**PCT** 



(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date 9 August 2001 (09.08.2001)



(10) International Publication Number WO~01/57188~A2

(51) International Patent Classification': C12N

(21) International Application Number: PCT/US01/03800

(22) International Filing Date: 5 February 2001 (05.02.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

09/496,914 3 February 2000 (03.02.2000) US 09/560,875 27 April 2000 (27.04.2000) US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US 09/496,914 (CIP)
Filed on 3 February 2000 (03.02.2000)
US 09/560,875 (CIP)
Filed on 27 April 2000 (27.04.2000)

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- (81) Designated States (national): AE, AG, AL, AM, AT. AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

#### Published:

 without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.



# NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

#### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

#### 2. BACKGROUND

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Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1350. The polypeptides sequences are designated SEQ ID NO: 1351-2700. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1350 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1350. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1350 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1350.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

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full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1 - 1350; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-1350. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 1351-2700); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1350; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

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The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

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The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, butilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and form a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases o disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

## 4. DETAILED DESCRIPTION OF THE INVENTION

#### **4.1 DEFINITIONS**

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It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

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As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 15 to about 50 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-1350.

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Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1350. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4<sup>20</sup> possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match  $(1 \div 4^{25})$  times the increased probability for mismatch at each nucleotide position  $(3 \times 25)$ . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

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The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

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The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

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The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophobicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

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The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

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The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

# 4.2 NUCLEIC ACIDS OF THE INVENTION

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Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1350; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1351-2700; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1351-2700. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1350; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1351-2700. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1350 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1350 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1350 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1350, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that

are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

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The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1350, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1350 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1350, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., Gene 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and Current Protocols in Molecular Biology, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1350, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### **4.3 ANTISENSE**

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1350, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO:1351-2700 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1350 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

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Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1350), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -a nomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

## 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO:1-1350). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

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In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

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#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

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The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

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The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

# 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1351-2700 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1350 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1350 or (b)

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polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:1351-2700 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1351-2700 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ 10 ID NO:1351-2700.

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Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1351-2700.

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The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat<sup>TM</sup> kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl<sup>TM</sup> or Cibacrom blue 3GA Sepharose<sup>TM</sup>; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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# 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

# 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

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another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

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For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction in vivo. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. 20 Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, e,g., cancer as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand. 25

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

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The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

#### 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

#### 4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

# 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

## 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

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Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

## 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

PCT/US01/03800 WO 01/57188

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of 10 stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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## 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

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A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

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Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

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A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

## 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

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Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapcutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β<sub>2</sub> microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

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Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

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Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

## 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

## 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin,
Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen'mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl,
Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

#### 4.10.12 RECEPTOR/LIGAND ACTIVITY

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A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

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The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

#### 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

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Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

## 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

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## 4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

#### 4.10.16 LEUKEMIAS

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Leukemias and related disorders may be treated or prevented by administration of a
therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see
Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

#### 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

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- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
  - (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
  - (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
  - (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
  - (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particularneurotoxins; and
  - (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

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- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
  - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

#### 4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

## 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

#### 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

#### 4.11 THERAPEUTIC METHODS

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The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

## 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

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A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

#### 4.12.1 ROUTES OF ADMINISTRATION

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Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

#### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

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comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

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Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

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A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications.

Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

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## 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC<sub>50</sub> as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the  $ED_{50}$  (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01  $\mu$ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1  $\mu$ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

#### 4.12.4 PACKAGING

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

### 4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab'}$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as  $IgG_1$ ,  $IgG_2$ , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

#### 5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

## 5.13.2 Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

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The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

## 5.13.2 Humanized Antibodies

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The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

## 5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

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An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

## 5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_{v}$  fragments.

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

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Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g.  $F(ab')_2$  bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

#### 5.13.6 Heteroconjugate Antibodies

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Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

### 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced antitumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

#### 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}$ Bi,  $^{131}$ In,  $^{90}$ Y, and  $^{186}$ Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

# 4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1350 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1350 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

## 4.15 TRIPLE HELIX FORMATION

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In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

PCT/US01/03800 WO 01/57188

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide. 10

## 4.16 DIAGNOSTIC ASSAYS AND KITS

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The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

### 4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide in vivo at the target site.

## 4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1350, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
  - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

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The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

## 4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1350. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1350 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

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Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

# 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude et al. (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

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More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

# 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer et al. (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI\*\*), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

## 4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

#### 5.0 EXAMPLES

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### 5.1 EXAMPLE 1

# Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

### 5.2 EXAMPLE 2

#### 5 Novel Contigs

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-1350 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO:189-282) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 189-282. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <a href="http://fasta.bioch.virginia.edu">http://fasta.bioch.virginia.edu</a>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-1350 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and Geneseq database October 12, 2000, update 21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the

closest homologue for SEQ ID NO:1-1350. The nearest neighbor results for SEQ ID NO: 1-1350 are shown in Table 2 below.

Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-1350. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/496,914.

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### TABLE 1

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	111 151 188 215 662-665 877 910 927
			976 1233 1319
adult brain	GIBCO	ABD003	41 49 74 101 111 120 132 141-142 151
			217 225 238 271 317 404 446 469 503
			513-514 535 550 564 573 666-669 798
		İ	898 910 927 976 1067 1083 1085 1178
	1	{	1254
adult brain	Clontech	ABR001	39 216 238 327 356 535 927 1056 1121
4441.01441			1178-1180 1199 1251
adult brain	Clontech	ABR006	74 611 949 1034 1136
adult brain	Clontech	ABR008	14 32 41 61 81 86 89 120 132 138 145
adult brain	Cionison		147 188 197 208 225 227-239 250 300-
			303 312 316 328-331 340 357-362 374
	1	•	380 384-391 408 414 446 448 464-467
			483 488 495-496 505 512 521 535 550
		}	566 571 577 585 590 594 598 634 641
			658 666 683 725 742 764 767 786 801
			805 810 823 826 829 831 836 841 887-
			923 927 934 943 950-951 963 976 995
	1		1000-1001 1006 1026 1034 1048 1057-
	1		1067 1086 1088 1090 1118 1120 1122-
	1	}	1128 1142 1162 1181-1192 1199 1204
	Ì		1218-1219 1225 1232 1253 1267 1271-
			1306 1342 1347 1349-1350
adult brain	Clontech	ABR011	49 238 1219
adult brain	BioChain	ABR012	74 238
adult brain	Invitrogen	ABR013	868 1268
adult brain	Invitrogen	ABT004	49 117 138 191 217 252 291 305 535
addit of the			566 596 663 670 746 798 816-819 876
			892 898 922 943 963 1034-1036 1121
cultured	Strategene	ADP001	41 74 101 138 211 238 304 537 582
preadipocytes			740 798 883 943 976 1067
adrenal gland	Clontech	ADR002	49 74 101 111 120 127 151 215 238
<b>44.</b> 51			240-247 316 330 363-364 404 414 534-
			535 833 924-940 950 963 976 1001
			1003 1067-1070 1118 1156 1193-1200
	}		1325
adult heart	GIBCO	AHR001	38 49 71-72 74-77 79 92 99 101 111
			118 129 132 138 151 158-163 182 195-
			203 215 217 238 264 269 353 384 398
			408 434-439 446 504 512-513 519 537
			562-573 577 611-614 616-619 658 661
			671-672 722 734 757-773 815 828-835
			874 891 898 919 926-927 976 988
			1021 1037 1041 1062 1067 1071 1080
			1083 1093 1122 1131 1185 1201 1254
			1308 1331 1335
adult kidney	GIBCO	AKD001	41 49 51 71-74 78-85 94 100-101 103-
			107 111 119-120 138 151 157 215 217-
			218 238 250 264 294 304 384 404 440
			446 454 477 504-505 509 514 518-519
			535 537 564 574-583 620-627 639 653
1			673-675 705 753 789 831 844 851 859
			877 909 918 927 956 963 976 1067
	1	1	1074 1083 1095 1178 1302 1331 1335
			10/4 1005 10/5 11/6 150
adult kidney	Invitrogen	AKT002	11-12 41 49 111-112 215-217 294 316
adult kidney	Invitrogen	AKT002	11-12 41 49 111-112 215-217 294 316 446 487 564 575 844 868 910 927 976
adult kidney	Invitrogen	AKT002	11-12 41 49 111-112 215-217 294 316

Sissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS: 518 537 545 549 580 582 592 594 634
			640 651-652 676-678 725 851 873 918
			952 976 1042 1067 1076 1083 1152
			8 111 121 151 180-182 188 215 537
ymph node	Clontech	ALN001	545 549 651 679-682 789 804-810 868
•		1	873 927 952 976 1042 1059 1335
			8 64 79 111 186 215-216 238 446 514
young liver	GIBCO	ALV001	519 537 564 653 683-684 698 753 798
_		ł	813 833 840 858 927 976 1038-1039
			1051 1085 1224 1245 1256
			40 71 292-293 305 384 468-469 496
adult liver	Invitrogen	ALV002	505 657 675 714 753 832 844 941-942
			976 1040 1076 1256 1293
			976
adult liver	Clontech	ALV003	8 32 36 38 41 49 51 71 74 79-80 101
adult ovary	Invitrogen	AOV001	104 111 120 122-125 138 140 143-149
			151 188-190 207-212 215-217 238 264
			316 384 409 440 445-446 496 504 512
			514 518-519 535 537 549-550 564 566
			571 580 582 600 618 638 657 667 681
		1	685-697 699 705 722 735-744 761 771
			815 833 842-865 868 875-876 918 926-
		<b>\</b>	927 950 952 963 976 1023 1042 1048
			1051 1059 1072 1076 1083 1117 1120
			1124 1131 1144 1174 1224 1268 1331
			1335
	<u> </u>	APL001	102 217 238 537 641 700
adult placenta	Clontech	APL001	663 851 1048
placenta	Invitrogen	ASP001	8 45 74 111 132 140 151 185 217 238
adult spleen	GIBCO	ASPOOL	294 414 446 477 504 514 534 545 549
		ł	592 722 873 883 952 976 1041-1042
			1083 1093-1094 1152 1224
	- lames	ATS001	72 107 111 113 126 140 151 183 215
testis	GIBCO	A13001	238 446 497 537 642 701-706 811 877
		1	927 962 976 1083 1117 1131
	Invitrogen	BLD001	41 151 191 402-405 409 414 496 545
adult bladder	Mymogen	BEEGG	592 607 706 873 952 1178 1329-1335
	Clontech	BMD001	8 58-62 65-68 74 79 108 111 116 137
bone marrow	Clouden	Bittero	147 151 164-174 213-215 238 305-307
			374 404 446 460 466 516 519 534 538-
			541 544-546 549-554 566 584 586 592
			596 607 610 628-629 643-645 652 707-
			708 774-789 844 866-871 873 919 927
		į	952 963 976 998 1034 1042 1064 1083
			1085 1120 1132 1152 1225 1229 1268
			1307 1310
hana marray	Clontech	BMD002	6 8 37-38 52 74 77 105 111 129 132
bone marrow	Cionicon		210 317 510-511 545 549 581 598 628
		j	638 724 766 789 844 860 868 873 919
			927 952 963 968 976 1042 1111 1141
		)	1160-1161 1229 1266 1346
hone	Clontech	BMD004	111 238 282 549 1083
bone marrow	Invitrogen	CLN001	52 260 264 299 494 536 545 564 592
adult colon	MAIGORCII	1	844 873 877 952 976 1042 1152 1268
			1336-1337
ļ	BioChain	CVX001	49 51 129 132 151 205 207 238 332-
adult cervix	BioChain	0 1 7 0 0 1	335 365-367 392-401 440 466 470-471
			518 537 597 629 832 877 927 976 1006
1	}		1085 1117 1129-1134 1192 1202-1205
		1	1219 1309-1328

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
endothelial cells	Strategene	EDT001	32 40-41 49 74 79 101 111 120 132
			138 151 204-206 215-217 238 269 316
	)		414 433 505 510 513 550 555 580 582
	1		596 675 722 745 798 814 836-841 851
			918 976 1041 1043 1073 1083 1131
			1331
Genomic clones	Genomic DNA	EPM001	525-532 927
from the short arm	from Genetic		
of chromosome 8	Research		47 525
Genomic clones	Genomic DNA	EPM003	47 323
from the short arm	from Genetic		
of chromosome 8	Research	ED 4004	525 927
Genomic clones	Genomic DNA	EPM004	323 921
from the short arm	from Genetic		
of chromosome 8	Research	ED 4005	531
Genomic clones	Genomic DNA	EPM005	331
from the short arm	from Genetic		
of chromosome 8	Research	ESO003	74 138 238
esophagus	BioChain	ESO002 FBR001	441-442 927
fetal brain	Clontech		215 893 927 1001
fetal brain	Clontech	FBR004	48 61 101 120 132 138 140 147 208
fetal brain	Clontech	FBR006	225 271 317 319 336 359 368 405-414
	1		519 550 571 594 686 715 722 764 824
		ļ	829 836 859 909 927 943 947 963 1057
	}	}	1067-1068 1104 1135-1140 1162 1206-
	}		1207 1235 1268 1288 1307-1308 1319
	1		1338-1350
	Ol. Analy	FBRs03	111 446
fetal brain	Clontech	FBT002	41 51 120 151 192-194 264 504 512
fetal brain	Invitrogen	TB1002	535 683 761 798 820-827 844 876 909
			963 976 1026 1048 1083 1144 1302
fetal heart	Invitrogen	FHR001	446 566 761
fetal kidney	Clontech	FKD001	51 74 111 127 140 151 184 294 537
letal kimiey	Cionicon		550 630-631 1319
fetal kidney	Clontech	FKD002	111 976 1083
fetal kidney	Invitrogen	FKD007	238 974
fetal lung	Clontech	FLG001	463 566 976 1074 1083 1093
fetal lung	Invitrogen	FLG003	41 238 330 407 415-416 537 573 844
			859 1048 1083 1116 1192
fetal liver-spleen	Columbia	FLS001	8 14 34-35 37 41 43 49 51 54-56 63-64
•	University	1	69-71 74 77 79 87-90 101 107 110-111
			114 120 128-131 138 140 147 150-155
		{	197 210 215 217 225 238 312 367 384
}			414 440 446 460 468 483 496 504-507 511-515 518-519 523 533-535 537 541
			511-515 518-519 523 533-535 537 541
}	1	1	544-545 547-550 555-560 564 566 571 577 582 585-586 598 636 646-647 649
			652 664 698 709-710 714 722-723 731
	{		735-736 746-753 761 784 798 823 829
	}		832 844 851 858-859 868 873 876 898
1	[		927 943 949 952 963 976 984 1002
			1021 1023 1040 1042 1044 1050 1083
	1		1021 1023 1040 1042 1044 1030 1033
1			1217 1251 1254 1256 1302 1308 1311
1			1319
			8 36-37 41-46 49 54 64 71 74 79 101
fetal liver-spleen	Columbia	FLS002	111 120 129 147 207 210 215-216 238
	University		250 330 353 359 366 383-384 414 478
			505 508-509 511 515-524 534-535 537
1		1	544-545 564 566 571 577 591 598 638
1		}	- 1 544*545 504 500 371 371 371 370 030

fetal liver  fetal liver  fetal muscle	Columbia University Invitrogen Clontech Invitrogen	FLS003 FLV001 FLV004	663 671 698 714 722 725 727 751 798 851 859 873 876 909 927 949 952 983- 984 1002 1023 1042-1044 1085 1095 1131 1144 1178 1199 1233 1240-1270 1331 1340 64 535 976 1256 8 101 120 138 217 446 468 535 566 580 722 730 749 844 918 943 976 1051
fetal liver  fetal liver  fetal muscle  fetal muscle	University Invitrogen Clontech	FLV001	984 1002 1023 1042-1044 1085 1095 1131 1144 1178 1199 1233 1240-1270 1331 1340 64 535 976 1256
fetal liver  fetal liver  fetal muscle  fetal muscle	University Invitrogen Clontech	FLV001	1131 1144 1178 1199 1233 1240-1270 1331 1340 64 535 976 1256 8 101 120 138 217 446 468 535 566
fetal liver  fetal liver  fetal muscle  fetal muscle	University Invitrogen Clontech	FLV001	1331 1340 64 535 976 1256 8 101 120 138 217 446 468 535 566
fetal liver  fetal liver  fetal muscle  fetal muscle	University Invitrogen Clontech	FLV001	64 535 976 1256 8 101 120 138 217 446 468 535 566
fetal liver  fetal liver  fetal muscle  fetal muscle	University Invitrogen Clontech	FLV001	8 101 120 138 217 446 468 535 566
fetal liver  fetal liver  fetal muscle  fetal muscle	University Invitrogen Clontech	FLV001	8 101 120 138 217 446 468 535 566 580 722 730 749 844 918 943 976 1051
fetal liver fetal muscle fetal muscle	Invitrogen  Clontech		8 101 120 138 217 446 468 535 566 580 722 730 749 844 918 943 976 1051
fetal liver fetal muscle fetal muscle	Clontech		580 722 730 740 844 918 943 976 1051
fetal muscle		FI V004	1 200 144 130 197 077 210 273 210 1031
fetal muscle		FI V004	1256 1331
fetal muscle			537 926 1256
fetal muscle	Invitrogen	FMS001	51 111 264 312 369-370 404 417-421
		PMSOOT	425 535 537 577 598 614 836 857 1141
			1208 1268
		FMS002	537
fetal skin	Invitrogen	FSK001	13-26 32 41 51 89 107 111 147 151
	Invitrogen	FSKUUI	225 264 316 405 422-429 488-494 496
			519 534-535 537 566 675 732 859 876-
			877 898 947 949-950 963 976 1001
			1062 1076 1083 1117 1144 1165 1268
			1281
	<del></del>	FSK002	537 812
fetal skin	Invitrogen	FSP001	87 549
fetal spleen	BioChain	FUC001	27-33 41 49 151 215 238 248-249 301
umbilical cord	BioChain	FUCUUI	316 446 495-503 519 521 534-535 537
			582 634 691 877 883 927 944-950 963
	•		976 1001 1075 1142-1143 1171 1218
			1243 1308
	omeo.	HFB001	41 49 57 79 87 103 111 120 132-135
fetal brain	GIBCO	DEDUVI	138 145 151 188 197 207 215 238 264
			271 294 316 367 414 440 446 466 504
			513-514 535 542-543 550 564 571 596
			635 648-654 675 711-715 722-723 798
1		1	832 872 876 883 927 976 1095 1144
			1168 1171 1178 1211 1335
	Invitrogen	HMP001	238
macrophage	Columbia	IB2002	49-50 77 81 89 105 111 136-138 140
infant brain	University	102002	151 161 175-179 185 216-217 264 295
	Oliversity		299 308-310 371-373 462 476 504 511-
			513 533 537 564 566 571 655-657 662
{		ĺ	683 716-720 723 752 790-803 829 832
			858-859 876 898 909 949 976 1045-
	i		1047 1076-1087 1090 1093 1116 1122
	ļ		1144 1209-1213 1225 1233 1256 1319
			1341
infant brain	Columbia	IB2003	41 50 77 104 132 215 238 508 512-513
miani orani	University		519 566 655 714 794 918 943 976 1067
	Olliversity		1092-1093 1233
i-fort broin	Columbia	IBM002	311 472-473 753 1214
infant brain	University		
i-Greater	Columbia	IBS001	51 111 376 474 790 876 949 1144 1204
infant brain	University	15000.	1221
luna Charlilan	Strategene	LFB001	151 316 462 514 534 582 675 939 1131
lung, fibroblast	Invitrogen	LGT002	1-7 41 74 79 94 115 120 138-139 156
lung tumor	HIMITOREII	1000	215 217 269 280 296 337 374-375 384
	ļ		404 446 454 475-480 498 514 518-519
			522 537 545 564 577 597 653 658 705
			721-724 754-756 779 859 868 872-874
			876-877 919 927 949 951-952 959 976
5		1	1002 1042 1048-1053 1076 1083 1088-
1	,	1	1089 1131 1144-1147 1216-1218 1229

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1293 1311 41 74 111 132 151 253 316 446 550
lymphocytes	ATCC	LPC001	634 844 927 976 1085 1268
	GIBCO	LUC001	8 11 41 74 86 91-98 101 109 111 120
leukocyte	GIBCO	LUCCOOL	147 151 212 215 218 238 252 288 312-
		ļ	314.316 338 359 408 427 443-447 505
		İ	510 512 514 518 534 545 549-550 561
			564 566 571 577 580 582 587-609 615
		ì	632-638 658-659 698 714 725-728 832
		- 20	836 841 859 866 873-874 882-883 918-
		}	919 927 943 952 963 976 1042 1076
		ļ	1083 1090 1148 1152 1168 1195 1219-
	ļ	}	
	ļ		1220 1224
leukocyte	Clontech	LUC003	74 100 215 232 238 339-341 446 545
.0			657 660 729 873 883 927 952 963 1008
	1		1042 1116 1120 1149-1150 1215 1222
Melanoma from cell	Clontech	MEL004	210 215 238 342 534 545 592 722 873
line ATCC #CRL	31021.301.		919 929 939 952 976 1071 1118 1218
1424	1		1235 1245
	Invitrogen	MMG001	8-10 40-41 49 73 80 114 138-140 147
mammary gland	HIAITIOREII	,	217 250-256 264 297-299 305 377-378
	ļ		398 446 481-486 505 512 537 545 549
			571 592 725 730-733 816 829 836 844
		)	868 873 876-877 898 926 943 951-960
			963 976 995 1034 1042 1048 1054-
			1055 1076 1083 1091 1093 1116-1117
		ĺ	1124 1152 1302
		1100001	39 101 111 138 238 361 1225 1251
induced neuron cells	Strategene	NTD001	1319
			74 225 976
retinoid acid induced	Strategene	NTR001	14 223 976
neuronal cells			129 225 238 304 313 361 657 976
neuronal cells	Strategene	NTU001	
pituitary gland	Clontech	PIT004	976
placenta	Clontech	PLA003	38 976
prostate.	Clontech	PRT001	111 188 238 257-258 564 724 961-966
prostato			1067 1095
rectum	Invitrogen	REC001	238 430-431 841 859 868 963 1001
rectum	11208	(	1116
salivary gland	Clontech	SAL001	8 151 402 432-433 446 496 868 952
Salivary gland	Cionicon		976 1083 1120 1151 1184
32 1 1 1 1 1	Clontech	SIN001	8 101 147 215 259-266 446 462 505
small intestine	Clontech	0111001	545 592 660 789 836 866 873 927 952
		1	963 967-978 1042 1120 1152 1223-
		1	1224
	-	SKM001	238 302 927 943 992 1031
skeletal muscle	Clontech		74 111 132 151 215-216 238 264 267-
spinal cord	Clontech	SPC001	270 343-344 353 379 516 537 566 740
			828 927 976 979-994 1092 1153-1159
		· i	
			1225 1250
adult spleen	Clontech	SPLc01	698 859 1042
stomach	Clontech	STO001	210 238 271-272 537 580 705 918 952
			995 1171
thalamus	Clontech	THA002	61 219-220 273-276 312 315 330 596
maiding.			963 996-1007 1059 1093 1160-1162
thimus	Clonetech	THM001	8 120 151 208 221 316-317 353 639
thymus	Cioneteen		750 867 874 878-881 927 963 1023
		j	1083 1094-1096 1124
	101-1-1	THMc02	8 61 114 129 132 210 225 231 306
thymus	Clontech	1 DIVICUZ	317-319 336 340 359 380 398 446 448
			463 512 519 545 554 587 598 698 724-
1	1	i	
			725 789 812 836 868 873 927 947 952

0:	RNA Source	Hyseq Library Name	SEQ ID NOS:
Tissue Origin	KIVA SOUICE	Tiysed Elecusy 1	976 1007 1042 1083 1085 1097-1116
			1122 1147 1177 1226-1229 1234 1311
			1313
i id aland	Clontech	THR001	14 41 49 76 94 111 144 151 183 188
thyroid gland	Clonicen	1111001	210 217 222 253 264 271 277-286 294
		1	320-326 345-352 361 381-382 446 467
			483 514 534 549-550 564 578 602 649
			844 882-883 927 950 956 976 1008-
			1028 1076 1083 1117-1120 1142 1163-
			1175 1230-1238 1308
4h.o.	Clontech	TRC001	223-225 238 287 353-354 514
trachea	Cionteen	110001	545 592 611 873 883-884 927
			952 1029-1031 1042 1151-1152
			1170 1176-1177 1239
	Clontech	UTR001	151 226 288-290 355 537 877
uterus	Ciontech	O I I COO I	885-886 976 1001 1032-1033
			1232

## TABLE 2

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
NO:	1			Score 460	100
1	B02829	Homo sapiens	Human G protein coupled receptor hRUP5 protein SEQ ID NO:10.		
	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	111	51
3	R26173	Homo sapiens	Part of Major Yo paraneoplastic antigen	293	76
3	K20173	110th oup to	(CDR62) encoded by clone pY2.		1
4	L29536	Homo sapiens	calcium channel L-type alpha 1 subunit	191	50
5	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	251	
6	M11507	Homo sapiens	transferrin receptor	120	95
<del>0</del> 7	AF099100	Homo sapiens	WD-reneat protein 6	1941	93
8	Y92338	Homo sapiens	Human cancer associated antigen precursor from	245	82
9	G01343	Homo sapiens	Human secreted protein, SEQ ID NO: 5424.	226	91
	AJ133798	Homo sapiens	conine VII protein	1127	68
10	G02449	Homo sapiens	Human secreted protein, SEQ ID NO: 6530.	584	99
11	X98330	Homo sapiens	ryangdine recentor 2	282	78
13	AL024498	Homo sapiens	dJ417M14.2 (novel serine/threonine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase))	293	100
			olfactory receptor OR93Ch	191	36
14	AF045577	Pan troglodytes		93	39
15	G03131	Homo sapiens	Human secreted protein, SEQ ID NO: 7212.	569	89
16	U26595	Rattus norvegicus	prostaglandin F2a receptor regulatory protein precursor		44
17	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	99	
10	Y36203	Homo sapiens	Human secreted protein #75.	165	75
18 19	U15647	Mus musculus	reverse transcriptase	106	40
		Homo sapiens	Human secreted protein, SEQ ID NO: 6782.	544	100
20	G02701 Y35923	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 172.	1691	100
			Human secreted protein, SEQ ID NO: 8111.	380	96
22	G04030	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	123	50
23 24	G02455 AF036329	Homo sapiens Homo sapiens	gonadotropin-releasing hormone precursor,	284	90
			second form Human secreted protein, SEQ ID NO: 8148.	96	32
25	G04067	Homo sapiens	Human secreted protein, SEQ 10 140. 8140.	100	34
26	S80119	Rattus sp.	reverse transcriptase homolog	101	35
27	U83303	Homo sapiens	line-1 reverse transcriptase	135	45
28	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	1	

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			SEO ID NO. 8148	83	42
29	G04067		Human secreted protein, SEQ ID NO: 8148.	116	72
30	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	96	67
31	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	58	32
32	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	2457	98
33	Y66688	Homo sapiens	Membrane-bound protein PRO1152.		95
34	Y87071	Homo sapiens	Human secreted protein sequence SEQ ID NO:110.	348	
76	U15131	Homo sapiens	p126	182	48
35 36	Y73464	Homo sapiens	Human secreted protein clone yl4_1 protein sequence SEO ID NO:150.	982	90
37	AL133215 Homo sapiens bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))		687	99	
38	AC067969	amino acids 3338-4088	Homo sapiens ryanodine receptor 1 (skeletal)	386	66
39	AL031588	Homo sapiens	dJ1163J1.1 (mostly supported by GENSCAN, FGENES and GENEWISE)	493	76
		Home re-ien-	Human secreted protein, SEQ ID NO: 7709.	110	51
40	G03628	Homo sapiens	CGI-35 protein	228	68
41	AF132969	Homo sapiens	Human secreted protein encoded by gene 45.	220	88
42	Y36268	Homo sapiens		105	35
43	X61048	Hydra sp.	mini-collagen hydroxyproline-rich protein	110	31
44	M76546	Helianthus annuus		139	70
45	U82288	Caenorhabditi s elegans	Rac-like GTPase	118	58
46	G03477	Homo sapiens	Human secreted protein, SEQ ID NO: 7558.	113	63
47	AF090942	Homo sapiens	PRO0657	90	59
48	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	72	56
49	AJ005560	Mus musculus	SPR2B protein		98
50	G02450	Homo sapiens	Human secreted protein, SEQ ID NO: 6531.	385	94
51	Y91649	Homo sapiens	Human secreted protein sequence encoded by gene 60 SEQ ID NO:322.	973	
52	U93563	Homo sapiens	putative p150	105	38
52	Y55927	Homo sapiens	Human STLK2 protein.	699	85
	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	145	56
54 55	AB008175	Mus musculus	hepatic nuclear factor 1-beta short form	356	74
	1469041	Homo sapiens	protein-tyrosine phophatase	165	41
56	M68941	Homo sapiens		338	76
57 58	AL031600 AF011417	Mus musculus	putative pheromone receptor	143	55
59	AF167320	Mus	zinc finger protein ZFP113	558	68
<u></u>	1100000	musculus	interferon regultory factor 7	263	96
60	U73036 X07984	Homo sapiens Mus musculus	protein-tyrosine kinase	297	69
	1,000	Homo sapiens	Human secreted protein clone cb98_4.	791	98
62	Y29861		1 6 -4	485	65
63	U35376 AF265555	Homo sapiens Homo sapiens	DID domain enzyme	785	74
			1 0EG ID MO. 7064	88	95
65 66	G03883 AF177390	Homo sapiens Manduca	antennal specific membrane protein AMP	274	54
		sexta	COPPO	614	100
67	AB040800	Homo sapiens		213	26
68	AF030027	Equine herpesvirus 4	24	261	95
69	G02965	Homo sapiens	Human secreted protein, SEQ ID NO: 7046.		98
70	W75770	Homo sapiens	Human oxidoreductase YTFO3.	1144	76
71	AB011135	Homo sapiens		239	
72	AB014885	Halocynthia roretzi	HrPOPK-1	813	78
73	AF045454	Cavia	phospholipase B	955	73
	J02870	porcellus Mus	laminin receptor	308	61

SEQ	Accession No.	Species	Description	Smith- Waterman	% Identity
D   10:	NO.			Score	
10		musculus			
75	Y00826	Rattus norvegicus	gp210 (AA 1-1886)	413	84
6	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	351	54
7	Y38422	Homo sapiens	Human secreted protein	468	76
8	Y14596	Homo sapiens	Human T-type voltage-gated Ca channel alpha- 1-I (hCavT3).	1357	99
79	Y14591	Human papillomaviru s type 68	APM-1 protein	767	100
30	AL137802	Homo sapiens	dJ798A10.2 (KIAA0445 protein)	71	34
31	AP000383	Arabidopsis thaliana	protein arginine N-methyltransferase-like protein	359	65
32	L46815	Mus musculus	DNA binding protein Rc	895	75
33	G01600	Homo sapiens	Human secreted protein, SEQ ID NO: 5681.	315	96
84	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	538	71
85	AB029002	Homo sapiens	KIAA1079 protein	134	42
85 86	Y28678	Homo sapiens	Human cw272 7 secreted protein.	325	62
87	Y99368	Homo sapiens	Human PRO1326 (UNQ686) amino acid	156	48
88	AJ225124	Mus musculus	hyperpolarization-activated cation channel, HAC3	487	95
89	AF177203	Homo sapiens	cerebral cell adhesion molecule	290	56
90	Y28280	Homo sapiens	Human G-protein coupled receptor GRIR-2.	326	79 95
91	L39891	Homo sapiens	polycystic kidney disease-associated protein	1751	99
92	AF064876	Homo sapiens	ion channel BCNG-1	953	53
93	AF170723	Homo sapiens	protein kinase STK10	151	37
94 .	X13292	Trypanosoma brucei	GPI-phospholipase C (AA 1 - 358)	1661	99
95	Y34127	Homo sapiens	Human potassium channel K+Hnov11.	1775	$\frac{1}{92}$
96	X03638	Rattus norvegicus	sodium channel protein I (aa 1-2009)	1995	99
97	AF134213	Homo sapiens	ubiquitin-specific protease	213	38
98	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	675	48
99	AF021935	Rattus norvegicus	mytonic dystrophy kinase-related Cdc42-binding kinase	867	98
100	AF279265	Homo sapiens	putative anion transporter l	160	60
101	AC007878	Homo sapiens	match to nuclear protein, NP220; note: sequence difference at residue 58	264	42
102	U22829	Mus musculus	P2Y purinoceptor		99
103	Y45023	Homo sapiens	Human sensory transduction G-protein coupled receptor-B3.	516	98
104	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	787 343	57
105	Y87342	Homo sapiens	119 SEO ID NO:119.		
106	AF169312	Homo sapiens	hepatic angiopoietin-related protein	74	52
107	AF116657	Homo sapiens	PRO1310	587	96
108	AE000401	Escherichia ∞li	sialic acid transporter		100
109	Y38395	Homo sapiens		182	94
110	Y78801	Homo sapiens	HP00631 amino acid sequence.	464	85
111	Z25535	Homo sapiens	nuclear pore complex protein hnup153	274	51
112	Y94939	Homo sapiens	sequence SEQ ID NO:84.		71
113	AF016365	Homo sapiens	hexokinase 1 isoform td	301	75
114	AC007956	Homo sapiens	unknown	520	92
115	M83738 AL157952	Homo sapiens Homo sapiens	protein-tyrosine phosphatase	251 484	91
	1	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	

~ <	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:				407	62
18	L41816	Homo sapiens	cam kinase l	627	93
	AJ006710	Rattus norvegicus	phosphatidylinositol 3-kinase	1646	94
20	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDPr		68
21	S39392	Homo sapiens	protein tyrosine phosphatase, PTPase {EC 3 1 3 48}	373	
-	U60805	Homo sapiens	oncostatin-M specific receptor beta subunit	262	88
22	Y44403	Homo sapiens	Human truncated tankyrase-1.	111	35
23	U88167	Caenorhabditi	contains similarity to C2 domains	219	29
24		s elegans	guanine nucleotide binding protein beta subunit	693	90
125	AF300648	Homo sapiens	4 apoptosis signal-regulating kinase 2	153	65
126	AB021861	Mus musculus		807	97
127	AF305210	Homo sapiens	concentrative Na+-nucleoside cotransporter hCNT3		73
128	M90360	Homo sapiens	protein kinase	220	86
129	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	574	
130	AF208043	Homo sapiens	IFI16b	496	67
131	AF208043 AF201734	Mus musculus	testis specific serine kinase-3	800	87
120	AE112006	Bos taurus	differentiation enhancing factor 1	159	74
132	AF112886	Homo sapiens	phospholipase C-beta-1b	554	85
133 134	AJ278314 W74802	Homo sapiens	Human secreted protein encoded by gene 73 clone HSQEL25.	1157	87
	1700000	IIIama sociesa	Pancreas-specific gene	668	96
135	AB020335	Homo sapiens Homo sapiens	A secreted protein encoded by clone dt674_2.	866	98
136 137	W80408 AC002563	Homo sapiens Homo sapiens	putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860)	5041	99
	1,000	Tlesse series	PRO3434, a novel secreted protein.	891	100
138 139	Y96736 AB024034	Homo sapiens Arabidopsis	DNA-damage inducible protein DDI1-like	147	55
		thaliana	Human GTPase regulator GRAF.	248	56
140	W97809	Homo sapiens	Human PLA2 protein.	125	46
141	Y51557 AF090113	Homo sapiens Rattus	AMPA receptor binding protein	623	93
		norvegicus	Human RECK cancer-inhibiting protein.	641	82
143 144	W26642 U87306	Homo sapiens Rattus	transmembrane receptor UNC5H2	578	84
145	AF264014	norvegicus  Homo sapiens	scavenger receptor cysteine-rich type 1 protein	727	92
			M160 precursor	140	40
146	W63683	Homo sapiens	Human secreted protein 3. galactose-1-phosphate uridyl transferase	513	81
147 148	M96264 D64014	Homo sapiens Escherichia	HrsA	818	90
149	M83316	Escherichia	pppGpp phosphohydrolase	915	95
150	AL163279	Homo sapiens	homolog to cAMP response element binding and	1261	99
			beta transducin family proteins	940	99
151	AF179867	Homo sapiens		392	61
152	R95332	Homo sapiens	ligand (clone 3TW).	370	92
153	AF151859	Homo sapiens	CGI-101 protein	489	81
154	X66957	Homo sapiens	hexokinase type 1		92
155	Y16355	Homo sapiens	alternatively spliced form	432	78
156	G00857	Homo sapiens	Human secreted protein, SEQ ID NO: 4938.	349	
157	AF159455	Mus musculus	zinc finger protein	352	74
l	L76191	Homo sapiens	interleukin-1 receptor-associated kinase	537	76
160	1 F101A1	Homo sapiens	putative gene, ankirin like, possible dual	670	98
158 159	AP001743	Holiko sapielis	specifity Ser/Thr/Tyr kinase domain	1	
	AP001743 AJ250425	Rattus norvegicus	specifity Ser/Thr/Tyr kinase domain Collybistin I	556	74

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:	Ì			610	100
62	Z22968	Homo sapiens	M130 antigen	336	92
63	AF181121	Homo sapiens	ATP-dependent Ca2+ pump PMR1		94
64	AF055636	Homo sapiens	leucine-rich glioma-inactivated protein precursor	455	
65	AF160798	Rattus norvegicus	calcium transporter CaT1	700	96
66	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	327	45
	*****	Homo sapiens	Human breast tumour-associated protein 68.	1072	99
67	Y48607 AB020741	Mus	NIK-related kinase	197	43
		musculus	PAR3	596	44
69	AF252293	Homo sapiens	diacylglycerol kinase eta	481	82
70	U59429	Cricetinae gen. sp.	_	386	42
171	AF035268	Homo sapiens	phosphatidylserine-specific phospholipase A1	507	82
72	AF127085	Mus musculus	semaphorin cytoplasmic domain-associated protein 3B		99
173	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	653	
174	G02979	Homo sapiens	Human secreted protein, SEQ ID NO: 7060.	538	97
175	U36488	Mus	embryonic stem cell phosphatase	168	55
		musculus Homo sapiens	Homo sapiens secreted protein gene clone	1022	100
176	W95629	House sabiens	am 196 4		
	AF289023	Homo sapiens	formiminotransferase cyclodeaminase form D	255	93
177			T-cell receptor alpha-chain (413 is 2nd base in	710	99
178	X04936	Homo sapiens	codon) non-ocogenic Rho GTPase-specific GTP	175	80
179	AF127481	Homo sapiens	exchange factor	517	94
180	G00978	Homo sapiens	Human secreted protein, SEQ ID NO: 5059.	671	96
181	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	862	100
182	AF110640	Homo sapiens	orphan seven-transmembrane receptor	766	84
183	AB020854	Bos taurus	orphan transporter short splicing variant	375	38
184	AF169691	Homo sapiens	cadherin-like protein VR8		99
185	AF126372	Homo sapiens	thyrotropin-releasing hormone degrading ectoenzyme	985	
186	L20966	Homo sapiens	phosphodiesterase	541	76
187	G02920	Homo sapiens	Human secreted protein, SEO ID NO: 7001.	254	93
188	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence SEO ID NO:42.	301	98
100	Y66713	Homo sapiens	Membrane-bound protein PRO1309.	694	100
189		Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	331	73
190 191	G03244 U36771	Rattus	sn-glycerol 3-phosphate acyltransferase	707	92
192	R05935	norvegicus  Homo sapiens	Secreted GPIIb subunit of multiple subunit polypeptide (MSP)GPIIb-IIIa.	157	72
193	M92084	Theileria	casein kinase II alpha subunit	364	50
		parva	Membrane-bound protein PRO1310.	448	90
194	Y66645	Homo sapiens		382	49
195	W95631	Homo sapiens	hi968 2.	680	99
196	AF255614	Rattus norvegicus	scaffolding protein SLIPR		41
197	AC021640	Arabidopsis thaliana	putative phosphatidate phosphohydrolase	300	
198	AF073967	Mus musculus	olfactory receptor	316	43
		domesticus	II Ctoin recentor UDD A 170	617	98
199	W01730	Homo sapiens		625	89
200	AF117948	Homo sapiens		636	94
201	AF128625	Homo sapiens		1303	100
202	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	701	99
203	Y53021	Homo sapiens	Human secreted protein clone qc646_1 protein sequence SEQ ID NO:48.	J	
204	AF227968	Homo sapiens	SH2-B beta signaling protein	182	79
1 204	12 22/700	Homo sapiens		375	100

SEQ D NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
<del>'</del>			{ovarian cancer critical region of deletion}		100
06	U18315	Sus scrofa	parathyroid receptor	122	60
07	AF255342	Homo sapiens	putative pheromone receptor V1RL1 long form	170	96
08	S52051	Rattus sp.	neurotransmitter transporter	715	94
	W63683	Homo sapiens	Human secreted protein 3.	840	99
09 10	D79992	Homo sapiens	similar to Drosophila photoreceptor cell-specific protein, calphotin.	541	82
	45115040	Homo sapiens	pancreas-enriched phospholipase C	1348	99
11	AF117948	Rattus	ankyrin binding cell adhesion molecule	471	69
12	U81035	norvegicus	neurofascin	798	56
.13	AF154846	Homo sapiens	zinc finger protein  FYVE finger-containing phosphoinositide kinase	933	93
.14	AF102777	Mus musculus		523	89
215	AL163303	Homo sapiens	putative gene containing transmembrane domain	563	78
216	U26595	Rattus norvegicus	prostaglandin F2a receptor regulatory protein precursor		98
217	G04095	Homo sapiens	Human secreted protein, SEQ ID NO: 8176.	644	
218	X75756	Homo sapiens	protein kinase C mu	314	81
	Y66723	Homo sapiens	Membrane-bound protein PRO1100.	770	98
219 220	D88577	Mus musculus	Kupffer cell receptor	567	40
121	AF258465	Homo sapiens	OTRPC4	853	100
221 222	AF021935	Rattus norvegicus	mytonic dystrophy kinase-related Cdc42-binding kinase	636	96
223	AL136527	Homo sapiens	bA215B13.1 (A kinase (PRKA) anchor protein 11)	693	100
	<u> </u>		WNT receptor Frizzled-4	690	99
224	AB032417	Homo sapiens	semaphorin VIa	703	68
225	AF030430	Mus musculus	putative dihydroxyacetone kinase (EC 2.7.1.2)	297	39
226	AE000218	Escherichia coli		2080	100
227	AF302150	Homo sapiens	phosphoinositol 3-phosphate-binding protein-2	265	88
228	AB024573	Mus musculus	GTP-binding like protein 2	316	40
229	AF122924	Xenopus laevis	Wnt inhibitory factor-1		100
230	G03205	Homo sapiens	Human secreted protein, SEQ ID NO: 7286.	229	92
231	X98260	Homo sapiens	M-phase phosphoprotein 11	265	
232	R92754	Homo sapiens	Human growth differentiation factor-12.	682	95
233	R75111	Homo sapiens	Glycosyl-phosphatidylinositol-specific phospholipase-D.	290	100
224	W69431	Homo sapiens	Human secreted protein cw1233_3.	235	97
234		Homo sapiens	serine palmitoyltransferase, subunit II	859	81
235	Y08686	Homo sapiens	atrophin-related protein ARP	117	37
236 237	AF118275 X81466	Mus musculus	Embryo Brain Kinase	460	62
238	U64857	Caenorhabditi s elegans	similar to the BPTI/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor (TFPI)	284	33
239	AJ250840	Mus	serine/threonine protein kinase	739	63
240	AJ223472	musculus Mus	transcription elongation factor TFIIS.h	222	38
241	Y94906	musculus Homo sapiens	Human secreted protein clone rb649_3 protein	353	52
			sequence SEQ ID NO:18.	591	99
242	AF169301	Homo sapiens	Na+/sulfate cotransporter SUT-1	667	93
243	L22022	Rattus norvegicus	orphan transporter v7-3		98
244	AF016191	Rattus norvegicus	potassium channel	1043	
245	AF097366	Homo sapiens	cone sodium-calcium potassium exchanger	645	98
245		Homo sapiens		497	98
246	Y29868	Homo sapiens		188	83
247	AF180475 Y17227	Homo sapiens		690	99
248					31

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
	<del> </del>	sexta	protein SCLP		ļ
250	AF192756	Kaposi's sarcoma- associated herpesvirus	Orf73	134	34
251	AB022694	Homo sapiens	MOK protein kinase	209	83
252	W55045	Homo sapiens	Neural adhesion molecule (ethb0018f2 product).	469	100
253	L46815	Mus musculus	DNA binding protein Rc	251	67
254	W68505	Homo sapiens	Human acid sensing ionic channel.	173	82
255	AF070066	Mus musculus	Citron-K kinase	1201	98
256	G02491	Homo sapiens	Human secreted protein, SEQ ID NO: 6572.	460	100
257	Z12841	Oryctolagus cuniculus	Phospholipase	368	80
258	Y95436	Homo sapiens	Human calcium channel SOC-3/CRAC-2.	1857	99
259	AJ222968	Mus musculus	L-periaxin	430	72
260	AJ250839	Homo sapiens	serine/threonine protein kinase	861	100
261	AJ249977	Homo sapiens	AMP-activated protein kinase gamma 3 subunit	758	98
262	AF141386	Rattus norvegicus	SLIT-2	198	62
263	AF022859	Homo sapiens	neuropilin-2(a0)	335	91
264	AF160477	Homo sapiens	Ig superfamily receptor LNIR precursor	387	99
265	Y44662	Homo sapiens	Human 14273 G-protein coupled receptor (GPCR).	204	56
266	U27269	Mus musculus	sodium glucose cotransporter	159	75
267	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	209	39
268	AF127389	Rattus norvegicus	putative taste receptor TR1	209	95
269	X98296	Homo sapiens	ubiquitin hydrolase	129	26
270	X78482	Streptococcus pyogenes	Fc-gamma receptor	109	26
271	AB009883	Nicotiana tabacum	KED	899	97
272	AF137367	Mus musculus	VPS10 domain receptor protein SORCS ionotropic glutamate receptor	460	86
273	L34938	Rattus norvegicus	dJ413H6.1.1 (hamster Androgen-dependent	188	74
274	AL022724	Homo sapiens	Expressed Protein LIKE PUTATIVE protein)		
275	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	173	94
276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	148	56
277	L40380	Homo sapiens	thyroid receptor interactor	430	96
278 279	AB046851 AC008075	Homo sapiens Arabidopsis	KIAA1631 protein Contains PF 00069 Eukaryotic protein kinase	157	43
000	1,00000	thaliana	domain. protein-tyrosine phosphatase	181	73
280	M83738	Homo sapiens Homo sapiens	unnamed protein product	439	91
281	AK024397	Homo sapiens	RNA helicase HDB/DICE1	497	84
282	AF141326 AF156530	Mus	ETS-domain transcriptional repressor PE1	605	76
283	חננסכו אי	musculus	210 dollari ambaripadan representati		
284	Y29336	Homo sapiens	Human secreted protein clone cs756_2 alternate reading frame protein.	647	100
285	Y73402	Homo sapiens	Human secreted protein clone yc25_1 protein sequence SEQ ID NO:26.	300	90
286	AF016411	Homo sapiens	KCNA3.1B	137	100
287	W89253	Homo sapiens	Human ALP.	688	97
288	AF112886	Bos taurus	differentiation enhancing factor 1	750	96
289	AF113131	Homo sapiens	host cell factor homolog LCP	367	44
290	U52111	Homo sapiens	plexin-related protein	698	100
291	AF026504	Rattus	SPA-1 like protein p1294	603	89

	Accession	Species	Description	Smith- Waterman	% Identity
	No.	I	}	Score	
10:		norvegicus			
	AF102854	Rattus	membrane-associated guanylate kinase-	124	53
292	AF 102854	norvegicus	interacting protein 2 Maguin-2		<u> </u>
	X99211	Drosophila	ubiquitin-specific protease	143	38
293	A99211	melanogaster			<del></del>
	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein	185	94
294	194943	Monto suprem	sequence SEO ID NO:92.		1
205	Y94890	Homo sapiens	Human protein clone HP02798.	108	59
295	AF019767	Homo sapiens	zinc finger protein	154	96
296	Y28568	Homo sapiens	Secreted pentide clone bd577 1.	568	84
297	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein	182	97
298	194943	Home suprem	sequence SEO ID NO:92.		
299	B08906	Homo sapiens	Human secreted protein sequence encoded by	605	69
299	B00900	Tiomo sapreme	gene 16 SEO ID NO:63.		
200	R58890	Homo sapiens	Human-32 cadherin-related molecule.	212	97
300	AF022859	Homo sapiens	neuropilin-2(a0)	277	100
301	Y71124	Homo sapiens	Human mitogenic regulator duox2.	716	97
302		Homo sapiens	Human receptor tyrosine kinase.	228	97
303	Y44297 D32050	Homo sapiens	alanyl-tRNA synthetase	192	80
304	U43586	Homo sapiens	protein kinase related to Raf protein kinases;	428	72
305	043380	Tionio supiens	Method: conceptual translation supplied by		
		1	author	l	95
306	R54872	Homo sapiens	Human H13 viral receptor mutant 4.	280	41
307	D78572	Mus	membrane glycoprotein	199	41
307	D16312	musculus			88
308	AF255614	Rattus	scaffolding protein SLIPR	639	88
300	A1 255011	norvegicus		1.60	89
309	S79463	Mus sp.	semaphorin homolog=M-Sema F	162	100
310	AF178941	Homo sapiens	ATP-binding cassette sub-family A member 2	736	36
311	U03413	Dictyostelium	calcium binding protein	151	30
J	032	discoideum	- TIODD	744	100
312	Y87347	Homo sapiens	Human signal peptide containing protein HSPP-	/44	100
J 12-		1	124 SEQ ID NO:124.	789 .	99
313	Z97055	Homo sapiens	dJ388M5.4 (putative GS2 like protein)	197	38
314	AC004010	Homo sapiens	similar to Leucine-rich transmembrane proteins;	197	1 30
			44% similarity to U42767 (PID:g1736918)	278	38
315	AL021392	Homo sapiens	dJ439F8.2 (supported by GENSCAN and	270	
İ			GENEWISE)	165	38
316	U70209	Mus	polycystic kidney disease I protein	1.05	
		musculus	coxsackie-adenovirus-receptor homolog	223	38
317	AF109643	Rattus	coxsackie-adenovirus-receptor nomorog	1	
		norvegicus	- utative transcription factor	138	84
318	AF104923	Homo sapiens	putative transcription factor activated protein kinase C receptor homolog	141	38
319	AF100287	Тгурапоѕота	activated protein kinase o receptor nomorog	1	
		vivax	Human secreted protein, SEQ ID NO: 4669.	125	51
320	G00588	Homo sapiens		459	97
321	Y21591	Homo sapiens	in 11 4 5 trianh acabate	232	97
322	D26070	Homo sapiens	receptor		
	1	<del></del>		306	88
323	Y27918	Homo sapiens			
			123. neuronal thread protein AD7c-NTP	209	70
324	AF010144	Homo sapiens		214	97
325	M19650	Homo sapiens	3 1 4 37)	1	
	1,,,,,,,,,	11		140	70
326	W80396	Homo sapiens		540	78
327	X75756	Homo sapiens	000 10 10 (272	721	99
	G02292	Homo sapiens	own ti tina massain	877	99
328	AF168990	Homo sapiens	100 - Albada baara ahain wariah e	581	80
329		Homo sapiens	region	ì	
	S67984				98
329 330			(4.4.10.4-4525)	2823	
329 330 331	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525		100
329 330			LDL-receptor related precursor (AA -19 to 4525) Human signal peptide containing protein HSPP-		100
329 330 331	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525) Human signal peptide containing protein HSPP- 107 SEQ ID NO:107.		

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:		ļ	similarity to P49205 (PID:g1345860)		
335	Y87347	Homo sapiens	Human signal peptide containing protein HSPP- 124 SEQ ID NO:124.	1111	67
336	AF006466	Mus	lymphocyte specific formin related protein	193	75
337	AF265555	musculus Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	632	97
		1	Amino acid sequence of hSlo3-2.	516	100
338	Y13443	Homo sapiens	putative GABA-gated chloride channel	189	100
339	Y07637	Homo sapiens	Human Grb7 effector 2.2412 protein.	2156	99
340	Y05734 AE000497	Escherichia	L-idonate transcriptional regulator	928	98
341		coli Escherichia	glycerol-3-phosphate dehydrogenase (EC	769	99
342	D90855	coli	1.1.99.5) chain A, anaerobic		100
343	D85613	Escherichia coli	membrane component	399	
344	M93239	Escherichia	transmembrane protein	232	100
345	M60177	Escherichia	enterobactin	759	99
346	D90699	Escherichia	Sensor protein copS (EC 2.7.3).	638	97
347	D90843	coli Escherichia	CapB protein.	552	100
348	M13422	Escherichia	49 kd protein	1193	96
	L10328	coli Escherichia	similar to drug resistance translocases	340	90
349		coli	enhancer-trap-locus-1	560	82
350	X69942	Mus musculus	apamin-sensitive small-conductance Ca2+-	463	80
351	AF239613	Homo sapiens	activated notassium channel	577	100
352	D90777	Escherichia coli	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) (b- hydroxybutyryl-CoA	311	100
353	D90863	Escherichia	dehydrogenase) (BhbD). similar to	311	98
		coli	Human transmembrane protein HP02000.	133	58
354 355	Y52386 Y31645	Homo sapiens Homo sapiens	Human transport-associated protein-7 (TRANP-	482	55
			7). Protein regulating gene expression PRGE-30.	119	51
356	Y58637	Homo sapiens	dual-specificity tyrosine phosphatase YVH1	1788	100
357 358	AF119226 Y87219	Homo sapiens Homo sapiens	Human secreted protein sequence SEQ ID	165	100
		Tions arriage	NO:258. beta-fibrinogen	233	93
359	J00132	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	70
360	G03789	Homo sapiens	Type III procollagen (prior art).	108	40
361 362	R28916 U16655	Rattus norvegicus	phospholipase C delta-4	649	65
262	G03110	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	95	42
363	G03119 U47276	Gallus gallus	chicken brain factor-2	104	34
364	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	183	65
365 366	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	118	46
367	X98258	Homo sapiens	M-phase phosphoprotein 9	564	75
368	AL021366	Homo sapiens	clCK0721Q.3 (Kinesin related protein)	3387	99
369	U70932	Peromyscus leucopus	reverse transcriptase	92	59
370	X86400	Homo sapiens	gamma subunit of sodium potassium ATPase	242	73
1200	C03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	56
371	G03172 U49974	Homo sapiens	mariner transposase	257	55
372	X13916	Homo sapiens	I DL-recentor related precursor (AA -19 to 4525)	21193	99
373 374	AF234765	Rattus norvegicus	serine-arginine-rich splicing regulatory protein SRRP86	1182	78
375	U49974	Homo sapiens	mariner transposase	172	55

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			Human secreted protein, SEQ ID NO: 6065.	221	67
76	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 4750.	600	100
77	G00669	Homo sapiens		1456	91
78	X52574	Mus musculus	GTP binding protein		
79	R69095	Homo sapiens	Anti-HIV Fab tat31 light chain.	68	37
80	J04974	Homo sapiens	alpha-2 type XI collagen	125	37
	AB002405	Homo sapiens	LAK-4p	530	43
81	U64830	Dictyostelium	protein tyrosine kinase	115	44
		discoideum	000 ID MO. 6007	618	98
383	G02916	Homo sapiens	Human secreted protein, SEQ ID NO: 6997.	617	93
384	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	4560	100
385	AJ245822	Homo sapiens	type I transmembrane receptor	2148	98
386	D86974	Homo sapiens	KIAA0220		50
387	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	142	1 59
388	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	99	
389	M12140	Homo sapiens	envelope protein	197	51
390	AJ293309	Homo sapiens	NHP2 protein	461	77
390 391	Y42751	Homo sapiens	Human calcium binding protein 2 (CaBP-2).	181	94
·	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	241	66
392		Homo sapiens	olfactory receptor protein	339	54
393	Y14442	Homo sapiens	Secreted protein clone da228 6.	957	100
394 395	W85607 Y76332	Homo sapiens	Fragment of human secreted protein encoded by	171	34
		i	gene 38.	250	100
396	G03930	Homo sapiens	Human secreted protein, SEQ ID NO: 8011.	105	35
397	AB032904	Hylobates syndactylus	dopamine receptor D4		1
200	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	861	.85
398 399	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	1047	92
			Human secreted protein clone cb98_4.	162	37
400	Y29861	Homo sapiens	similar to rat integral membrane glycoprotein;	527	78
401	D87002	Homo sapiens	accession number Z21513.	i	'
	1E100754	Homo sapiens	ancient ubiquitous protein AUP1 isoform	853	95
402	AF100754	Gallus gallus	alpha-2-macroglobulin receptor	258	60
403	X74904 AF075462	Mus	ADP-ribosylation factor-directed GTPase	545	89
		musculus	activating protein isoform b	162	30
405	X92887	Human endogenous	pol/env	102	
		retrovirus K			
406	Y30162	Homo sapiens	Human dorsal root receptor 4 hDRR4.	325	72
400	AK022626	Homo sapiens	unnamed protein product	2833	99
407	L13802	Homo sapiens	ribosmal protein small subunit	264	92
408	Y91600	Homo sapiens	Human secreted protein sequence encoded by	1788	89
			gene 9 SEQ ID NO:273.  Secreted protein encoded by gene 30 clone	2004	99
410	W88745	Homo sapiens	HTSEV09.		82
411	AB043953	Mus musculus	Chat-H	2628	
412	Y86233	Homo sapiens		1014	92
			NO:148.	265	71
413	U10542	Pan troglodytes	MHC class I A		
414	AF155097	Homo sapiens	NY-REN-7 antigen	850	95
414		Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	88	48
415	G03203	Homo sapiens	· · · · · · · · · · · · · · · · · · ·	266	89
416	Y57911			481	60
417	W27651	Homo sapiens	70	3077	87
418	Y76884	Homo sapiens		289	68
419	AF255559	Notothenia	aipha tubulin		
		coriiceps	Human secreted protein, SEQ ID NO: 6065.	209	74
420 421	G01984 AL109827	Homo sapiens Homo sapiens	dJ309K20.2 (acrosomal protein ACR55 (similar		96
	AC008075	Arabidopsis	to rat sperm antigen 4 (SPAG4))) F24J5.4	112	35
422					

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	4 F221706	Homo sapiens	Alu co-repressor 1	1090	100
423	AF231705 AF234887	Homo sapiens	FLAMINGO 1	6268	97
424 425	Y35942	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 191.	1961	99
456	AB009288	Homo sapiens	N-copine	635	98
426 427	L12392	Homo sapiens	Huntington's Disease protein	16080	99
	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	768	98
428	AJ293573	Homo sapiens	zinc finger protein Cezanne	542	87
429 430	Y84441	Homo sapiens	Amino acid sequence of a human RNA- associated protein.	2074	100
431	G02850	Homo sapiens	Human secreted protein, SEQ ID NO: 6931.	723	95
432	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	73	42
433	AF159296	Lycopersicon esculentum	extensin-like protein	613	48
434	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	135	44
435	X73874	Homo sapiens	phosphorylase kinase	3442	97
436	AF161426	Homo sapiens	HSPC308	268	74
437	Y30812	Homo sapiens	Human secreted protein encoded from gene 2.	1055	52
438	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	168	56
439	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2294	96
440	X02344	Homo sapiens	beta-tubulin	311	95
441	AF168418	Homo sapiens	activating signal cointegrator 1	1882	100
442	L11672	Homo sapiens	zinc finger protein	795	54
443	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	93	26
444	A52140	unidentified	HUMAN NDR	2451	100
445	X98330	Homo sapiens	ryanodine receptor 2	9356	99
446	AF116712	Homo sapiens	PRO2738	227	49
447	AF245447	Homo sapiens	sphingosine kinase type 2 isoform	576	99
448	AF133086	Homo sapiens	membrane-type serine protease 1	2630	94
449	U87305	Rattus norvegicus	transmembrane receptor UNC5H1	817	93
450	AF081249	Homo sapiens	JAW1-related protein MRVI1A long isoform	4568	99
451	AC005498	Homo sapiens	R31665_1	316	62
452	M60235	Homo sapiens	granule membrane protein-140	464	73 88
453	AB036706	Homo sapiens	intelectin	730 263	81
454 455	G00918 Y22634	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 4999.  Human cytokine inducible regulatory protein-1	192	67
456	Y36705	Homo sapiens	(CIRP-1).  Fragment of human secreted protein encoded by gene 62.	106	40
467	101225	Home coniens	DNA encoding human growth hormone receptor.	3282	96
457 458	N91325 M19155	Homo sapiens Plasmodium falciparum	S-antigen precursor	110	36
459	Y13377	Homo sapiens	Amino acid sequence of protein PRO257.	509	98
460	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	149	43
461	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	184	54
462	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	135	33
463	X84960	Triticum aestivum	low molecular weight glutenin	1781	85
464	W19919	Homo sapiens	Human Ksr-1 (kinase suppressor of Ras).	502	59
465	AF189764	Mus musculus	alpha/beta hydrolase-l	101	30
466	U93569	Homo sapiens	p40	1172	99
467	Y41528	Homo sapiens	Fragment of human secreted protein encoded by gene 77.	1172	52
468	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.		97
469 470	AJ000008 X70922	Homo sapiens Mus	PI3-kinase neurotoxin homologue	5832 118	47
	1	musculus		1.00	75
471	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	198	1 /2

SEQ	Accession	Species	Description	Smith-	%
D D	No.	} -		Waterman	Identity
40:		<b>!</b>		Score	ļ
			gene 62.		1
173	G02313	Homo sapiens	Human secreted protein, SEQ ID NO: 6394.	328	100
174	Y07007	Homo sapiens	Breast cancer associated antigen precursor	1013	97
+ /4	107007	110illo supiciis	sequence.		
175	W93254	Homo sapiens	Human ESRP1 protein.	943	80
	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	236	65
176			Human secreted protein encoded by gene 44	202	60
477	Y02693	Homo sapiens	clone HTDAD22.		
		<u> </u>	Human secreted protein, SEQ ID NO: 5951.	267	100
478	G01870	Homo sapiens	Human secreted protein, SEQ 15 10. 5551.	3427	92
479	AF102777	Mus	FYVE finger-containing phosphoinositide kinase	3421	12
		musculus		123	53
480	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	221	77
481	W87701	Homo sapiens	A human membrane fusion protein designated	221	''
			SYTAX1.		30
482	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	131	39
483	AF210651	Homo sapiens	NAG18	124	59
484	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	343	50
485	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
486	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein	149	73
100	013174		3	L	
487	Y76167	Homo sapiens	Human secreted protein encoded by gene 44.	627	100
488	AJ275213	Homo sapiens	stabilin-1	1244	91
488 489	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	313	65
		Homo sapiens	Huntington's Disease protein	16081	100
490	L12392	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	197	66
491	G03789		laminin-binding protein	228	70
492	J03799	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein	128	41
493	U15174	Homo sapiens		1.20	1
		<u> </u>	Human secreted protein encoded by gene 44	197	67
494	Y02693	Homo sapiens		177	10,
			clone HTDAD22.	889	94
495	AC005175	Homo sapiens	R31449_3	229	61
496	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	1	48
497	AB030237	Canis	D4 dopamine receptor	90	40
		familiaris		-	-
498	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	228	65
499	U70935	Peromyscus	reverse transcriptase	213	52
		maniculatus			
500	U48508	Homo sapiens	skeletal muscle ryanodine receptor	26406	99
501	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	105	58
502	AF119851	Homo sapiens	PRO1722	156	62
503	AF113685	Homo sapiens	PRO0974	116	50
504	U79458	Homo sapiens	WW domain binding protein-2	322	59
505	W29651	Homo sapiens	Human secreted protein CD124_3.	608	55
506	W85459	Homo sapiens	Secreted protein encoded by clone dh1135_9.	986	70
		Homo sapiens	Human secreted protein HUSXE77, SEQ ID	115	33
507	Y86265	riomo sapiens	NO:180.	1	
660	47 160124	17	bA243J16.3 (similar to MYLK (myosin, light	184	92
508	AL160175	Homo sapiens	polypeptide kinase))	1	1
		<del></del>		97	62
509	U43360	Peromyscus	reverse transcriptase	1	1
		maniculatus	TY	117	63
510	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.		100
511	W79092	Homo sapiens	Human secreted protein dn740_3.	1058	
512	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	205	64
	AJ133439	Homo sapiens	GRIP1 protein	2151	100
513	AE003456	Drosophila	CG6393 gene product	259	42 .
514	1	melanogaster		L	1
	1		p46XiEg22	128	40
514	7.17206	Xenopus		1	
	Z17206	Xenopus		1	
514	1	laevis	large tumor suppressor )	1766	94
514 515 516	AF104413	laevis Homo sapiens	large tumor suppressor 1 Human secreted protein, SEO ID NO: 7878.	1766 92	94
514 515 516 517	AF104413 G03797	laevis Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7878.		
514 515 516 517 518	AF104413 G03797 AF151083	Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7878.  HSPC249	92 444	40 98
514 515 516 517	AF104413 G03797	laevis Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	92	40

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:			SEO ID NO. 7871	159	59
521	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	259	40
522	AF121857	Homo sapiens	sorting nexin 7	82	37
523	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.		73
524	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	253	
525	AF119851	Homo sapiens	PRO1722	162	57
526	Y27761	Homo sapiens	Human secreted protein encoded by gene No. 47.	154	57
527	G02707	Homo sapiens	Human secreted protein, SEQ ID NO: 6788.	70	45
528	U47924	Homo sapiens	C8	1112	86
529	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	84	45
530	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	111	60
531	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	92	65
532	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	75	29
533	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	182	48
534	AF068286	Homo sapiens	HDCMD38P	861	100
535	U07707	Homo sapiens	epidermal growth factor receptor substrate	228	60
536	G01955	Homo sapiens	Human secreted protein, SEQ ID NO: 6036.	484	75
537	AF219232	Gallus gallus	qin-induœd kinase	206	53
538	AF135022	Homo sapiens	mediator	128	100
539	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	141	59
540	AF016430	Caenorhabditi s elegans	contains similarity to a BR-C/TTK domain	853	39
541	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	408	66
542	M29487	Homo sapiens	integrin alpha subunit precursor	517	81
543	AF102530	Mus musculus	olfactory receptor F3	327	73
544	Y73431	Homo sapiens	Human secreted protein clone yb186_1 protein sequence SEQ ID NO:84.	386	100
545	AE004833	Pseudomonas acruginosa	probable TonB-dependent receptor	279	42
546	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	264	53
547	Y69192	Homo sapiens	A human monocyte-macrophage apolipoprotein B receptor protein.	1772	67
548	Y91493	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:166.	176	100
549	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
550	AF044588	Homo sapiens	protein regulating cytokinesis 1; PRC1	1953	88
551	Y29332	Homo sapiens	Human secreted protein clone pe584_2 protein sequence.	1224	94
552	X98330	Homo sapiens	ryanodine receptor 2	24621	99
553	Y42782	Homo sapiens	Human UC Band #331 protein.	684	95
554	AB025258	Mus musculus	granuphilin-a	501	41
555	AJ010346	Homo sapiens	RING-H2	1468	100
556	W92388	Homo sapiens	Human TR-interacting protein S239a.	538	92
557	AF119851	Homo sapiens	PRO1722	175	59
558	AF117756	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP150	183	32
559	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	319	68
560	D86214	Mus musculus	Ca2+ dependent activator protein for secretion	1010	93
561	AF187325	Canis	melanoma antigen	287	55
663	1 77001001	familiaris	OXAIL	2512	99
562 563	AJ001981 Z17238	Homo sapiens Rattus	glutamate receptor subtype delta-1	338	66
564	W30638	Homo sapiens	Partial human 7-transmembrane receptor	371	100
	1	<del> </del>	HAPO167 protein.	467	97
565 566	AC005620 Y99358	Homo sapiens Homo sapiens	R33590_1 Human PRO1772 (UNQ834) amino acid	1138	78
	AL031177	Homo sapiens	sequence SEQ ID NO:63. dJ889M15.3 (novel protein)	1002	58
567					

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:				231	100
69	AF097518	Homo sapiens	liver-specific transporter	1532	100
70	AB035698	Homo sapiens	Misshapen/NIK-related kinase MINK-1	1064	100
571	Y07096	Homo sapiens	Colon cancer associated antigen precursor sequence.		
572	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	735	55
573	Y66639	Homo sapiens	Membrane-bound protein PRO290.	254	45
574	AB037108	Homo sapiens	seven transmembrane domain orphan receptor	1883	99
		Homo sapiens	This gene is novel.	836	100
575	D43949		Human breast tumour-associated protein 57.	108	50
576	Y48596	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	141	75
577	G00352	Homo sapiens	Human secreted protein, SEQ ID 1101 1150	140	65
578	R95913	Homo sapiens	Neural thread protein.	201	70
579	AK025116	Homo sapiens	unnamed protein product	77	70
580	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:388.		
581	AF196779	Homo sapiens	JM10 protein	450	100
	AF188706	Homo sapiens	g20 protein	330	98
582		Canis	D4 dopamine receptor	64	56
583	AB030234	familiaris	•		
	602621	Homo sapiens	Human secreted protein, SEQ ID NO: 6702.	345	90
584	G02621		dJ963E22.1 (Novel protein similar to NY-REN-2	268	85
585	AL096828	Homo sapiens	Antigen)		
		<del>  ,</del>	Human secreted protein encoded from gene 9.	235	35
586	Y30819	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	132	56
587	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.  Human secreted protein, SEQ ID NO: 6953.	182	79
588	G02872	Homo sapiens	Human secreted protein, SEQ 1D NO. 0733.	764	80
589	AF235017	Mus	2P1 protein	/04	
590	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone	329	81
591	Y30709	Homo sapiens	HPMBQ32.  Amino acid sequence of a human secreted	110	43
		TY	protein.  A human seven transmembrane signal transducer	1369	92
592	Y53875	Homo sapiens	nolypeptide.		
593	Y53051	Homo sapiens	Human secreted protein clone dd119_4 protein	1112	97
	1/05/50	Homo sapiens	Human secreted protein encoded by gene No. 92.	763	79
594	Y27658	Homo sapiens	Human secreted protein, SEQ 1D NO: 7879.	156	58
595	G03798	Mus	COP1 protein	2215	95
596	AF151110	musculus	COI I protoni		
			Human secreted protein, SEQ ID NO: 7867.	157	65
597	G03786	Homo sapiens	putative secreted protein ZSIG37	143	40
598	AF192499	Mus	putative secreted protein 20103?		
		musculus	DD01947	236	76
599	AF119855	Homo sapiens	PRO1847	212	73
600	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	567	88
601	Y00295	Homo sapiens	Human secreted protein encoded by gene 38.	2015	74
602	AF184971	Homo sapiens	class II cytokine receptor ZCYTOR7	1	96
603	AF061936	Homo sapiens	diacylglycerol kinase iota	773	93
604	AL096828	Homo sapiens	TO DENLO	1333	
605	AB033106	Homo sapiens		3915	100
	X75756	Homo sapiens	protein kinase C mu	3916	99
606		Homo sapiens		5758	99
607	D86983			1377	99
608 609	W69341 W88627	Homo sapiens Homo sapiens		339	82
		Homo sapiens	HPMBQ32.	116	62
610	Y27868	_	107.	2164	100
611	AF202636	Homo sapiens	angiopoietin-like protein PP1158	218	82
612	AF090944	Homo sapiens			59
613	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	195	
614	M87053	Rattus norvegicus	lens membrane protein	450	84
615	AC004232	Homo sapiens	FPM315	163	37
	1 AUJU4232	1 LIOUIO Sabiens	Human secreted protein, SEQ ID NO: 6065.	205	79

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	Y91524	Homo sapiens	Human secreted protein sequence encoded by gene 74 SEQ ID NO:197.	821	99
		L.,		2258	99
18	AJ245621	Homo sapiens	CTL2 protein  Human secreted protein encoded by gene 75.	108	64
19	Y76198	Homo sapiens	transferrin receptor 2 alpha	3922	94
20	AF067864	Homo sapiens	Transmembrane protein dppC	573	90
521	D90721	Escherichia coli		730	100
522	W75858	Homo sapiens	Human secretory protein of clone CS752-3.	733	100
523	Y94982	Homo sapiens	Human secreted protein vb12_1, SEQ ID NO:4.	637	83
524	AF034745	Mus musculus	LNXp80	94	46
625	U42580	Paramecium bursaria Chlorella virus 1	Pro-rich, IPPPNMSLPLS (3x)		70
626	U79260	Homo sapiens	unknown	194	50
627	R95913	Homo sapiens	Neural thread protein.	99	100
628	G03450	Homo sapiens	Human secreted protein, SEQ ID NO: 7531.	427	100
529	Y36281	Homo sapiens	Human secreted protein encoded by gene 58.	590	76
630	Y02693	Homo sapiens	Human secreted protein encoded by gene 44	165	
631	G02139	Homo sapiens	Human secreted protein, SEQ ID NO: 6220.	268	96
632	U16996	Homo sapiens	protein tyrosine posphatase	351	80
633	AF121857	Homo sapiens	sorting nex in 7	2019	100
634	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number 1.25899	340	77
635	Y07090	Homo sapiens	Renal cancer associated antigen precursor sequence.	277	64
636	AB013382	Homo sapiens	DUSP6	414	76
637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	315	71
638	M95762	Rattus norvegicus	GABA transporter	924	89
639	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	219	60
640	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	137	79
641	AC008075	Arabidopsis thaliana	F24J5.4	121	33
642	W74824	Homo sapiens	Human secreted protein encoded by gene 96 clone HAQBK61.	615	62
(42	AB015982	Homo sapiens	serine/threonine kinase	485	98
643 644	Y25806	Homo sapiens	Human secreted protein fragment encoded from gene 23.	162	46
(15	AF122904	Homo sapiens	membrane protein DAP10	474	100
645		Homo sapiens		200	38
646	AF233323	Homo sapiens		1203	99
647	W48804	Homo sapiens		1440	98
648	AF257330	Homo sapiens		233	73
649	Y36203		000 10 10 (06)	173	78
650 651	G02872 Y32199	Homo sapiens Homo sapiens	1 mcc	1012	100
652	AB032909	Hylobates agilis	dopamine receptor D4	122	32
653	AK021848	Homo sapiens	unnamed protein product	186	69
654	W73411	Homo sapiens	1 dby Care No	57	37
655	L22455	Rattus	mu opioid receptor	116	34
	1-003112	norvegicus	Human secreted protein, SEQ ID NO: 7193.	110	45
656	G03112	Homo sapiens		459	97
657 658	G02345 W88627	Homo sapiens Homo sapiens	Secreted protein encoded by gene 94 clone	291	75
			HPMBQ32. Human secreted protein, SEQ ID NO: 6913.	134	65
659	G02832	Homo sapiens		333	96
660	Y91423	Homo sapiens	gene 11 SEQ ID NO:144.		

~~ (	Accession No.	Species	Description	Smith- Waterman	% Identity
10:	.10.			Score	1-0-
	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	168	68
62	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	375	43
			Human GTP binding protein APD08.	629	100
663	W75771	Homo sapiens	Human GIP binding protein Al Dos.	480	55
64	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like)	400	
l			protein (hs6M1-21))	978	96
665	AB037734	Homo sapiens	KIAA1313 protein		84
666	W82841	Homo sapiens	Human cerebral protein-1.	192	87
667	W82841	Homo sapiens	Human cerebral protein-1.	182	
	AB030184	Mus	contains transmembrane (TM) region and ATP	757	68
668		musculus	binding region dopamine receptor D4	85	37
669	AB032919	Hylobates muelleri		746	81
670	AF107295	Rattus	outer membrane protein	/46	
	-	norvegicus	leukocyte surface protein	394	93
671	Z33642	Homo sapiens	Secreted protein clone du410_5.	261	91
672	W85608	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	106	48
673	G03203	Homo sapiens	Human secreted protein, 3EQ ID 110. 7201.	2388	99
674	AL035587	Homo sapiens	dJ475N16.4 (KIAA0240)	1134	53
675	Y59668	Homo sapiens	Secreted protein 108-005-5-0-C1-FL.	174	74
676	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	1013	95
677	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDPr		
678	L11625	Mus	receptor protein-tyrosine kinase	545	96
		musculus	dJ167A19.3 (novel protein)	745	100
679 680	AL031427 AJ133430	Homo sapiens Mus	olfactory receptor	528	77
		musculus		179	70
681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	336	76
682	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	118	100
683	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.		
684	U43360	Peromyscus maniculatus	reverse transcriptase	100	37
			Human secreted protein, SEQ ID NO: 4966.	162	60
685	G00885	Homo sapiens	unnamed protein product	590	100
686	AK001518	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
687	G01982	Homo sapiens	Human cancer associated antigen precursor	2405	99
688	Y92241	Homo sapiens	(MO-REN-46).	423	36
689	AC024792	Caenorhabditi s elegans	contains similarity to TR:P78316		
690	Y27868	Homo sapiens		183	81
691	Y56514	Homo sapiens	107. Human Jurkat cell clone P2-15 AIM10 longest	180	88
1	1		ORF protein sequence.	1539	99
692	Y27795	Homo sapiens	Human secreted protein encoded by gene No. 79.	428	98
693	Y36268	Homo sapiens	Human secreted protein encoded by gene 43.		89
694	U12465	Homo sapiens	ribosomal protein L35	308	99
695	Y45272	Homo sapiens	Human secreted protein encoded from gene 16.	1517	
696	AF191838	Homo sapiens	TANK hinding kinase TBK1	1242	98
697	Y02693	Homo sapiens	1 idad bu gang 44	275	75
698	Y87280	Homo sapiens	Human signal peptide containing protein HSPP-	576	90
		Homo sapiens	.57 SEQ ID NO:57.	729	99
699	¥97999	}	ID NO:1.	610	79
700	AJ006701	Homo sapiens		2357	100
	AF209198	Homo sapiens	zinc finger protein 277	709	45
701	AJ298841	Mus	torsinA protein		ļ
701 702	1.62200	musculus			
702		Homo saniens	unnamed protein product	622	98
	AK021729 Z46787	Homo sapiens Caenorhabdit s elegans		920	51

1	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:			550 m NO. 6592	125	58
	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	121	95
	R95326	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 2DD).		39
08	G03002	Homo sapiens	Human secreted protein, SEO ID NO: 7083.	125	
09	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	516	98
10	M63577	Saccharomyc es cerevisiae	SFP1	131	59
711	AB026291	Rattus	acetoacetyl-CoA synthetase	467	85
	501011	norvegicus  Homo sapiens	protein tyrosine phosphatase (PTP-BAS, type 3)	368	44
712	D21211 AF044033	Marmota	olfactory receptor	615	83
		marmota	Human secreted protein, SEQ ID NO: 7642.	251	100
/14	G03561	Homo sapiens	Human secreted protein, SEQ 10 110. 7042.	1380	100
/15	AB033062	Homo sapiens	KIAA1236 protein	80	73
716	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	835	99
717	Y96864	Homo sapiens	SEQ. ID. 37 from WO0034474.	234	100
718	AJ243396	Homo sapiens	voltage-gated sodium channel beta-3 subunit	578	99
719	U47334	Homo sapiens	similar to chicken gamma aminobutyric acid receptor beta4 subunit	1096	100
720	AB020598	Homo sapiens	peptide transporter 3	570	74
721	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.		100
722	J05046	Homo sapiens	insulin recentor-related receptor	6787	41
723	AF001958	Ambystoma tigrinum	electrogenic Na+ bicarbonate cotransporter;	111	
724	AF127084	Mus musculus	semaphorin cytoplasmic domain-associated protein 3A	5253	94
	3/64/02	Homo sapiens	GABA transporter	3114	99
725 726	X54673 AF016191	Rattus	potassium channel	370	100
727	AB029559	norvegicus Rattus	BATI	139	35
		norvegicus Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	2186	97
728	Y28503		plexin-B1/SEP receptor	729	56
729 730	AJ011415 Z93096	Homo sapiens Homo sapiens	bK390B3.1 (manic fringe (Drosophila) homolog)	142	68
731	Z10062	Homo sapiens	cDNA encoding a human vanilloid receptor homologue Vanilrep1.	675	99
				492	94
732	AF161382	Homo sapiens		3826	99
733 734	AB029033 AE000493	Homo sapiens Escherichia	putative transport protein	592	97
735	AL033379	Homo sapiens	dJ417O22.2 (novel 7 transmembrane receptor (rhodopsin family) protein similar to high- affinity lysophosphatidic acid receptor homolog)	2173	99
736	AF132599	Homo sapiens	Classicated T lumphocytes	245	56
			acetylcholine receptor delta subunit	883	99
737	X55019	Homo sapiens		1978	100
738	X91906	Homo sapiens		1444	98
739	AB026116	Homo sapiens	organic anion transporter 4	83	24
740	D00570	Mus musculus	open reading frame (196 AA)	118	40
741	W03626	Homo sapiens		614	100
742	U66059	Homo sapiens		2751	99
743	AF119815	Homo sapiens		148	93
744	X16663	Homo sapiens		448	95
745	W67838	Homo sapiens	clone HLTCJ63.		100
746	W57260	Homo sapien:	Human semaphorin Y.	2414	65
747	W21578	Homo sapien	Alzheimer's disease protein encoded by DNA from plasmid pGCS2232.	968	
L	Y94935	Homo sapien		622	100
748			Judgeties on 4		106
748	AL022238	Homo sapien		314	85

EQ D	Accession No.	Species	Description	Smith- Waterman Score	% Identity
IO:   51	AB025258	Mus	granuphilin-a	773	41
-		musculus		900	99
52	Y52386	Homo sapiens	Human transmembrane protein HP02000.	2527	99
53	Y48586	Homo sapiens	Human breast tumour-associated protein 47.	694	100
154	AJ272207	Homo sapiens	putative G protein-coupled receptor 92	979	68
755	M85183	Rattus norvegicus	vasopressin receptor		71
756	AF190501	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6	388	
757	Y02692	Homo sapiens	Human secreted protein encoded by gene 43 clone HTADX17.	461	87
758	Z22535	Homo sapiens	ALK-3	439	98
759	R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	564	97
760	W74902	Homo sapiens	Human secreted protein encoded by gene 175 clone HE8BI92.	1217	99
		77	Human secreted protein, SEQ ID NO: 7787.	223	88
761	G03706	Homo sapiens	KIAA0869 protein	4433	99
762	AB020676	Homo sapiens	unnamed protein product	2285	99
763	AK026992	Homo sapiens Homo sapiens	glucocorticoid receptor AF-1 coactivator-1	573	100
764 765	AF173358 AF268066	Mus	netrin 4	2019	89
	-	musculus	Human breast tumour-associated protein 46.	1169	89
766 767	Y48585 AF230378	Homo sapiens Mus	interleukin-1 delta	309	45
768	AF121975	Mus Mus	odorant receptor S18	268	62
		musculus	RanBPM	611	57
769 770	AB008515 Y09945	Homo sapiens Rattus	putative integral membrane transport protein	458	50
		norvegicus	AD026	688	99
771 772	AF226731 Y27132	Homo sapiens Homo sapiens	Human glioblastoma-derived polypeptide (clone OA004FG).	1384	100
	1/07022	Uemo coniens	NOV/plexin-A1 protein	1821	98
773 774	X87832 AB025258	Homo sapiens Mus	granuphilin-a	500	41
		musculus	HSPC040 protein	232	93
775	AF125101	Homo sapiens	Human secreted protein, SEQ ID NO: 6896.	314	95
776	G02815	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	191	68
777	G02493	Homo sapiens	Sequence of pre-human atrial natriuretic peptide.	213	45
778	R03301	Homo sapiens	bA353C18.2 (novel protein)	232	100
779 780	AL357374 AF100346	Homo sapiens Homo sapiens	neuronal voltage gated calcium channel gamma-	1434	89
781	Y19566	Homo sapiens	Amino acid sequence of a human secreted protein.	103	52
	1,,,,,,,,,	77	1.1	1098	93
782 783	Y36233 AF084464	Homo sapiens Rattus	GTP-binding protein REM2	141	30
784	W49042	norvegicus  Homo sapiens		2693	99
			LBP-3.	1904	91
785	AF238381	Homo sapiens		547	100
786	Y91870	Homo sapiens	L'ENTER 7	1062	94
787	Y71062	Homo sapiens		8684	98
788	AF117754	Homo sapiens	complex component TRAP240	2848	96
789	AL049569	Homo sapiens		745	96
790	AF151848	Homo sapiens		1421	95
791	Y08639	Homo sapiens		644	99
792 793	Y41706 AF121228	Homo sapiens Homo sapiens	thyroid hormone receptor-associated protein	1037	100
			complex component TRAP95	124	62
794 795	G04072 Y69384	Homo sapiens Homo sapiens	Amino acid sequence of a 14274 receptor	119	100
1			protein.	1250	99
1	W40215	Homo sapiens	Human macrophage antigen.	1358	77

CEO	Accession	Species	Description	Smith-	%
SEQ	No.	Species	2.00	Waterman	Identity
ID	No.			Score	
NO: 797	AF258340	Homo sapiens	hepatocellular carcinoma-associated antigen 112	1151	99
	AF159615	Homo sapiens	FGF recentor activating protein 1	461	98
798	Y59863	Homo sapiens	Human normal uterus tissue derived protein 26.	797	99
799		Homo sapiens	Human T1-receptor ligand III splice variant 2.	572	92
800	W70459	Homo sapiens	renin	1913	93
801	L00073		CRI protein.	11963	97
802	P92219	Homo sapiens	CKI protein.		
		(human)	ANP-A receptor preprotein (AA -32 to 1029)	5199	98
803	X15357	Homo sapiens	Human secreted protein from clone EC172_1.	4018	95
804	W64473	Homo sapiens	oligophrenin-4	2067	100
805	AJ243874	Homo sapiens	Human secreted protein, SEQ ID NO: 5812.	284	100
806	G01731	Homo sapiens		1562	83
807	Z24680	Homo sapiens	garp	1364	90
808	AF171669	Homo sapiens	glycoprotein-associated amino acid transporter LAT2		96
809	W70321	Homo sapiens	Secreted protein CC198_1.	1154	99
810	W74843	Homo sapiens	Human secreted protein encoded by gene 115 clone HOVBA03.	855	
011	AF108831	Homo sapiens	K:Cl cotransporter 3	4561	100
811	AF108831 AF092135	Homo sapiens	PTD014	862	100
812 813	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	784	100
814	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
815	AF051151	Homo sapiens	Toll/interleukin-1 receptor-like protein 3	3850	99
816	W95630	Homo sapiens	Homo sapiens secreted protein gene clone gn114 1.	358	100
		Homo sapiens	Human secreted protein, SEQ ID NO: 5163.	549	100
817	G01082	Homo sapiens	CGI-41 protein	1106	95
818	AF151800	Homo sapiens	low density lipoprotein receptor	3980	100
819	L00352		IGF-I receptor	5832	99
820	X04434	Homo sapiens	Human secreted protein, SEQ ID NO: 7925.	572	100
821	G03844	Homo sapiens	TERA	396	48
822	AF212220	Homo sapiens	Human glycophosphatidylinositol-anchored	4897	99
823	Y50125	Homo sapiens	protein GPI-122.		
	15166550	I I ama soniens	ASB-3 protein	2675	98
824	AF156778	Home sapiens	neuronal voltage-gated calcium channel gamma-	1105	100
825	AF096322	Homo sapiens	2 subunit		
826	Y07972	Homo sapiens	Human secreted protein fragment #2 encoded from gene 28.	1540	100
			potassium channel Kv8.1	2435	95
827	AB032013	Homo sapiens	BCL9	5284	96
828	Y13620	Homo sapiens	Human secreted protein sequence encoded by	541	98
829	Y91474	Homo sapiens	gene 24 SEQ ID NO:147.		
		1V and applicant	glypican	1625	87
830	X54232	Homo sapiens	acetylcholine receptor beta-subunit preprotein	2540	100
831	X14830	Homo sapiens Homo sapiens	Human chondromodulin-like protein, Zchm1.	1002	100
832	Y71262	i momo sapiens	Trainer Chord CEO ID NO: 7054	638	96
		77	I Human secreted arates and 11 No. 7727.		
833	G03873	Homo sapiens	Human secreted protein, SEQ ID NO: 7954.	1389	93
833 834	G03873 AC003030	Homo sapiens Homo sapiens	R29828_1		93 87
833 834 835	G03873 AC003030 Y38422	Homo sapiens Homo sapiens Homo sapiens	R29828_1 Human secreted protein.	1389 964	
833 834	G03873 AC003030	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans	R29828_1 Human secreted protein. glycine-rich	1389 964 85	87 36
833 834 835	G03873 AC003030 Y38422	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	1389 964 85 998	87 36 75
833 834 835 836 837	G03873 AC003030 Y38422 U41557	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor	1389 964 85 998	87 36 75 60
833 834 835 836 837	G03873 AC003030 Y38422 U41557 AL121889 AJ011415	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor A secreted protein encoded by clone cw1543_3.	1389 964 85 998 1580 1105	87 36 75 60 67
833 834 835 836 837 838 839	G03873 AC003030 Y38422 U41557 AL121889 AJ011415 W80398	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens Homo sapiens Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor A secreted protein encoded by clone cw1543_3. Human secreted protein, SEQ ID NO: 4943.	1389 964 85 998 1580 1105 255	87 36 75 60 67 92
833 834 835 836 837 838 839 840	G03873 AC003030 Y38422 U41557 AL121889 AJ011415 W80398 G00862	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens Homo sapiens Homo sapiens Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor A secreted protein encoded by clone cw1543_3. Human secreted protein, SEQ ID NO: 4943. Human secreted protein, SEQ ID NO: 6731.	1389 964 85 998 1580 1105 255 644	87 36 75 60 67 92 97
833 834 835 836 837 838 839 840 841	G03873 AC003030 Y38422 U41557 AL121889 AJ011415 W80398 G00862 G02650	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor A secreted protein encoded by clone cw1543_3. Human secreted protein, SEQ ID NO: 4943. Human secreted protein, SEQ ID NO: 6731. FGFR signalling adaptor SNT-1	1389 964 85 998 1580 1105 255 644 2629	87 36 75 60 67 92 97 99
833 834 835 836 837 838 839 840	G03873 AC003030 Y38422 U41557 AL121889 AJ011415 W80398 G00862	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens Homo sapiens Homo sapiens Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor A secreted protein encoded by clone cw1543_3. Human secreted protein, SEQ ID NO: 4943. Human secreted protein, SEQ ID NO: 6731. FGFR signalling adaptor SNT-1 Human secreted protein clone yc27_1 protein sequence SEQ ID NO.114.	1389 964 85 998 1580 1105 255 644	87 36 75 60 67 92 97
833 834 835 836 837 838 839 840 841 842 843	G03873 AC003030 Y38422 U41557 AL121889 AJ011415 W80398 G00862 G02650 AF036717 Y73446	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor A secreted protein encoded by clone cw1543_3. Human secreted protein, SEQ ID NO: 4943. Human secreted protein, SEQ ID NO: 6731. FGFR signalling adaptor SNT-1 Human secreted protein clone yc27_1 protein sequence SEQ ID NO.114.	1389 964 85 998 1580 1105 255 644 2629	87 36 75 60 67 92 97 99 100
833 834 835 836 837 838 839 840 841 842 843	G03873 AC003030 Y38422 U41557 AL121889 AJ011415 W80398 G00862 G02650 AF036717 Y73446 G02872	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor A secreted protein encoded by clone cw1543_3. Human secreted protein, SEQ ID NO: 4943. Human secreted protein, SEQ ID NO: 6731. FGFR signalling adaptor SNT-1 Human secreted protein clone yc27_1 protein sequence SEQ ID NO.114. Human secreted protein, SEQ ID NO: 6953.	1389 964 85 998 1580 1105 255 644 2629 1089	87 36 75 60 67 92 97 99 100
833 834 835 836 837 838 839 840 841 842 843	G03873 AC003030 Y38422 U41557 AL121889 AJ011415 W80398 G00862 G02650 AF036717 Y73446	Homo sapiens Homo sapiens Homo sapiens Caenorhabditi s elegans Homo sapiens	R29828_1 Human secreted protein. glycine-rich  dJ1076E17.1 (KIAA0823 protein (continues in AL023803)) plexin-B1/SEP receptor A secreted protein encoded by clone cw1543_3. Human secreted protein, SEQ ID NO: 4943. Human secreted protein, SEQ ID NO: 6731. FGFR signalling adaptor SNT-1 Human secreted protein clone yc27_1 protein sequence SEQ ID NO.114. Human secreted protein, SEQ ID NO: 6953. CGI-52 protein	1389 964 85 998 1580 1105 255 644 2629 1089	87 36 75 60 67 92 97 99 100

SEQ	Accession	Species	Description	Smith-	%
D`	No.			Waterman	Identity
<b>1</b> 0:	}			Score	ļ
			to AF038969 (PID:g2827207)		
48	X99886	Homo sapiens	monocyte chemotactic protein-2	160	76
349	AC005587	Homo sapiens	similar to mouse olfactory receptor 13; similar to	963	98
,47	11000550.	7.0.2	P34984 (PID:g464305)		
350	AB038237	Homo sapiens	G protein-coupled receptor C5L2	1767	100
351	AF124490	Homo sapiens	ARF GTPase-activating protein GIT1	3415	98
352	Y86217	Homo sapiens	Human secreted protein HWHGU54, SEQ ID	1189	99
552	18021/	Homo sapiens	NO:132.		
	1 200 4541	77	chloride channel protein 7	3748	99
353	AF224741	Homo sapiens	furin (AA 1-794)	3550	99
354	X17094	Homo sapiens	Fragment of human secreted protein encoded by	1245	99
355	W78245	Homo sapiens		1243	"
			gene 19.	1926	100
356	R97569	Homo sapiens	Interleukin-2 receptor associated protein p43.	3211	99
357	Y41765	Homo sapiens	Human PRO1083 protein sequence.		84
358	AF057306	Homo sapiens	transmembrane proteolipid	481	
359	AK025116	Homo sapiens	unnamed protein product	374	69
860	Y41312	Homo sapiens	Human secreted protein encoded by gene 5 clone	824	100
		-	HLDRM43.		
362	Y25776	Homo sapiens	Human secreted protein encoded from gene 66.	895	99
863	Y74188	Homo sapiens	Human prostate tumor EST fragment derived	96	30
-05	1	)	protein #375.		<u></u>
864	AF167473	Homo sapiens	heme-binding protein	870	99
865	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	211	67
	X54870	Homo sapiens	Type II integral membrane protein	1201	100
866	G00700	Homo sapiens	Human secreted protein, SEQ ID NO: 4781.	640	99
867		Homo sapiens	Human secreted protein fragment encoded from	388	88
868	68 Y07894	Homo sapiens	gene 43.		
	100100	77	preproenkephalin (	1349	95
869	J00123	Homo sapiens	Human secreted protein sequence encoded by	1048	98
870	Y91632	Homo sapiens	Human secreted protein sequence encoded by	1040	1 70
		<del></del>	gene 25 SEQ ID NO:305.  GABA-alpha receptor beta-3 subunit	237	93
871	L04311	Homo sapiens	GABA-alpha receptor beta-3 subunit	960	94
872	Y29988	Homo sapiens	Human cytokine family member EF-7 protein.	1124	99
873	AF161382	Homo sapiens	HSPC264	464	100
874	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.		96
875	Y27572	Homo sapiens	Human secreted protein encoded by gene No. 6.	573	
876	M15530	Homo sapiens	B-cell growth factor	171	56
877	W63681	'Homo sapiens	Human secreted protein 1.	1652	99
878	L27867	Rattus	neurexophilin	1448	98
		norvegicus			
879	Y10835	Homo sapiens	Amino acid sequence of a human secreted	321	100
			protein.		
880	W88991	Homo sapiens	Polypeptide fragment encoded by gene 144.	936	100
881	AF118670	Homo sapiens	orphan G protein-coupled receptor	1971	100
882	AF208865	Homo sapiens	EDRF	528	100
883		Homo sapiens	cathepsin L	209	72
			04410951112	348	100
	Y18462		Human secreted protein clone dn10/3 12 Drotein		
	Y94950	Homo sapiens	Human secreted protein clone dh1073_12 protein		
884	Y94950	Homo sapiens	sequence SEQ ID NO:106.	404	100
884 885	Y94950 AF070661	Homo sapiens  Homo sapiens	sequence SEQ ID NO:106.  HSPC005		100
884 885 886	Y94950 AF070661 Y04315	Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23.	385	100
884 885 886 887	Y94950 AF070661 Y04315 X92744	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1	385 375	100
884 885 886 887	Y94950 AF070661 Y04315	Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23.  hBD-1  Human secreted protein sequence clone	385	100
884 885 886 887 888	Y94950 AF070661 Y04315 X92744 Y22496	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23.  hBD-1  Human secreted protein sequence clone cn621 8.	385 375 994	100 100 94
884 885 886 887 888	Y94950 AF070661 Y04315 X92744 Y22496 Y41293	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.	385 375 994 4595	100 100 94
884 885 886 887 888 889	Y94950  AF070661  Y04315  X92744  Y22496  Y41293  G03714	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.	385 375 994 4595	100 100 94 99 63
884 885 886 887 888 889	Y94950 AF070661 Y04315 X92744 Y22496 Y41293	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014	385 375 994 4595 147 1012	100 100 94 99 63 99
884 885 886 887 888 889 890	Y94950  AF070661  Y04315  X92744  Y22496  Y41293  G03714	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014  neuronal pentraxin II	385 375 994 4595 147 1012 2002	100 100 94 99 63 99 98
884 885 886 887 888 889 890 891	Y94950  AF070661  Y04315  X92744  Y22496  Y41293  G03714  AF208856  U29195	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014  neuronal pentraxin II  Burkitt lymphoma receptor 1	385 375 994 4595 147 1012 2002 1953	100 100 94 99 63 99 98 100
884 885 886 887 888 889 890 891 892 893	Y94950  AF070661  Y04315  X92744  Y22496  Y41293  G03714  AF208856  U29195  X68149	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014  neuronal pentraxin II  Burkitt lymphoma receptor 1	385 375 994 4595 147 1012 2002	100 100 94 99 63 99 98
884 885 886 887 888 889 890 891 892 893	Y94950  AF070661  Y04315  X92744  Y22496  Y41293  G03714  AF208856  U29195	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014  neuronal pentraxin II  Burkitt lymphoma receptor 1  Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.	385 375 994 4595 147 1012 2002 1953 537	100 100 94 99 63 99 98 100
884 885 886 887 888 889 890 891 892 893 894	Y94950  AF070661 Y04315 X92744 Y22496  Y41293 G03714 AF208856 U29195 X68149 Y94914	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014  neuronal pentraxin II  Burkitt lymphoma receptor 1  Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.	385 375 994 4595 147 1012 2002 1953	100 100 94 99 63 99 98 100
884 885 886 887 888 889 890 891 892 893 894	Y94950  AF070661 Y04315 X92744 Y22496  Y41293 G03714 AF208856 U29195 X68149 Y94914  W61630	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014  neuronal pentraxin II  Burkitt lymphoma receptor 1  Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.  Clone HNFGW06 of EGFR receptor family.	385 375 994 4595 147 1012 2002 1953 537	100 100 94 99 63 99 98 100 100
884 885 886 887 888 889 890 891 892 893 894 895 896	Y94950  AF070661 Y04315 X92744 Y22496  Y41293 G03714 AF208856 U29195 X68149 Y94914  W61630 M24110	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014  neuronal pentraxin II  Burkitt lymphoma receptor 1  Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.  Clone HNFGW06 of EGFR receptor family.  GOS19-2 peptide precursor	385 375 994 4595 147 1012 2002 1953 537 326 481	100 100 94 99 63 99 98 100 100
884 885 886 887 888 889 890 891 892 893 894	Y94950  AF070661 Y04315 X92744 Y22496  Y41293 G03714 AF208856 U29195 X68149 Y94914  W61630	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	sequence SEQ ID NO:106.  HSPC005  Human secreted protein encoded by gene 23. hBD-1  Human secreted protein sequence clone cn621_8.  Human soluble protein ZTMPO-1.  Human secreted protein, SEQ ID NO: 7795.  BM-014  neuronal pentraxin II  Burkitt lymphoma receptor 1  Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.  Clone HNFGW06 of EGFR receptor family.	385 375 994 4595 147 1012 2002 1953 537	100 100 94 99 63 99 98 100 100

901 M 902 W 903 G( 904 Y( 905 A) 906 A 907 A 908 A 909 Y 910 A 911 Y 912 Z 913 Y 914 G 915 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 D 924 Y 925 A 926 C 927 Y 928 Y 928 Y 929 A 930 A	A27288 V85737 J01349 J00261 JF039688 JB007836 JB007836 JB017507 JK000056 JK6299 JF231023 JY14134 JF172854 JK172854 JK172	Homo sapiens Homo sapiens	Sequence of human lipocortin. oncostatin M Polypeptide with transmembrane domain. Human secreted protein, SEQ ID NO: 5430. Human secreted protein encoded by gene 4. antigen NY-CO-3 Hic-5 Apg12 unnamed protein product Human secreted protein HFOXB55, SEQ ID NO:214. protocadherin Flamingo I Vascular endothelial cell growth inhibitor beta protein sequence. Human GDF-3 (hGDF-3) polypeptide encoding cDNA. SEQ ID NO 475 from WO9922243. Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F22162 1 ST7 protein Human signal peptide containing protein HSPP-62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein c17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56. down-regulated in gastric cancer Human secreted protein, SEQ ID NO: 7449.	Score 1835 1297 749 650 1133 771 2544 224 1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785 55	100 99 100 99 99 99 100 100 100
March   Marc	A27288 V85737 J01349 J00261 JF039688 JB007836 JB007836 JB017507 JK000056 JK6299 JF231023 JY14134 JF172854 JK172854 JK172	Homo sapiens Homo sapiens	oncostatin M Polypeptide with transmembrane domain. Human secreted protein, SEQ ID NO: 5430. Human secreted protein encoded by gene 4. antigen NY-CO-3 Hic-5 Apg 12 unnamed protein product Human secreted protein HFOXB55, SEQ ID NO:214. protocadherin Flamingo 1 Vascular endothelial cell growth inhibitor beta protein sequence. Human GDF-3 (hGDF-3) polypeptide encoding cDNA. SEQ ID NO 475 from WO9922243. Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F722162_1 ST7 protein Human signal peptide containing protein HSPP-62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	1297 749 650 1133 771 2544 224 1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	99 100 99 99 99 100 100 100 98 100 100 100 48 90 99 100 99 100 88 100 100 98
1002   W   1002   W   1003   Graph	V85737  V85737  V85737  V85737  V81349  V80261  V8039688  V8007836  V800056  V86299  AF231023  V14134  Z90420  Y19757  G03172  U14971  AF172854  AC005525  AF166350  Y87285  Y36131  AF193766  Y95013  X75208  Y96202  AB039886  G03368  Y48606	Homo sapiens Homo sapiens	Polypeptide with transmembrane domain.  Human secreted protein, SEQ ID NO: 5430.  Human secreted protein encoded by gene 4.  antigen NY-CO-3  Hic-5  Apg 12  unnamed protein product  Human secreted protein HFOXB55, SEQ ID  NO:214.  protocadherin Flamingo 1  Vascular endothelial cell growth inhibitor beta protein sequence.  Human GDF-3 (hGDF-3) polypeptide encoding cDNA.  SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253.  ribosomal protein S9  cardiotrophin-like cytokine CLC  F22162_1  ST7 protein  Human signal peptide containing protein HSPP-62 SEQ ID NO:62.  Human secreted protein #3.  cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66.  protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.	749 650 1133 771 2544 224 1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	100 99 99 99 100 100 98 100 100 100 48 90 99 100 99 100 88 100 100 99 100 100
903 G0 904 Y0 905 Al 906 A 907 A 908 A 909 Y 910 A 911 Y 912 Z 913 Y 914 G 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 X 924 Y 925 A 926 G 927 X 928 Y 929 A 930 A 931 X 932 G	101349 100261 115039688 115039688 115039688 115039688 115039688 115039688 115039688 115039688 11503968 11503968 11503968 11503172	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 5430.  Human secreted protein encoded by gene 4.  antigen NY-CO-3  Hic-5  Apg 12  unnamed protein product  Human secreted protein HFOXB55, SEQ ID  NO:214.  protocadherin Flamingo I  Vascular endothelial cell growth inhibitor beta protein sequence.  Human GDF-3 (hGDF-3) polypeptide encoding cDNA.  SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253.  ribosomal protein S9  cardiotrophin-like cytokine CLC  F22162_1  ST7 protein  Human signal peptide containing protein HSPP-62 SEQ ID NO:62.  Human secreted protein #3.  cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66.  protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.	650 1133 771 2544 224 1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	99 99 99 100 100 98 100 100 100 100 48 90 99 100 99 100 88 100 100 100 98
1004   Y(0)	700261 AF039688 AB007836 AB017507 AK000056 786299 AF231023 Y14134 Z90420 Y19757 G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 4. antigen NY-CO-3 Hic-5 Apg 12 unnamed protein product Human secreted protein HFOXB55, SEQ ID NO:214. protocadherin Flamingo 1 Vascular endothelial cell growth inhibitor beta protein sequence. Human GDF-3 (hGDF-3) polypeptide encoding cDNA. SEQ ID NO 475 from WO9922243. Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F72162_1 ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	1133 771 2544 224 1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	99 99 100 100 98 100 100 100 100 48 90 99 100 99 100 88 100 100 100 98
905 AJ 906 A 906 A 907 A 908 A 909 Y 910 A 911 Y 912 Z 913 Y 914 G 915 U 915 U 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 X 924 Y 925 A 926 C 927 X 928 X 929 A 930 A 931 X 932 C	AF039688 AB007836 AB017507 AK000056 AF231023 AF231023 AF13134 AF19757 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens	antigen NY-CO-3  Hic-5  Apg 12  unnamed protein product  Human secreted protein HFOXB55, SEQ ID  NO:214.  protocadherin Flamingo 1  Vascular endothelial cell growth inhibitor beta protein sequence.  Human GDF-3 (hGDF-3) polypeptide encoding cDNA.  SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253.  ribosomal protein S9  cardiotrophin-like cytokine CLC  F22162_1  ST7 protein  Human signal peptide containing protein HSPP- 62 SEQ ID NO:62.  Human secreted protein #3.  cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.	771 2544 224 1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	99 100 100 98 100 100 100 100 48 90 99 100 99 100 88 100 100 100 98
906 A 907 A 908 A 909 Y 910 A 911 Y 912 Z 913 Y 914 G 915 U 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 X 924 Y 925 A 926 G 927 X 928 Y 929 A 930 A	AB007836 AB017507 AK000056 AB017507 AK000056 AF231023 AF231023 AF131023 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens	Hic-5 Apg 12 unnamed protein product Human secreted protein HFOXB55, SEQ ID NO:214. protocadherin Flamingo 1 Vascular endothelial cell growth inhibitor beta protein sequence. Human GDF-3 (hGDF-3) polypeptide encoding cDNA. SEQ ID NO 475 from WO9922243. Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F22162 1 ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	2544 224 1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	100 100 98 100 99 100 100 100 48 90 99 100 99 100 88 100 100 100 98
906 A 907 A 908 A 909 Y 910 A 911 Y 912 Z 913 Y 914 G 915 U 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 X 924 Y 925 A 926 G 927 X 928 Y 929 A 930 A	AB017507 AK000056 786299 AF231023 Y14134 Z90420 Y19757 G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens	unnamed protein product Human secreted protein HFOXB55, SEQ ID NO:214. protocadherin Flamingo I Vascular endothelial cell growth inhibitor beta protein sequence. Human GDF-3 (hGDF-3) polypeptide encoding cDNA. SEQ ID NO 475 from WO9922243. Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F22162 I ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	224 1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	100 98 100 99 100 100 100 48 90 99 100 99 100 88 100 100 100 98
907 A 908 A 909 Y 910 A 911 Y 912 Z 913 Y 914 G 915 U 915 U 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 Y 924 Y 925 A 926 G 927 Y 928 Y 929 A 930 A	AK000056 (86299 AF231023 Y14134 Z90420 Y19757 G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	unnamed protein product Human secreted protein HFOXB55, SEQ ID NO:214. protocadherin Flamingo I Vascular endothelial cell growth inhibitor beta protein sequence. Human GDF-3 (hGDF-3) polypeptide encoding cDNA. SEQ ID NO 475 from WO9922243. Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F22162_1 ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	1537 427 7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	98 100 99 100 100 100 48 90 99 100 99 100 88 100 100 100 98
908 A 909 Y 910 A 911 Y 912 Z 913 Y 914 G 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 X 924 Y 925 A 926 G 927 X 928 X 929 A 930 A 931 X 932 G	AK000056 (86299 AF231023 Y14134 Z90420 Y19757 G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	unnamed protein product Human secreted protein HFOXB55, SEQ ID NO:214. protocadherin Flamingo I Vascular endothelial cell growth inhibitor beta protein sequence. Human GDF-3 (hGDF-3) polypeptide encoding cDNA. SEQ ID NO 475 from WO9922243. Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F22162_1 ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	100 99 100 100 100 48 90 99 100 99 100 88 100 100 100 98
909 Y 910 A 911 Y 912 Z 913 Y 914 G 915 U 915 U 916 A 917 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 Y 924 Y 925 A 926 G 927 Y 928 Y 929 A 930 A 931 Y 932 G	(86299 AF231023 Y14134 290420 Y19757 G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein HFOXB55, SEQ ID NO:214.  protocadherin Flamingo 1  Vascular endothelial cell growth inhibitor beta protein sequence.  Human GDF-3 (hGDF-3) polypeptide encoding cDNA.  SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253.  ribosomal protein S9  cardiotrophin-like cytokine CLC  F22162 1  ST7 protein  Human signal peptide containing protein HSPP-62 SEQ ID NO:62.  Human secreted protein #3.  cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66.  protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.	7393 1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	99 100 100 100 48 90 99 100 99 100 88 100 100 100 98
911 Y 912 Z 913 Y 914 G 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 927 Y 928 Y 929 A 930 A	Y14134 Z290420 Y19757 G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Vascular endothelial cell growth inhibitor beta protein sequence.  Human GDF-3 (hGDF-3) polypeptide encoding cDNA.  SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F22162 1 ST7 protein  Human signal peptide containing protein HSPP-62 SEQ ID NO:62.  Human secreted protein #3. cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	1319 1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	100 100 48 90 99 100 99 100 88 100 100 98
911 Y 912 Z 913 Y 914 G 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 927 Y 928 Y 929 A 930 A	Y14134 Z290420 Y19757 G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Vascular endothelial cell growth inhibitor beta protein sequence.  Human GDF-3 (hGDF-3) polypeptide encoding cDNA.  SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F22162 1 ST7 protein  Human signal peptide containing protein HSPP-62 SEQ ID NO:62.  Human secreted protein #3. cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	1950 1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	100 100 48 90 99 100 99 100 88 100 100 100 98
912 Z 913 Y 914 G 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 926 G 927 Y 928 Y 929 A 930 A	290420 Y19757 303172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	protein sequence.  Human GDF-3 (hGDF-3) polypeptide encoding cDNA.  SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F22162 1 ST7 protein  Human signal peptide containing protein HSPP-62 SEQ ID NO:62.  Human secreted protein #3. cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	100 48 90 99 100 99 100 88 100 100 100 98
913 Y 914 G 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 926 G 927 Y 930 A 931 Y 932 G	Y19757 G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	cDNA.  SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253.  ribosomal protein S9 cardiotrophin-like cytokine CLC F22162_1 ST7 protein  Human signal peptide containing protein HSPP- 62 SEQ ID NO:62.  Human secreted protein #3. cytokine-like protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	1361 112 886 1204 1963 4711 430 465 724 357 5256 813 785	100 48 90 99 100 99 100 88 100 100 100 98
914 G 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 926 G 927 S 928 Y 929 A 930 A	G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	SEQ ID NO 475 from WO9922243.  Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F722162_1 ST7 protein  Human signal peptide containing protein HSPP- 62 SEQ ID NO:62.  Human secreted protein #3. cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56.	112 886 1204 1963 4711 430 465 724 357 5256 813 785	48 90 99 100 99 100 88 100 100 100 98
914 G 915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 926 G 927 S 928 Y 929 A 930 A	G03172 U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 7253. ribosomal protein S9 cardiotrophin-like cytokine CLC F72162_1 ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56. down-regulated in gastric cancer	886 1204 1963 4711 430 465 724 357 5256 813 785	90 99 100 99 100 88 100 100 100 98
915 U 916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 926 C 927 Y 928 Y 929 A 930 A	U14971 AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	ribosomal protein S9 cardiotrophin-like cytokine CLC F22162_1 ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56. down-regulated in gastric cancer	1204 1963 4711 430 465 724 357 5256 813 785	99 100 99 100 88 100 100 100 98
916 A 917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 926 C 927 Y 928 Y 929 A 930 A	AF172854 AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	cardiotrophin-like cytokine CLC F22162_1 ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56. down-regulated in gastric cancer	1204 1963 4711 430 465 724 357 5256 813 785	100 99 100 88 100 100 100 98
917 A 918 A 919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 926 C 927 Y 928 Y 929 A 930 A	AC005525 AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	F22162_1 ST7 protein Human signal peptide containing protein HSPP- 62 SEQ ID NO:62. Human secreted protein #3. cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56. down-regulated in gastric cancer	1963 4711 430 465 724 357 5256 813 785	99 100 88 100 100 100 98
918 A 919 Y 920 Y 921 A 922 Y 923 X 924 Y 925 A 926 C 927 X 928 Y 930 A 931 X 932 C	AF166350 Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	ST7 protein  Human signal peptide containing protein HSPP- 62 SEQ ID NO:62.  Human secreted protein #3.  cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66.  protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.  down-regulated in gastric cancer	4711 430 465 724 357 5256 813 785	100 88 100 100 100 98
919 Y 920 Y 921 A 922 Y 923 > 924 Y 925 A 926 C 927 Y 928 Y 930 A 931 S 932 C	Y87285 Y36131 AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human signal peptide containing protein HSPP-62 SEQ ID NO:62.  Human secreted protein #3.  cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66.  protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.  down-regulated in gastric cancer	430 465 724 357 5256 813 785	100 88 100 100 100 98
921 A 922 Y 923 D 924 Y 925 A 926 G 927 Y 928 Y 930 A 931 Y 932 G	AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein #3.  cytokine-like protein C17  Human secreted protein vc48_1, SEQ ID NO:66.  protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.  down-regulated in gastric cancer	724 357 5256 813 785	100 100 100 98
921 A 922 Y 923 A 924 Y 925 A 926 G 927 Y 928 Y 930 A 931 Y 932 G	AF193766 Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	cytokine-like protein C17 Human secreted protein vc48_1, SEQ ID NO:66. protein tyrosine kinase-receptor IkappaB kinase (IKK) binding protein, Y2H56. down-regulated in gastric cancer	724 357 5256 813 785	100 100 100 98
922 Y 923 Z 924 Y 925 A 926 C 927 Y 928 Y 929 A 930 A 931 Y 932 C	Y95013 X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human secreted protein vc48_1, SEQ ID NO:66.  protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.  down-regulated in gastric cancer	357 5256 813 785	100 100 98
923	X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens	protein tyrosine kinase-receptor  IkappaB kinase (IKK) binding protein, Y2H56.  down-regulated in gastric cancer	5256 813 785	100 98
923	X75208 Y96202 AB039886 G03368 Y48606	Homo sapiens Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	813 785	98
924 Y 925 A 926 C 927 Y 928 Y 929 A 930 A 931 Y 932 C	AB039886 G03368 Y48606	Homo sapiens	down-regulated in gastric cancer	785	
925	AB039886 G03368 Y48606		down-regulated in gastric cancer		/8
926 (6 927 ) 928 ) 929 (7 930 (7 931 ) 932 (6	G03368 Y48606		The secreted protein SEO ID NO: 7449	55	- 50
927 S 928 S 929 A 930 A 931 S 932 G	Y48606	I TAGITIO DEPICES	Human Secreted protein, one The Tro. 7 10.		50
928 Y 929 A 930 A 931 Y 932 G		Homo sapiens	Human breast tumour-associated protein 67.	539	100
929 A 930 A 931 Y 932 G	Y36151	Homo sapiens	Human secreted protein #23.	668	100
930 A 931 N 932 G	AF110399	Homo sapiens	elongation factor Ts	1666	100
932 (	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2763	99
932 (	Y73328	Homo sapiens	HTRM clone 082843 protein sequence.	931	100
	G01959	Homo sapiens	Human secreted protein, SEQ ID NO: 6040.	274	100
		Homo sapiens	B-cell receptor associated protein	1469	100
	U47924		Human secreted protein, SEQ ID NO: 7908.	529	93
	G03827	Homo sapiens	mitochondrial ABC transporter 3	196	63
	AB039371	Homo sapiens	rab8	1064	100
936	X56385	Canis	rado		
937	B08906	familiaris Homo sapiens	Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.	117	44
		<del>  ,,                                  </del>	alpha-1 acid glycoprotein precursor	1064	99
	M13692 Y53886	Homo sapiens Homo sapiens	A suppressor of cytokine signalling protein	515	42
940	Y16630	Homo sapiens		1904	99
941	AC005102	Homo sapiens	(PAR). small inducible cytokine subfamily A member	627	99
			24	1289	81
942	M12886	Homo sapiens		1049	98
943	AF226046	Homo sapiens	GK003		100
944	Y36078	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 463.	.L	
945	M22877	Homo sapiens	cytochrome c	565	100
	W67869	Homo sapiens	Human secreted protein encoded by gene 63	551	93
947	W67859	Homo sapiens	1,11,	283	100
		<del> </del>	5.000 50	789	100
	W85726	Homo sapiens	<del></del>	4236	100
949 950	AJ242015	Homo sapiens	LANGUM II DECIRITI	567	99

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:	. 10.			1314	100
	AF110645	Homo sapiens	candidate tumor suppressor p33 ING1 homolog		70
51	Y36111	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 496.	402	
	15010100	Homo sapiens	APC10	990	100
53	AB012109		transmembrane protein BRI	1405	100
54	AF246221	Homo sapiens	putative transmembrane GTPase	1883	100
55	AF054986	Homo sapiens	Human secreted protein fg949_3.	1879	100
56	W74726	Homo sapiens	Human viral receptor protein (ACVRP).	1581	100
957	Y27096	Homo sapiens	Human viral receptor protest (NOVIG).	1920	100
58	AJ222967	Homo sapiens	cystinosin 1500 3 matein	587	100
559	Y53052	Homo sapiens	Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.		100
250	G02694	Homo sapiens	Human secreted protein, SEQ ID NO: 6775.	283	96
960	AF151855	Homo sapiens	CGI-97 protein	1214	65
961	U26592	Homo sapiens	diabetes mellitus type I autoantigen	250	
962		Homo sapiens	dJ475B7.2 (novel protein)	3796	100
963	AL050306	Homo sapiens	PTD004	2089	100
964 965	AF078859 AB020315	Homo sapiens	homologue of mouse dkk-1 gene: Acc#	1466	100
		<u> </u>	AF030433 precursor polypeptide (AA -22 to 1185)	6580	99
966	X04571	Homo sapiens	hepatocellular carcinoma antigen gene 520	993	99
967	AF146019	Homo sapiens	hepatocellular carcillolla antigen gene 320	632	100
968	AF071002	Homo sapiens	minK-related peptide 1; MiRPI	3545	100
969	AB021227	Homo sapiens	membrane-type-5 matrix metalloproteinase	1579	100
970	AF180920	Homo sapiens	cyclin L ania-6a	5621	99
971	AF105365	Homo sapiens	K-Cl cotransporter KCC4	739	100
972	AF083248	Homo sapiens	ribosomal protein L26 homolog	6295	100
973	AJ132429	Homo sapiens	hyperpolarization-activated cyclic nucleotide gated cation channel hHCN4		100
254	W61619	Homo sapiens	Clone HTPFF86 of TM4SF superfamily.	454	100
974	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	
975		Homo sapiens	ABCA1	11763	99
976	AF275948	Homo sapiens	everine/alutamate transporter	2552	100
977 978	AB026891 AF117657	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP80	3348	99
979	AF044201	Rattus	neural membrane protein 35; NMP35	1570	92
		norvegicus	neuroendocrine-specific protein-like protein 1	1170	99
980	AF119297	Homo sapiens	potassium channel modulatory factor	1983	99
981	AF155652	Homo sapiens	Human stomach carcinoma clone HP10412-	1553	99
982	W88499	Homo sapiens	encoded protein.	2012	98
983	Z.56281	Homo sapiens	interferon regulatory factor 3	2160	100
984	AB026125	Homo sapiens	ART-4	172	70
985	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.		
	AD00000	Homo sapiens	b-chemokine receptor CCR4	1895	100
986	AB023888	Homo sapiens	Human H1075-1 secreted protein 5' end.	712	100
987 988	W27291 AF153450	Manduca	juvenile hormone esterase binding protein	226	32
		sexta	Human secreted protein, SEQ ID NO: 7778.	194	88
989 990	G03697 AF204159	Homo sapiens Homo sapiens	potassium large conductance calcium-activated	1486	100
	1		channel beta 3a subunit	558	99
991	G02061 AL031266	Homo sapiens Caenorhabditi	Human secreted protein, SEQ ID NO: 6142.  VM106R.1	327	40
992	AL031200	s elegans		1.535	
	126740	Homo sapiens	Membrane-bound protein PRO1124.	4730	99
993	Y66749	Homo sapiens		141	77
994	G01246		corin	5811	99
995 996	AF133845 AF117756	Homo sapiens Homo sapiens		4999	100
			11	284	93
997	W62066	Homo sapiens		725	100
998	Y87173	Homo sapiens	NO:212	1654	99
l	J	177	Amino acid sequence of protein PRO263.		
000	V13370	Homo sapiciis			
999	Y13379 Y95008	Homo sapiens Homo sapiens		676 1747	100

SEQ	Accession	Species	Description	Smith-	% Identity
D	No.			Waterman	Identity
NO:				Score 398	96
1002	G01234	Homo sapiens	Human secreted protein, SEQ ID NO: 5315.	2150	100
003	W73420	Homo sapiens	Human secreted protein encoded by Gene No.	2130	1 100
			24.	742	100
1004	X12791	Homo sapiens	19kD SRP-protein (AA 1 - 144)	642	100
005	M23323	Homo sapiens	membrane protein		98
1006	X63745	Homo sapiens	KDEL receptor	326	99
1007	Y35997	Homo sapiens	Extended human secreted protein sequence, SEQ	824	99
			ID NO. 382.	02	35
1008	AB032918	Hylobates moloch	dopamine receptor D4	92	99
1009	Y91680	Homo sapiens	Human secreted protein sequence encoded by gene 81 SEQ ID NO:353.	1372	
1010	AL136125	Homo sapiens	dJ304B14.1 (novel protein)	825	98
1011	G03733	Homo sapiens	Human secreted protein, SEQ ID NO: 7814.	379	98
1012	Y17531	Homo sapiens	Human secreted protein clone BL205 14 protein.	818	97
1013	G00724	Homo sapiens	Human secreted protein, SEQ ID NO: 4805.	462	100
1014	AF288092	Naegleria gruberi	haem lyase	114	37
1015	AB045292	Homo sapiens	M83 protein	3867	99
1015	X15940	Homo sapiens	ribosomal protein L31 (AA 1-125)	644	100
1017	Y94873	Homo sapiens	Human protein clone HP02632.	1876	100
1017	AL024498	Homo sapiens	dJ417M14.1 (novel protein)	589	100
1019	X83425	Homo sapiens	Lutheran blood group glycoprotein	3054	99
1020	W03516	Homo sapiens	Prostaglandin DP receptor.	1864	100
1020	G03960	Homo sapiens	Human secreted protein, SEQ ID NO: 8041.	398	100
1022	Y91689	Homo sapiens	Human secreted protein sequence encoded by gene 93 SEQ ID NO:362.	768	100
1022	AE000660	Homo sapiens	hADV36S1	573	100
1023 1024	AF132965	Home sapiens	CGI-31 protein	1550	100
1024	W92380	Homo sapiens	Human TR-interacting protein S103a.	1466	97
1026	R66278	Homo sapiens	Therapeutic polypeptide from glioblastoma cell line.	830	100
1027	X65614	Homo sapiens	S100P calcium-binding protein	476	100
1027	Y41741	Homo sapiens	Human PRO704 protein sequence.	1323	100
1028		Homo sapiens	RAMPI	806	100
1029	AJ001014	Homo sapiens	Human secreted protein 2.	1354	99
1030	W63682	Homo sapiens	unnamed protein product	766	100
1031	AK023007	Homo sapiens	Human SR-BI class B scavenger.	2672	99
1032 1033	W97900 Y82453	Homo sapiens	Human TGC-440 secretory protein SEQ ID NO:1.	639	99
1034	Y73473	Homo sapiens	Human secreted protein clone yd178_1 protein sequence SEQ ID NO:168.	752	93
1035	Y86468	Homo sapiens	Human gene 48-encoded protein fragment, SEQ ID NO:383.	96	90
1055	1100813	Homo sapiens	mitochondrial ATP synthase subunit 9 precursor	698	100
1036	U09813	Homo sapiens	calpain	3699	99
1037	AJ242832	Homo sapiens	acetylcholine receptor epsilon subunit CHRNE	2574	100
1038	X66403		polyhomeotic 2	1310	100
1039	AJ242730	Homo sapiens Mus	DNA binding protein DESRT	1453	80
1040 -	AF169968	musculus	Division & Process	1	
1041	X52563	Bos taurus	permability increasing protein	383	29
1041		Homo sapiens	Human secreted protein, SEO ID NO: 4449.	75	50
1042	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	60	53
1043	G02532	Homo sapiens	interleukin 8 receptor B	1850	100
1044	M94582		bG256O22.1 (similar to IGFALS (insulin-like	1704	50
1045	AL080239	Homo sapiens	growth factor binding protein, acid labile subunit))		
	1.51222	17	HSPC040 protein	580	100
1046 1047	AF125101 W74809	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 81	176	100
			clone HMWDN32.	2201	100
1048	AL022238	Homo sapiens		1559	99
1049		Homo sapiens	Secreted protein encoded by gene 134 clone HAIBP89.		
	1	Homo sapiens		2820	100

				Smith-	1 %
SEQ	Accession	Species	Description	Waterman	Identity
-	No.	•		Score	Identity
10:					98
051	W78324	Homo sapiens	Fragment of human secreted protein encoded by	1318	98
150	¥7 / 632-7	7201110 01111111111111111111111111111111	gene 81		100
062	Y21851	Homo sapiens	Human signal peptide-contianing protein (SIGP)	1643	95
052	121031	110tho suprais	(clone ID 2328134).		
		Arabidopsis	putative protein	661	62
053	AL163815		putative protein		
		thaliana	Human secreted protein encoded by gene 77.	262	100
1054	Y76200	Homo sapiens	TC10-like Rho GTPase	1160	100
055	AJ276567	Homo sapiens	Human secreted protein encoded by gene No. 54.	154	96
056	Y27620	Homo sapiens	Human secreted protein encoded by gene 140: 54.	745	100
1057	D14530	Homo sapiens	ribosomal protein	1132	100
1058	AF132000	Homo sapiens	TADA1 protein	920	100
1059	AL031778	Homo sapiens	dJ34B21.1 (novel BZRP (benzodiazapine	920	100
. [	12001111		receptor (peripheral) (MBR, PBR, PBKS, IBP,	1	1
}			Isoquinoline-binding protein)) LIKE protein)		<del>    -   -     -                        </del>
1000	AF227135	Homo sapiens	candidate taste receptor T2R9	134	33
1060		Homo sapiens	Human secreted protein encoded by gene No. 9.	1392	100
1061	Y27575		HB15	1088	100
1062	Z11697	Homo sapiens	putative transmembrane protein	819	100
1063	AF123757	Homo sapiens	novel retinal pigment epithelial cell protein	2932	99
1064	AF155135	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
1065	Y41674	Homo sapiens	Human channel-related molecule HCRV12.	2575	100
1066	AJ250042	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	770	85
1067	Y36087	Homo sapiens	Extended human secreted protein sequence, SEQ	1 '''	1 33
			ID NO. 472.	301	100
1068	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein	301	100
1000	174757		paguance SEO ID NO:124.	<del></del>	
1069	Y94959	Homo sapiens	Human secreted protein clone mc300_1 protein	301	100
1009	1 34333	110mo supreme	sequence SEO ID NO:124.		
1000	111/6/525	Homo sapiens	Human leukocyte cell clone HP00804 protein.	2014	99
1070	W64535		pot. ORF III	148	50
1071	X03145	Homo sapiens	dJ889M15.3 (novel protein)	821	91
1072	AL031177	Homo sapiens	dJ889M13.3 (nover protein)	249	62
1073	X82200	Homo sapiens	gpStaf50 Human secreted protein, SEQ ID NO: 7294.	99	47
1074	G03213	Homo sapiens	Human secreted protein, SEQ ID NO. 1234.	506	55
1075	Y36233	Homo sapiens	Human secreted protein encoded by gene 10.	424	98
1076	G03187	Homo sapiens	Human secreted protein, SEQ ID NO: 7268.	332	76
1077	L25899	Homo sapiens	ribosomal protein L10		97
1078	Y91447	Homo sapiens	Human secreted protein sequence encoded by	898	197
1070	1,77		gene 48 SEQ ID NO:168.	1	
1079	G01862	Homo sapiens	Human secreted protein, SEQ ID NO: 5943.	290	89
	AB039723	Homo sapiens	WNT receptor frizzled-3	1376	92
1080			Na/PO4 cotransporter homolog	269	100
1081	AB020527	Homo sapiens	ribosmal protein small subunit	499	80
1082	L13802	Homo sapiens	Human secreted protein encoded by gene 42	143	81
1083	W75098	Homo sapiens		1	
		_1	clone HSXB125.	83	51
1084	G03564	Homo sapiens		88	43
1004			1 TT seemend protein SHI HI NU A144		
	G04063	Homo sapiens		1 174	64
1085	G04063		PP 00657	124	64
1085 1086	G04063 AF090942	Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598.	129	41
1085 1086 1087	G04063 AF090942 G00517	Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172.	129 126	41 36
1085 1086 1087 1088	G04063 AF090942 G00517 G04091	Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. Genrotein coupled receptor 14	129 126 364	41 36 82
1085 1086 1087 1088 1089	G04063 AF090942 G00517 G04091 AF140631	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14	129 126 364 114	36 82 32
1085 1086 1087 1088 1089 1090	G04063 AF090942 G00517 G04091 AF140631 G04063	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144.	129 126 364	41 36 82
1085 1086 1087 1088 1089 1090	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp.	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein	129 126 364 114	36 82 32
1085 1086 1087 1088 1089 1090	G04063 AF090942 G00517 G04091 AF140631 G04063	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone	129 126 364 114 146	36 82 32 83
1085 1086 1087 1088 1089 1090	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41.	129 126 364 114 146 405	36 82 32 83
1085 1086 1087 1088 1089 1090	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41. Secreted protein clone fh123_5.	129 126 364 114 146 . 405	36 82 32 83 100
1085 1086 1087 1088 1089 1090 1091 1092	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41. Secreted protein clone fh123_5. Human secreted protein clone pm514_4 protein	129 126 364 114 146 405	41 36 82 32 83 100
1085 1086 1087 1088 1089 1090 1091 1092	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41. Secreted protein clone fh123_5. Human secreted protein clone pm514_4 protein	129 126 364 114 146 405 4358 1013	41 36 82 32 83 100 97 99
1085 1086 1087 1088 1089 1090 1091 1092	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708 W85612 Y53012	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41. Secreted protein clone fh123_5. Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30. Human cancer associated antigen precursor from	129 126 364 114 146 405 4358 1013	36 82 32 83 100
1085 1086 1087 1088 1089 1090 1091 1092	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens	PRO0657  Human secreted protein, SEQ ID NO: 4598.  Human secreted protein, SEQ ID NO: 8172.  G-protein coupled receptor 14  Human secreted protein, SEQ ID NO: 8144.  LMW G-protein  Secreted protein encoded by gene 175 clone  HEMAM41.  Secreted protein clone fh123_5.  Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30.  Human cancer associated antigen precursor from	129 126 364 114 146 405 4358 1013	41 36 82 32 83 100 97 99
1085 1086 1087 1088 1089 1090 1091 1092 1093 1094	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708 W85612 Y53012	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41. Secreted protein clone fh123_5. Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30. Human cancer associated antigen precursor from clone NY-REN-62.	129 126 364 114 146 405 4358 1013	41 36 82 32 83 100 97 99 100 60
1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708 W85612 Y53012 Y92345 AF090942	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO0657  Human secreted protein, SEQ ID NO: 4598.  Human secreted protein, SEQ ID NO: 8172.  G-protein coupled receptor 14  Human secreted protein, SEQ ID NO: 8144.  LMW G-protein  Secreted protein encoded by gene 175 clone  HEMAM41.  Secreted protein clone fh123_5.  Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30.  Human cancer associated antigen precursor from clone NY-REN-62.  PRO0657	129 126 364 114 146 405 4358 1013	41 36 82 32 83 100 97 99 100 60 58
1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708 W85612 Y53012 Y92345 AF090942 L24521	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41. Secreted protein clone fh123_5. Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30. Human cancer associated antigen precursor from clone NY-REN-62. PRO0657 transformation-related protein	129 126 364 114 146 . 405 4358 1013 409	41 36 82 32 83 100 97 99 100 60
1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708 W85612 Y53012 Y92345 AF090942 L24521 X56932	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41. Secreted protein clone fh123_5. Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30. Human cancer associated antigen precursor from clone NY-REN-62. PRO0657 transformation-related protein 23 kD highly basic protein	129 126 364 114 146 405 4358 1013 409 147 166 490	41 36 82 32 83 100 97 99 100 60 58
1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097	G04063 AF090942 G00517 G04091 AF140631 G04063 S72304 W88708 W85612 Y53012 Y92345 AF090942 L24521	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus sp. Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO0657 Human secreted protein, SEQ ID NO: 4598. Human secreted protein, SEQ ID NO: 8172. G-protein coupled receptor 14 Human secreted protein, SEQ ID NO: 8144. LMW G-protein Secreted protein encoded by gene 175 clone HEMAM41. Secreted protein clone fh123_5. Human secreted protein clone pm514_4 protein sequence SEQ ID NO:30. Human cancer associated antigen precursor from clone NY-REN-62. PRO0657 transformation-related protein 23 kD highly basic protein Human secreted protein, SEQ ID NO: 8144.	129 126 364 114 146 405 4358 1013 409 147 166	41 36 82 32 83 100 97 99 100 60 58 70

SEQ ID	Accession No.	Species	Description	Smith- Waterman Score	% Identity
NO:				183	72
1101	AF119851		PRO1722	207	62
1102	G04086	Homo sapiens	Human secreted protein, SEQ ID NO: 8167.	91	52
1103	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	128	69
1104	X74856	Mus musculus	ribosomal protein L28		
	002700	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	130	62
1105	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	48
1106	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7121.	69	43
1107	G03040		HCF-binding transcription factor Zhangfei	744	99
1108	AF039942	Homo sapiens	high affinity immunoglobulin epsilon receptor	738	94
1109	AF201951	Homo sapiens	beta subunit	223	79
1110	AF111108	Mus musculus	transient receptor potential 2		59
1111	AF119900	Homo sapiens	PRO2822	144	
1112	Y16589	Homo sapiens	A protein that interacts with presentlins.	265	39
1112	G02872	Homo sapiens	Human secreted protein, SEO ID NO: 6953.	178	67
1114	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	164	63
		110	Human secreted protein encoded from gene 1.	1217	99
1115	Y30811	Homo sapiens	APEG precursor protein	130	40
1116	X51394	Xenopus laevis		442	65
1117	M27826	Homo sapiens	neutral protease large subunit	72	60
1118	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	491	97
1119	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.		97
1120	Y35906	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 155.	244	
	002214	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	65
1121	G03714	Homo sapiens	Human secreted protein encoded by gene 81.	110	90
1122	Y00337	Homo sapiens	two pore domain K+ channel; TASK-2	703	94
1123	AF084830	Homo sapiens	membrane interacting protein of RGS16	442	88
1124	AF212862		Human secreted protein from clone CW795 2.	191	53
1125	W64469	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	154	100
1126	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	165	100
1127 1128	G01361 Y84320	Homo sapiens Homo sapiens	Human cardiovascular system associated protein	815	99
			kinase-1.	88	73
1129	G02105	Homo sapiens	Human secreted protein, SEQ ID NO: 6186.	700	100
1130	Y32923	Homo sapiens	Transmembrane domain containing protein clone HP01512.		91
1131	Y29817	Homo sapiens	Human synapse related glycoprotein 2.	260	
1132	Y91644	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:317.	525	96
1133	Y91449	Homo sapiens	Human secreted protein sequence encoded by	542	100
	1		gene 49 SEQ ID NO:170.	2399	93
1134	AB017908	Homo sapiens	4F2 light chain	312	55
1135 1136	X51760 Y99426	Homo sapiens Homo sapiens	Human PRO1604 (UNQ785) amino acid	917	72
		1	sequence SEQ ID NO:308.	102	50
1137	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	768	91
1138	AF155106	Homo sapiens	NY-REN-36 antigen	117	50
1139	AL031055	Homo sapiens	transport proteins)		
1140	AF011359	Bos taurus	regulator of G-protein signaling 7	138	96
1140	Y70018	Homo sapiens	12	623	100
	<del></del>	<del></del>		113	38
1142	G04091 AB030235	Homo sapiens Canis	D4 dopamine receptor	89	48
1144	Y94922	familiaris Homo sapiens	Human secreted protein clone pv6_I protein	539	88
			sequence SEQ ID NO:50.	398	96
1145	X99962	Homo sapiens		168	79
1146	G03807	Homo sapiens	CEO ID NO. 7703	512	85
1147	G03712	Homo sapiens		705	76
1148	Y28279	Homo sapiens		247	36
1149	U13642	Caenorhabditi	exon 5 similar to transmemorane domain of 5.	1	

EQ	Accession	Species	Description	Smith- Waterman	% Identity
5	No.			Score	
io:	1			500.1	
			cerevisiae zinc resistance protein  Human secreted protein, SEQ ID NO: 7519.	117	62
150	G03438		Human secreted protein, SEQ ID NO: 5084.	181,	80
151	G01003		Human secreted protein, SEQ ID NO: 7879.	198	63
1152	G03798	Homo sapiens	DNA binding protein	95	41
153	X88799	Oryza sativa	TR3beta	155	96
1154	D85245	Homo sapiens	Tumour suppressor protein, p53.	341	87
1155	R74272 Y86265	Homo sapiens Homo sapiens	Human secreted protein HUSXE77, SEQ 1D	99	41
			NO:180. Human secreted protein, SEQ ID NO: 6658.	263	98
1157	G02577	Homo sapiens	putative organic anion transporter	185	42
1158	AF104334	Homo sapiens	Human secreted protein, SEQ ID NO: 5474.	173	57
1159	G01393	Homo sapiens	Human GTP binding protein APD08.	224	81
1160	W75771	Homo sapiens	M-ABC2 protein	410	83
1161	AF216833	Homo sapiens	Human secreted protein encoded by gene 10	1156	100
1162	W67816	Homo sapiens	clone HCEMU42.	230	70
1163	AF119851	Homo sapiens	PRO1722	113	31
1164	Y87252	Homo sapiens	Human signal peptide containing protein HSPP- 29 SEQ ID NO:29.		82
1165	W64537	Homo sapiens	Human liver cell clone HP01148 protein.	338	64
1165	AF269286	Homo sapiens	TICK	134	51
1167	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	149	90
1168	D90789	Escherichia	Dipeptide transport system permease protein DppC.	411	
		coli	TG0847 protein	344	90
1169	R63783	Homo sapiens Homo sapiens	Human secreted protein encoded from gene 18.	478	98
1170	Y45274	Homo sapiens	Mr 110 000 antigen	347	96
1171	D64154	Homo sapiens	organic anion transporter OATP-B	311	67
1172	AB026256	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	60	52
1173	G00357 D87717	Homo sapiens	similar to human GTPase-activating protein(A49869)	178	59
			ribosomal protein	391	78
1175	M64716	Homo sapiens		285	67
1176	R08330	Homo sapiens Homo sapiens	ribosomal protein L12	242	72
1177	L06505	Homo sapiens	essenic cation transporter (OCT2)	276	88
1178	AJ251885	Homo sapiens	Human secreted protein, SEO ID NO: 7339.	155	90
1179	G03258 G01207	Homo sapiens	Human secreted protein, SEQ ID NO: 5288.	282	62
1180	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	249	
	17161604	Homo sapiens	HSPC176	138	90
1182	AF161524	Homo sapiens	Human secreted protein, SEO ID NO: 7870.	282	66
1183	G03789 Y02671	Homo sapiens	Human secreted protein encoded by gene 22	107	71
	100000	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	88	69
1185	G03797	Homo sapiens		118	46
1186	G03564 AB032905	Hylobates	dopamine receptor D4	96	37
	<u> </u>	concolor	Human secreted protein, SEQ ID NO: 5037.	292	78
1188	G00956	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	178	79
1189	G03258	Homo sapiens	Human secreted protein, SEO ID NO: 7442.	324	76
1190	G03361 AF117755	Homo sapiens Homo sapiens		187	70
1192	Y70455	Homo sapiens	Human membrane channel protein-5 (MECHP-	202	67
			5).	99	42
1193	G03052	Homo sapien:		192	76
1194	G02607	Homo sapien:		2001	98
1195		Homo sapien	Homo sapiens CI542_2 clone secreted protein.  Human GABAB receptor 1d protein sequence.	239	69
1196	Y14104	Homo sapien		149	90
1197	X61972	Homo sapien		145	51
1198	G00534	Homo sapien Homo sapien	s Human secreted protein HELHN47, SEQ ID	1089	89
1199	1 1 00200		NO:175.		

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
~ <	No.			Score	Identity
10:				404	50
	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	202	49
	M27826	Homo sapiens	neutral projease large souths.	265	61
1203	Y73424	Homo sapiens	Human secreted protein clone yi4_1 protein sequence SEQ ID NO:70.		98
1204	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	625	
1205	Y36203	Homo sapiens	Human secreted protein #75.	219	59
1206	U78111	Gallus gallus	AO	205	57
	AF095448	Homo sapiens	putative G protein-coupled receptor	416	76
1207	AF116715	Homo sapiens	PRO2829	127	75
1208	AF116713 AF099137	Homo sapiens	MaxiK channel beta 2 subunit	475	95
1209 1210	AF205718	Homo sapiens	hepatocellular carcinoma-related putative tumor	423	79
1211	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	224	70
			Human secreted protein, SEQ ID NO: 4800.	117	44
1212	G00719	Homo sapiens	Human secreted protein, SEQ ID NO: 5090.	351	73
1213	G01009	Homo sapiens	PRO0657	124	70
1214	AF090942	Homo sapiens	Human secreted protein encoded by gene 17	99	77
1215	Y14427	Homo sapiens	clone HSIEA14		<u> </u>
1015	C03005	Homo sapiens	Human secreted protein, SEQ ID NO: 7986.	173	57
1216	G03905	Homo sapiens	Human transmembrane protein HTMPN-21.	1173	100
1217	Y57897	Homo sapiens	hla-dr antigen alpha chain	454	78
1218	J00194	Homo sapiens	Secreted protein 76-28-3-A12-FL1.	470	92
1219 1220	Y59709 W81576	Homo sapiens	EBV-induced G-protein coupled receptor (EBI-	725	100
1221	W96745	Homo sapiens	polypeptide.     High affinity immunoglobulin E receptor-like	650	98
1222	Y35911	Homo sapiens	protein (IGERB).  Extended human secreted protein sequence, SEQ	135	31
•		L	ID NO. 160.  Human secreted protein encoded by gene 21.	260	95
1223	Y00278	Homo sapiens		568	90
1224	AF161422	Homo sapiens	HSPC304	202	95
1225	U14970	Homo sapiens	ribosomal protein S5 Human secreted protein, SEQ ID NO: 5814.	610	100
1226	G01733	Homo sapiens		333	56
1227	AF099973	Mus musculus	schlafen2	155	81
1228	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	801	63
1229	AF217188	Mus musculus	YPIB		100
1230	AF176813	Homo sapiens	soluble adenylyl cyclase	275	100
1231	X98333	Homo sapiens	organic cation transporter	1704	53
1232	W74955	Homo sapiens	Human secreted protein encoded by gene 77	212	
1233	Y94940	Homo sapiens	1/0 1	526	100
1234	U76618	Mus musculus	N-RAP	482	82
1002	A FO44034	Homo sapiens	hook2 protein	380	97
1235	AF044924	Homo sapiens		417	100
1236	G01459	Homo sapiens	adapter protein	164	84
1237	AF000018 W88633	Homo sapiens	did by cone 100 clone	250	90
	11100000	Homo sapiens		697	98
1239	W29660	Oryctolagus	peroxisomal Ca-dependent solute carrier	154	52
1240	AF004161	cuniculus	interference in Trig 24	709	97
1241	Y92710	Homo sapiens			88
1242	Y95002	Homo sapiens		325	100
1243	Y44905	Homo sapiens	partial protein.	511	97
1244	AF284422	Homo sapiens	cation-chloride cotransporter-interacting protein	1888	93
1245	Y53629	Homo sapiens	BMS115.		97
1	AB039371	Homo sapiens	mitochondrial ABC transporter 3 Extended human secreted protein sequence, SEQ	389 168	39
1246	I ADVITO				

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
D	No.	1		Score	
10:			ID NO. 160.		
1248	AF072509	Rattus	glutamate receptor interacting protein 2	559	90
1240	A1072507	norvegicus		L	100-
1249	AF247042	Homo sapiens	tandem pore domain potassium channel TRAAK	661	98
1250	B08974	Homo sapiens	Human secreted protein sequence encoded by	1087	97
1200			gene 27 SEQ ID NO:131.	858	59
1251	L15313	Caenorhabditi	putative	030	] ]
		s elegans	Human secreted protein clone it217_2 alternate	278	75
1252	Y29338	Homo sapiens	reading frame protein.	1 2.0	
		<b></b>	Human G-protein receptor HPRAJ70.	211	92
1253	W01730	Homo sapiens	Human secreted protein, SEQ ID NO: 7155.	294	83
1254	G03074	Homo sapiens	Human secreted protein, SEQ ID NO: 5899.	253	91
1255	G01818	Homo sapiens	eppin-1	222	54
1256	AF286368 AF220264	Homo sapiens	MOST-1	87	93
1257	G02227	Homo sapiens	Human secreted protein, SEO ID NO: 6308.	281	78
1258	Y07970	Homo sapiens	Human secreted protein fragment #2 encoded	81	94
1259	10/3/0	110mle suprems	from gene 26	1	
1260	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain	986	100
1200	103332		ligand (clone 3TW).	172	36
1261	AF140674	Homo sapiens	zinc metalloprotease ADAMTS6	237	67
1262	U28369	Homo sapiens	semaphorin V	288	71
1263	Y07049	Homo sapiens	Renal cancer associated antigen precursor	280	1 '1
		1	sequence.	187	80
1264	Y36153	Homo sapiens	Human secreted protein #25.  Human cytokine signal regulator CKSR-2 SEQ	723	93
1265	Y78114	Homo sapiens		/25	
	1	1	ID NO:2.  Amino acid sequence of protein PRO334.	191	100
1266	Y13397	Homo sapiens	phosphatidylinositol 5-phosphate 4-kinase	859	95
1267	AF030558	Rattus	gamma	ļ	
1060	U73167	norvegicus  Homo sapiens	candidate tumor suppressor gene LUCA-1	159	96
1268	AF190664	Mus	LMBR2	552	76
1209	Al 190004	musculus	4.5		
1270	AL050332	Homo sapiens	dJ570F3.1 (homolog of the rat synaptic ras	820	98
1270	1120000		GTPase-activating protein p135 SynGAP)	131	95
1271	G02126	Homo sapiens	Human secreted protein, SEQ ID NO: 6207.	253	$\frac{1}{92}$
1272	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1280	100
1273	AL035661	Homo sapiens	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthethase (acetate-coA ligase))	1200	
	1.5061516	1/1/2	S3-12	3523	61
1274	AF064748	Mus musculus	- IA		
1275	D17554	Homo sapiens	TAXREB107	377	78
1275	Y30715	Homo sapiens	C Lucron anamata d	643	90
12/0	150715		protein	705	100
1277	AF146760	Homo sapiens	septin 2-like cell division control protein	707	46
1278	Y05069	Homo sapiens	Human PIGR-2 protein sequence.	281	85
1279	X59668	Oryctolagus	aorta CNG channel (rACNG)	20'	ر ا
		cuniculus	Transpir CEO ID NO: 5132	489	98
1280	G01051	Homo sapiens		120	43
1281	G03411	Homo sapiens		1635	100
1282	AF055084	Homo sapiens	odd-skipped related 1 protein	357	98
1283	AF117814	Mus	odd-skipped foldled i protein		
160	1100010	musculus Xenopus	NaDC-2	535	60
1284	U87318	laevis	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
1205	AF061346	Mus	Edp1 protein	452	68
1285	AF001340	musculus			
1286	AB030182	Mus	contains transmembrane (TM) region	582	68
1250	AB030102	musculus			<del></del>
1287	A13595	synthetic	immunosuppresive protein PP15	185	97
120/	1.13373	construct			100
1288	AF254411	Homo sapiens	ser/arg-rich pre-mRNA splicing factor SR-A1	837	98
1289		Rattus	serine/threonine protein kinase TAO1	319	98
1		norvegicus			

~~ (	Accession No.	Species	Description	Smith- Waterman Score	% Identity
10:				523	100
290	AF038563	Homo sapiens	membrane associated guanylate kinase 2	468	100
291	AF034837	Homo sapiens	double-stranded RNA specific adenosine deaminase	937	87
292	M15888	Bos taurus	endozepine-related protein precursor		45
293	AB010692	Arabidopsis thaliana	ATP-dependent RNA helicase-like protein	636	
204	AF209923	Homo sapiens	orphan G-protein coupled receptor	1570	100
294 295	W67828	Homo sapiens	Human secreted protein encoded by gene 22	504	98
1296	AC004832	Homo sapiens	similar to 45 kDa secretory protein; similar to CAA10644.1 (PID:g4164418)	648	65
1297	X80035	Oryctolagus	cysteine rich hair keratin associated protein	575	70
		cuniculus	Human secreted protein, SEQ ID NO: 6726.	223	97
1298	G02645	Homo sapiens	Human delta3 fragment #4.	122	32
1299	Y59440	Homo sapiens	Leukocyte seven times membrane-penetrating	459	81
1300	W70504	Homo sapiens	type recentor protein JEG18.	3916	99
1301	Y67315	Homo sapiens	Human secreted protein BL89_13 amino acid sequence.		96
1302	M77693	Homo sapiens	spermidine/spermine N1-acetyltransferase	174 254	69
1302	G01331	Homo sapiens	Human secreted protein, SEQ ID NO: 5412.		99
1303	G01491	Homo sapiens	Human secreted protein, SEQ ID NO: 5572.	747	98
1304	AF148509	Homo sapiens	olpha 1 2-mannosidase	602	98
1305	G01658	Homo sapiens	Human secreted protein, SEO ID NO: 5739.	333	98
1307	Y90899	Homo sapiens	D1-like dopamine receptor activity modifying	332	
1200	AF033120	Homo sapiens	n53 regulated PA26-T2 nuclear protein	348	52
1308	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	147	66
1309	AF063243	Bos taurus	ribosomal protein 1.30	296	90
1310 1311	AF224494	Mus musculus	arsenite inducible RNA associated protein	688	70
			HTRM clone 2709055 protein sequence.	1154	100
1312 1313	Y73342 Y99419	Homo sapiens Homo sapiens	Human PRO1780 (UNQ842) amino acid sequence SEQ ID NO:282.	1145	78
			PRO1777	433	97
1314 1315	AF116667 W75100	Homo sapiens Homo sapiens	Human secreted protein encoded by gene 44	807	97
	l		clone HE8CJ26.  APOBEC-1 stimulating protein	789	100
1316	AJ272078	Homo sapiens		2607	98
1317	AB041533	Homo sapiens	sperm antigen	806	92
1318	U19617	Mus musculus	Elf-1	768	100
1319	U82598	Escherichia coli	ferric enterobactin transport protein	709	100
1320	D90892	Escherichia coli	SORBITOL-6-PHOSPHATE 2- DEHYDROGENASE (EC 1.1.1.140) (GLUCITOL-6- PHOSPHATE DEHYDROGENASE) (KETOSEPHOSPHATE	709	
		 	REDUCTASE).	601	92
1321	W67847	Homo sapiens	clone HPBCJ74.	466	93
1322	AJ276101	Homo sapiens		504	97
1323	AJ276101	Homo sapiens		1584	100
1324	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1277	89
1325	U91561	Rattus norvegicus	pyridoxine 5'-phosphate oxidase	1606	100
1326	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1531	90
1327	Y32206	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2825826.	<u> </u>	
1200	AF151048	Homo sapiens		657	85
1328		Homo sapiens	olfactory receptor	1645	100
1329	Y10530	Homo sapiens	guarine nucleotide exchange factor	4314	99
1330 1331	AF180681 AF111856	Homo sapiens			99
	. J			2171	100
1332	Y13583	Homo sapiens	G-protein coupled receptor	1395	100

SEO.	Accession	Species	Description	Smith-	%
SEQ ID	No.	Species	•	Waterman	Identity
NO:	110.	1		Score	105
	Y25755	Homo sapiens	Human secreted protein encoded from gene 45.	1380	96
1334		Homo sapiens	protocadherin gamma A5	4742	99
1335	AF152325	Home sapiens	transcription factor BTF3	639	81
1336	X74070		protein phosphatase 2C	1931	95
1337	AF095927	Rattus	protein phosphatase 20	1	
	<u> </u>	norvegicus	Human secreted protein, SEQ ID NO: 7958.	621	100
1338	G03877	Homo sapiens	Human secreted protein, SEQ 15 1vo. 755.	626	100
1339	AL008582	Homo sapiens	bK223H9.2 (ortholog of A. thaliana F23F1.8)	5820	99
1340	X61615	Homo sapiens	leukemia inhibitory factor receptor	7528	97
1341	Y01519	Homo sapiens	A carcinogenesis-inhibiting protein.	2372	100
1342	AF207600	Homo sapiens	ethanolamine kinase		97
1343	U54807	Rattus	GTP-binding protein	1167	197
15 15	02.00.	norvegicus			<del></del>
1344	AC020579	Arabidopsis	putative phosphoribosylformylglycinamidine	3283	51
1344	ACOZOSTS	thaliana	synthase; 25509-29950		122
1345	Y28576	Homo sapiens	Secreted peptide clone pe503_1.	944	100
	W74787	Homo sapiens	Human secreted protein encoded by gene 58	1171	100
1346	W/4/0/	Tionio sapiene	clone HHFHN61.		
46.45	10000	Homo sapiens	guanylate binding protein isoform I	2636	87
1347	M55542		28.4 kDa protein	1329	100
1348	AF183428	Homo sapiens	Fas-ligand associated factor 3	167	24
1349	U70669	Homo sapiens	cardiac voltage gated potassium channel	562	99
1350	AF295530	Homo sapiens	Cardiac voltage gated potassium enames		
			modulatory subunit		

## TABLE 3

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence 337	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  TPSLIHQAPTPCPAGLWG/PPNGHYHGS*PGC
1	1331	A				HWPQAPHRA***GLLPPRWLGHGLPGGPAAP WAASQWVDGVAGRLPGPAWSWHASGAAPA QPGPL*LLVPGSSGLPDPRDP IRNSSIRPMKERETKLSAKHMITCSASYDIRGL
2	1352	A	27	100	366	QIETT\YHHTPIRMAKIQKT/GHHQC**ECGAT GTLIHGWWGCKVVEPLGKTVWQIPK HASAHASVVLKDNSELEQQLGATGAYRARA
3	1353	A	40	3	314	LELEAEVAEMRQMLQLEHPFVNGADKLRPD SMYVHLNEL*QSLVENMLLTVVDTH\RTPI*R
4	1354	A	74	2	292	TASALFSCPDGGSLAGFAGRRASFHLECLKR QKDRGGDISQKTVLPLHLVHHQVAHTFGQAT VTCQQARQSPG*RTNPE/ALQWVLPVSDGWH VLPLP
5	1355	A .	78	114	850	ENCRVASNLPGVFFSEDTAQSGSYMRISAHPP NAGGEVSNGPKRKLTLMLNFSLPSSGLNAGA FYALSTLLNRMVIWHYPGEEVNAGRIGLTIVI AGMLGAVISGIWLDRSKTYKETTLVVYIMDT GGAWWCYTFYLGTGDTCG*CFITAGVIMGFF MTGYLPLGFEFAVEL\SYPESEGISSGLLNISA QVFGIIFTISQGQIIDNYGTKPGNIFLCVFLTLG AALTAFIKADLRRQKANKETLEN
6	1356	A	81	97	376	EWFSYMLGSNMSVYHSP*SLEPLCKVLSES*A YLRVPFIRILLNAR*IRKAYKRMSLEIKLLIRE *CLFQEMGLSLQWLYSARGDFFRATSRL
7	1357	A	93	2	872	TLSSACLIGDAWKELTIVAGAVSNQLLVWYP ATALADNKPVAPDRRISGHVGIIFSMSYLESK GLLATASEDRSVRIWKGGDLRVPGGRVQNIG HCFGHSARVWQVKLLENYLISAGEDCVCLV

SEQ   ID NO: of nucleotide   No: of peptide   No: of nucleotide					<del></del>	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Acoustic Acid E=Glutamic Acid.
			hod	1			F=Phenvialanine, G=Glycine, H=Histidine,
Sequence   94496		1 ' '					I=Isoleucine, K=Lysine, L=Leucine,
Sequence   914   Sequence   914   Sequence   915   Sequence   914   Sequence   915   Sequence   916   Sequence   916   Sequence   917   Sequence   918   Sequ	1					to last amino	M=Methionine, N=Asparagine, P=Proline,
Samino acid residue of sequence peptide residue of sequence of peptide residue of sequence of peptide sequence   Sequen	1 -	uence					O=Glutamine, R=Arginine, S=Serine,
residue of peptide   sequence   y=Tyrosine, x=Unknown, *Supe codon, pepsible nucleotide tellion, *pessible nucleotide tinscrition   NHSEGELQAFRCHQGRGIRALAAHERQAWV   TIGGDDSCIRL WHLVGRCYRGLGDLOSILQ	uence	}		714			T=Threonine, V=Valine, W=Tryptophan,
Pepilde   Pepilde   Pepissible nucleotide deletion, "Prossible nucleotide insertion   Pepilde   Pepilde   Pepilde   Pepilde insertion   Pepilde			)	ļ			V=Tyrosine, X=Unknown, *=Stop codon,
		1	Ì				/=possible nucleotide deletion, \=possible
WSHEGELLOAFRGHIGGRAFAHEROVAN	ì	1	Ì				nucleotide insertion
	ļ	<del></del>	<del> </del>	<del> </del>	sequence		WSHEGEILQAFRGHQGRGIRAIAAHERQAWV
**RRGQVLGAAARG**TFEVLLPAGGSSWSRIC	1		İ	Į.			ITGGDDSGIRLWHLVGRGYRGLG/DLGSLLQ
RIVCYGOWGRSCQGCPHQHSNCCCGPDYW   WEGAQLELGPAWL   RIDGE		l	l		1		VP**ARYTQGCDSGWLLATAGSD*YRGPVSL
WEGAQLELGPAWL		ì	}		ļ		*RRGQVLGAAARG*TFPVLLPAGGSSWSRGL
1358		1	Į.	}	·		RIVCYGQWGRSCQGCPHQHSNCCCGPDPVS
S		ļ.	1			_	WEGAQLELGPAWL
	9	1358	A	106	3	350	FSSLLSGRISTLRDETGAILIDGDPAACAPIIKF
1359   A   115   49   186	1	1330			Ì	·	LLTEELHLRGVSIYVLRHEAQIYGITPLVCAL
1359   A				1			LI/CRRL*SDSCMRAALNDRGLYQVLILDGLY
1360		l	(	1	1		QCLGFVDSDSRKMVS1L1
1360   A   123   2   1249	9	1359	A	115	49	186	QAWAIFKGKY KEGDIGGPAV WATALACALIV
FEEVORLRFEVHDISSNEHGILKEADFLGGME   CTLGGIVSQRKLSKSLLKIGHTAGKSSITVIA     ELLSGNDDYVELAFNARKLIDDKOFFSKSDFF     LEIFRMNDDATQLVHRTEVVMNNLSPAWK     SFKVSVINSLCSGDFDRRLKCIVWDWDSNGK     SFKVSVINSLCSGDFDRRLKCIVWDWDSNGK     KPAKKKNYKNSGTVINLNCKHKMHSPLDYI     MGGCQIQFTVAIDFTASNGDFRNSCSLHYIHP     YQPNEYLKALVAVGEICQDYDSDKMFPAFGF     GARIPPEYTDSHDFAINFNEDNFECAGIQGVV     EAYQSCFPKAPTFTGFTNICPHSSRK VAKFR     SEGN*HQGRAFAIIFLVDFQQVGVYSQDMGP     DNPGGHFV     ACARKQLLGRTVFIWFVGQLLGGELKGYSKT     NTTSSRPASSRGTLSSSSSSSSLTNDALPSSL     KSDSTITTSGLVPFRSSCVSSLTNDALPSSL     KSDSTITTSGLVPFRSSCVSSSLTNDALPSSL     KSDSTITTSGLVPFRSSCVSSSLTNDALPSSL     KSDSTITTSGLVPFRSSCVSSSLTNDALPSSL     KSDSTITTSGLVPFRSSCVSSSLTNDALPSSL     KSDSTITTSGLVPFRSSCVSSSLTNDALPSSL     KSDSTITTSGLVPFRSSCVSSSLTNDALPSSL     KSDSTSTRTLSGVPFRSSCVSSVSSP     KSDSTSRTANDALSTRT     KSDSTSTRT							KSSEFNEGPERERMDV
TI 1361 A 147 614 9 ACARKQLLGRTVFIWFVQQLLGGLKGYSKT  11 1361 A 147 614 9 ACARKQLLGRTVFIWFVQQLLGGLKGYSKT  12 1362 A 177 12 416 LIFSENADSLCVSPFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	10	1360	A	123	2	1249	KUCKI QEK VUKI E VIKI CURI V I SKELI I VDI I
EELSGNIDDYVELAFNARKLIDDKFFSKSDFY LEIFRAMDDATQQL/HRIEVVMNNLSPAWK SFKVSVNSLCSGDPDRRLKCI/WDWDSNGK HIDFIGEFTSTFKEMRGAMEGKQVQWECNPK YKAKKKNYKNSGTVILNILCKIHKMHSFLDYI MGGCQIQFTVAIDFTASNGDFRNSCSLHYHIP YQPNEYLKALVAVGEICQDYDSDKMFPAFGF GARIPPEYTDSHDFAINFNEDIPSRCSLGJGWV EAYGSCPWAPFTFTGFTNICPHSSRKVAKFRR SEGN*HQGRAFAIIFILVDFQQVGVYSQDMGP DNPGGHFV  ACARKQLLGRTVFIWFVGQLLGGELKGYSKT NTISSRPASSRGTLSSSSSSSSITADALPSSL KSDSTITTSGLVPFPRSSLCVNPAKSSVSSEVSSI KILLSSSVKYLE*KRTSCCFPDSSESLSVDLAFSSL SDEVSMGTSSRKPINSSSLGALKMSATSVG SGSESPTFFLTGLQSPPSTRPEPGLTTARNS TILTRDC  12 1362 A 177 12 416 LIPSEFALDSLVDPRVRSRKQFFVIYPVYDTAI DTKHFSLLDGNVGEPDMSAGFCPNHKAAM VIFLDRVYGIEVQPFLHILLEGGFLPDLRAA ASLDT/AEIGAMPFLLS*LFTLCLMMFFTIYPFI NILTMNVY  13 1363 A 249 535 105 WTFHRHLSPAPLIVCDQGTCVVSYYPQNIVQ MPDTQMEQGLMHLFLDGNA*PHSVECYCPS TFEIAIKITSFVLYFHAPYRAPEVLLRSSYYSSPI DVWAVGSIMAELYMLRPLPPGTSEVDEIFKIC QVLGTFKWSTLVPKHYRAPEVLLRSSYYSSPI DVWAVGSIMAELYMLRPLPPGTSEVDEIFKIC QVLGTFKWSTLVPKHYRAPEVLLRSSYYSSPI DVWAVGSIMAELYMLRPLPPGTSEVDEIFKIC QVLGTFKWSTLVPKHYRAPEVLLRSSYYSSPI DVWAVGSIMAELYMLRPLPPGTSEVDEIFKIC THAFKINGKNPINGLUSATITYCYAAICHELLS TMYMMRPLCTATVNATNKMGFLNSQVN THAFFILDICYSSVTAQDAAEPTVSKPILVWGYIT *SFFFIESWGTNGCLLSAITYACYAAICHELLS TMYMMRPLCTATVNATNKMGFLNSQVN THYPIET*HPVKQMIKWQ*LTATVNAITNKMGFLNSQVN THYPIET*HPVKQMIKWQ*LTATVNAITNKMGFLNSQVN THYPIET*HPVKQMIKWQ*LTATVNAITNKMGFLNSQVN THYPIET*HPVKQMIKWQ*LTATVNAITNKMGFLNSQVN THYPIET*HPVKQMIKWQ*LTATVNASKV KQTPNSETAPSVCRUNLVPDKCG  16 1366 A 263 104 481 FCFRTTEEDGGDDCVVSVWIKQRNNSCVK SKDYTSKYNIFILGENT*KDIPTITSKHTKMW VSSLAMKEMLTKTIM VSSLAMKEMLTKTIM  VSSLAMKEMLTKTIM  VSSLAMKEMLTKTIM  VSSLAMKEMLTKTIM VSSLAMKEMLTK			1				FEEVORERFEVHDISSINHNOEREADI EGGINE
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KQTPNSETAPSVCRNLVFDKCG  KQTPNSETAPSVCRNLVFDKCG  FCIFRTTEEDRGGDDCVVSVWTKQRNNSCVK SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNIFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM LVVGITGTRHHARVIFIFLVETGFPHVGQAGL			1		1		TETPIET*HPVKOMIKWQ*LTAWLRNRGYKKI
16 1366 A 263 104 481 FCIFRTTEEDRGGDDCVVSVWTKQRNNSCVK SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM			1				KOTPNSETAPSVCRNLVFDKCG
SKDVFSKPVNIFWALEESVLGVKARQPRPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV  17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM LVVGITGTRHHARVIFIFLVETGFPHVGQAGL	16	1266		263	104	481	FCIERTTEEDRGGDDCVVSVWTKORNNSCVK
AGNTFEMTCK VSSKNIKSPRYSVLIMAEKPV GDLSSPNETK YIISLDQDSVVKLENWTDASRV  17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM LVVGITGTRHHARVIFIFLVETGFPHVGQAGL	10	1300	1 ^	203	1 -0.	_	SKOVESKPVNIFWALEESVLGVKARQPKPFFA
17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM	1		Į		{		AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV
VSSLAMKEMLTKTTM  VSSLAMKEMLTKTTM  LVVGITGTRHHARVIFIFLVETGFPHVGQAGL							GDLSSPNETKYIISLDQDSVVKLENWIDASRV
VSSLAMKEMLTKTTM  LVVGITGTRHHARVIFIFLVETGFPHVGQAGL	17	1367	- <del> </del>	298	68	208	RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW
18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL ELLTSGDPPALASQSAGITGMSHCARPKGHFG	1 1	1,30,	[ ]				VSSLAMKEMLTKTTM
ELLTSGDPPALASQSAGITUMSHCARPAGHFG	18	1368	A	300	904	1	LVVGITGTRHHARVIFIFLVETGFFHVUQAGL
	1.0		1			!	ELLISGDPPALASQSAGITUMSRCARFROHFG

PCT/US01/03800

					D distand and	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-Americ Acid. E-Glutamic Acid.
IO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	O=Glutamine R=Arginine, S=Serine,
ence	1		914	ng to first		TaThreonine V=Valine, W=Tryptophan,
	1		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		residue of	sequence	/=possible nucleotide deletion, \=possible
	ł		İ	peptide		nucleotide insertion
	1		Ì	sequence		IHLK*MFYTMSQKMP*PTINLILLLIIPGNLNIF
		<del>                                     </del>	1			KPNMGWLGPKTAFV*KDEVLSGIPFAKGRCR
	{	}	i	1	]	KPNMGWLGPK I AF V KDEVLSOM I TELESTON
	1	{		{		WK*DY*C/LQEVTDPIMEKGKKKKRTASFFK
	1	1	ì			GQPHQSTNALLRRCVR*RYHLS\TVETAGLP*
	1	1	ì	1	1	KNTGHIPGQPFLFKLVFKC*NVICI**QYKW*Q
	1	1	1	1	,	NIGVKNKSFCPH*SSSPSL*FIGHHSRNF/CSFK
	1		1			TEPHSVVQAGGQWRNLSSLQAPPPGLMPLSR
	i	1	1	1		ISLMSSWDYRRPPQ
	1	<del></del>	302	3	445	NSPSRWAKIQMFEHTFCG*GCG/ER/NVHIHCS
19	1369	A	302	13	) ''2	WICRI RPIL WRAVREYLSKLKNAELSFDPGV
	Ì	1	1	1	1	CLIDIVAIDMPTSI*DEKEALLFAFLAFHE*HC
	ł	1	{	1	1	KSRIWAVIO/CIHLWDWLRKL*CFHRMKFYA
	1	1	1			I AVINDERHI I SHIWKDVONILLK
		1		J	1339	FFECGKEVPLEEONKHPGPRATTSPGA/HARA
20	1370	Α	304	1	1339	LI SAGEFTAGVGLSP*AIHSFVWLCTFIQHGA
	1	{		1		GGPCHOPGGSPGPWMHTTQAGHLWEGAYPC
	1		1	}		GSSTWHOVPGOLGGSWGPRERSLLGSFIRCS
	ļ	}	1	1		CDUPPER WMSPNOKPPTENPGVMGKVWK
	1	1	}	i	}	LMPGESPLIWEAEGKEDHLSPEGQGHSE/PVA
	1	1	l l	1	ļ	PLHSSLGNTVKP*PKNQKPKQNRSRHGQ\GF
	1	1			1	MAGQGQSRPAAR*PPCPALTPASHSAGTWPP
	}	1				RICRTVPGGPCPSPSGFRSCRR*GFSA*TRSWP
		}	1		1	DAEPPSTPDTAPRCCTQSDTSSQGPQ*S*WRR
	1	1			1	CRALPGRLCSAPAAGLRRARPRLSESRRGNSF
	i	ļ	1		ļ	PASPAAASARCPSWGPSCPARPPSRPAAGTEP
	ł	- {	}			AAPSRCTAWLRGEREPGPRPPGRRPRSGRGP
	ļ	1	}	ł		AAPSRCIAWLRUEREFURIT ONG ROOMS
	ì					VSFAPEVLSLPAVRQTKSWRWRNEEEITRPW
	l	1	1	<b>\</b>		ALVRSRGG
21	1371	IA	326	799	1587	GSQVLPPPPSQDSATLPQDA*GPRAAPGQPVC
21	13/1	1	320			E*GLQGAGVRRLRGEVLCQPQP*GAL*EQCL
	1	l l	1			HLSFSPRQGAAPDTEPSAWGPAPTGATGPGL
		1	ı	1	j	LRHVRLFSAGAPRGAATPCPPALLHGPAWPP
	Į	1		İ		ARPMFRGHPPVRPLGPWGKVAAGPRALCLA
	- }	- }	i			GVPAVQGECATKPSG*GL*PAHLRGPPGPEV
	1	1				QWHWQLSAGRDPVPAEDPPL*EGPLGPGGPA
	ì					AAQAEPGADPEPEDKDQAAESRPAGAMSLS
	1	1			j	OGSGPVGGOGLR
				146	652	PHI ENPHPEHSEPGAPLT*STLSWSILSPREPS
22	1372	A	327	140	032	GAPCYPGHPHI.ENPHLEHLLTWRTVIWSILI
l l				- }		PCAPCYPEHPHI EHPLTWSTPHLEHPSPGEPL
ĺ		1		- 1		SCRIPTRSH HRDHPLP*CLSTEESPI*GWGSL
Ì					1	APPSTPLVLDVAPPGPQPASSCPGRDSCYSVE
1		1	Ì	1		CTVVSP
	}	1			_	CIVSSCOGTRKPCHLEDANKINKQSPTLEKIE
23	1373	A	348	397	2	T OF ST # V/KO*I IVAFKYVOILHPRKKYFQKPI
<del></del>	1	[	1		!	NNEKRKMKKRKEEKKKCRERMQRRSKWRI
1		1		ì	1	EEKKE*RREE\EERKKEKEDRKERRKETSPRO
		)		1		CENTE VICE CENTRALIZED IN CONTROL OF THE CONTROL OF
					i	SRRLLRD GRALDTAAGSPVQTAHGLPSDALAPLDDSM
24	1374	- <del> </del> A	362	170	352	GRALDIAAGSTVQIATIGLE SDALAG EDDSIN
24	.   15/4	1 ''		1		WEGRTTAQWSLHRKRHLARTLLVSRVRGPO
125	1275	-	384	373	128	YLITTILETGYLWKNRHSDQ*KRTENPERDQ
25	1375	A	304	1 3.5	1	KYPKVDFCKSNSMKNRLCNKWHWINWIFI
1		1	- 1	1	1	VVINI NI KPHTKI TPNIKKN
				202	165	FVKNTNPFIFSGTNLTIWIRSI*RKSDEINQKI
26	1376	A	397	383	1 105	*MEKYSISLDRRLNTVKMSFLPNLIYKFNTIS
1					i	VIDANT
,	1	l_			200	V CV A TOVMVNI*KLIV FLYANDEQLEIEMN
			406	103	380	ALUMAN O ANTON THE TANK TO THE TANK TO THE TANK
27	1377	_   A	1 400	1 - 00	1	IVP\FNGSKNKIAFTNLTKYONIONKHAENII
27	1377	^	400	100		IVP\FNGSKNKIAFTNLTKYQNIQNRHAENYI LVNKIEDLNKWRNVLLSWIGRRNIINTMT

		14-4	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
10: of	NO: of	поп	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iuci-	peptide	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
æq-	uence	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	1		714	amino acid	of peptide	T=Threoning V=Valing W=Tryptophan,
		ì	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	l	į .	1		Soquence	/=possible nucleotide deletion, \=possible
	1	1		peptide	i	nucleotide insertion
	1	<u> </u>		sequence	427	TICINKENNLDEIK/FLERHKLSKLTQEEVENL
28	1378	Α	408	14	421	ITLKTSRETELVINK*VIPHKEKPGPDSFIGEF
	)	ł	1	ł	ļ	YQTFKEEL/II/ILHKLFQTIKYGRILPNSVYETSI
	1	1	1	1		TLKPKPEKDL\KENYRPLPLSNIDAK\LNKTLA
	1	1	1	1		NRI**HIR
		1	{			IYSKMCMERQRLNN*ILKKNKVRGIAVPDVK
29	1379	A	434	395	128	VYYKPTVIK/TSWIL*KDSHIVEWNRLENLEID
	13.5	1	1	1	1	VYYKPIVIK/ISWIL-KDSHIVE WIKKEELEE
	1	1	ì			PN/IKRLILDKGAEATEWRKDSFFRQWQ
20	1380	A	455	2	228	FFFETESHSVTQAGVQWCNPGFKRFSCFGLSS
30	1300	^	133	{ -		SWDYRYAPPRP\ANF\*FLVETGFYYVAQAGL
	1	ì	i	[		KLLSPGDLPALAS
		<del> </del>	462	393	2	QLMFDKGVKNIH\WGWTPPFTK*YWKNWISI
31	1381	Α	402	393	1 -	CRRMNI NPYL SRYIKINSR/KDLTVRPEPIKLV
			1	1		FENTOKTIODTGLGK*FIAKTSKAQSTKTNK*
	1		i	1.	1	KRQTRYIKLK\KKSTASKENNRVKRQPLE*EK
	İ	1	{	1		TEAN
		J			471	VKPVEIAVELVKPIEYK*HLLSDPAIPLSGI*LK
32	1382	A	474	125	4/1	FIK A VT/RRICTPMFAAPVSVIA/RN*KQSK/CQ
	Į	ì	1	Ì		KQ*YVHRMEYYTTIKRSEILICTTTWVDFRNT
		1	1	j		ILRETDRIHKTTYDVISLI
						KSACSFICSEEQPASPSPLKPGTYASET\RPRDP
33	1383	A	488	1825	2	HAAGPRRDSSEAETRRPRGA/DGSGTVVKGT
-			į .	1		PGSPAPPCSWGHGG\ETEGAG*CPAAPGTDLR
	1		į.	1	<b>\</b>	APGGSAGS*\GLPSAGGSRGRKGWRAAGRQP
		Į.	1			STR*GRPGRHGGRGE*AGHPEPRQSALQSAG
	1		1	1	1	STR*GRPGRHGGRGE AGII EI ROSAEGOTE
	- [	1	1			L/ASSPEPMGAALAEDGSGDSRGAGPRPQE*P
	ł	1				PSVLSRS\GS*G*G*AASGTASSPRSHSSRLGPP
		- {	1	1		SAGFHGLRCGQPPFAAAPPGPWPGTGRPAGG
1	1	1		i		AGSPPAAAGTAPPATRGAQSRRQNRTAGRNA
ļ	ļ		}	]		SPQTAAGAGSPVQWALSRATG*TGETGSWC
1	(	ŀ	j			AGGTHQATHLTAAWVCPPTWSVRPGGSGPA
!	Í	1	ļ	Ì		AGLGR*GRHPAQSPPLPVPRG*PAWPQEAPSP
ļ		ì	ì	1	}	SPASSEVALSSGSCWPDQAPGPARGSPPAPLA
ł	Ì	ì		1	i	PAWPAAGRGRQR*GRQSAHPPPRR*STAVSL
	]		<b>\</b>	1	1	CCTS+WRRSP+AGTRTOOC+SPWLVPACSSRP
1	1		1	}	1	I *PCTPRPSTOOSPOTTGTPGRSAGPGHPRS*
	1	ı	1			L CORCRACTORI GAOTVASPH*GHWPIALSCI
		1	l	i	- 1	I WASASPPGPEAPPOTGACIGINCKI KAASAN
1	1	i				RSSVAPACA*GWQ*AGSPPAVLRGPP*RVRE
1		1				GALTHRPRAPDE
]					<del></del>	A DG A SVGRAOA AEG*RGGPTGRPPSALGVS/I
34	1384	A	497	422	2	AGRAGRAGEGRPVPPAYPLCKSAQTSGPPKA
				1	1	RLS\PPLASCGGRGPPGGAACATCAPPAGPAR
	1		1	1	1	SSRCRRSPPE*GPR*PSRPARPSPGSAASRRQ
	-	İ				22KCKKV2LLE-OLK-LDIG VIG DI CONTROLOGO
	Ì	-				KLTPCRCQFRGLCA
35	1385	A	509	156	475	PTPYPGE*QAAFLLRGPGLRPPA/DPSLR/HRN
33	1303	1 ^	""		1	LTELVVAVTDENIVGLFAALLAERRVLLTAS
1	1	1	1	1		KLSTLTSCDHAFCALLYPMRWEHVLIPTLPPI
1		i	1	[		II DYC+CPPLPRT
				$\frac{1}{3}$	1631	FEESEVCHLYCVSPTPGPHGRLATWL/PGLLA
36	1386	A	512	13	100.	ELGI AAGGOTLCPAGELPGHARAQASGAPG
			-	1		VI LAVPGRRRVHTCGPGPAAPSTRGECPPPAL
					Į.	GHTRPARPRPV\PFAPAVPOEPGGQGHGAA/I
		Ì				PATGHSAPRGCPPARAAPTGSATPAPPPAAC.
1		1		1		AFHSAWSVPPAGRQQG*RVPAPAFRRTTPGT
1		1		1	<b>\</b>	PGQHLLDRPGAPPAQGSGPAPAPPPRLAGPA
1	}	}	}			GPAAPPPGPPAASWHSSLSKSSSSL\GWSPPL
!	1			İ	1	GPAAPPPGPPAAS WITSOLONOSOSLIU WOFFE
1		1				
	ļ					VGPGSLQ*TPPPQGPHLSGSCGGTSSWRGQR AAVARRLRSWNACGLSRVAGRSSASYPGRE

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid, E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in	nucleotide location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	[		914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
Ų	Į –			residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ	l		peptide	1	nucleotide insertion
	Ì	ļ	1	sequence		GRPSQSQ*PAGPPGMRGCCLRGW*PSSSGSD
	<del></del>		1			GRPSQSQ+PAGPPOMRGCCLRG W 1355GBD
	ì		ì		1	GPGPHPASTWLRAGKTGPSPPACGCA*LPPPS
	İ		1			VSAAPQSPRTRCPRGCAAAAGLCVLAAAGAS
	1	l	1			HGA\GLPGVRVHTQRVHIH*GAG\GCQTPRPR
	}	1	1		1	LRSLPVLGLPAPRCPVSAHPWHRRSGSSCHA
	}	l	1			ARLVPRHPAPGCP**TG*\PLITGFPEP*A*GLP
	1	1		<u> </u>	į	NHQAVGLEASGALQAGHRDELPTMVQLLDH
	1	1	1			CDDVDI KGRPHAP
		1		828	1 1	FRI PLAAGA/RGAAEPRVAVSMAPDPSAKIH
37	1387	A	620	020	1	WEASPEMOSK CHOKGKNNOTECENHVRFLQ
	j	}	ł	1		DINSTHI VACGTHAFOPLCAAIDAEAFILPIS
	ì	1		1		FEEGKEKCPYDPARGFTGLIIDGGLYTATKYE
	1	1	1	1		FRSIPDIRRSRHPHSLRTEETPMHWLNG*EDE
			1	1		AQDDGG*GTISSFLLPWPADHPTPKSPGEPVH
	[			1		SIPVCCQVRGQPQSGGKESPACLKSLSNCLTH
		1	- {	1		\DAEFVFSVLVRESKASAVGDDDKVYYFFTE
	Į.	1	Ĭ	ł		RATEKESGSFTQSRSSHRVARGIPPL
	1	1	1			FRAMVSSTLKLGISILNGGNAEVQ/QGNRGKG
38	1388	A	739	1	427	TSEEGKEG*EVPV*LPVSPPLPRPLQKMLDYL
50	1000		Į.			KDKKEVGFFQSIQALMQTC\GEKVMADDEFT
	1	Į.		{		QDLFRFLQLLCEGHNNDFQNYLRTQTGNTTT
	l l	{		(	1	QDLFRFLQLLCEGHNNDFQN1LK1Q1GN111
		i i	1			INIIICTVDYLLRLQESI
39	1389	A	767	1	1030	TLDLTGPLLLGGVPNVPKDFRGRNRQFGGCM
39	1369	1	'''			RNLSVDGKNVDMAGFIANNGTREGCAARRN
			1	Ì		FCDGRRRQNGGTCVNRWNMYLCECPLRFGG
	ì		{			KNCEQGEWPASSIPPVTAAWEALLLDVPGTT
	1	1	1			VRGLHIQVRQPLVVYAAFTVDSHRPLQETVL
	- }	}	1	1		RRAPAPASGVPSPSGVGWDR*AGPAEPSPSIP
		į	1	ļ		ATVIISVPWYLGLMFRTR\KEDSVLMEATSGG
	ì		İ	}		PTSFRLQVTGAPCHQGTC*VGARGRDPMLSG
		1	- (	İ		I DVTDGEWHHLLIELKNVKEDSEMKHLVIM
		- (	- (			TI DYGMDOVSWHLHLLWG*TLPPAQGKTGA
			1	Ì	1	SEDKVSVRRGFRGCMQVRGGCGGRGEACPS
	1		1	Ì		CAAPRI
				69	399	IHKITIHKEDI NKWKYILCSGMERLSTVMIPVV
40	1390	A	801	69	377	POITYKENA*O\VILKETW*E*GAKITILRKNKL
ĺ				1		RGLVLVPLSTC*VKYLLDKVLPHIKTYYEAR
1				1	1	VNIK SVVI VOVTIM
ł	-				100	SMLKERK VFQFPSCLFFQYITWLGPPYHVLFD
41	1391	A	835	7	195	SSVTNFSIGAK*DILQSVMNCLYAKRIPCVT
						GSTHASGYDKTPDFILQVPVAVEGHIIHWIES
42	1392	A	841	1	415	KASFGDECSHHAYLHDQFWSYWNSLKHRTW
1 '-	1	1	- 1			QGIGTVASNLSQL*TLNAPFPELLLFRSLARTG
1	1			ļ	}	QGIGTYASNLSQL*TLNAFFFELLLFRSLARTO
1	1		(			FVLT*\RFGPGLVIYWYGFIQELDCNRERGILL
1				1		KACFPTNIVTL
12	1202	A	845	358	92	PALSPAPVPQKKGSPLPLDPCLGPSSWLLSVG
43	1393	^	7			LGWPRL*PRRGPGDPGSLPATPPLLTPPHTLLF
1	1			- {	1	ODDMI PPSHAGLARPPPPEPISVP
			0.52	452	1	LPOYCEEPRI SPKSKLVKHSAL**PSALKPPTK
44	1394	A	853	432	1.	SPRCIPRTSLYFTICC/PPALOL/SPIEDPPALYKS
1		!			ļ	DETHIMLES A SOPLNOAPTLVKGHPPSRFLQG
	}	- 1	Ī	1		QVSCPPQPTLPREKPLPLHLRPPPRPAQPPLPR
1	{	1				PLTFSTRRNVDPEIPERFR
Į.	1					GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG
	1395	A	894	379	162	QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT
45	1			1		QEEYD/KLKILS-FQISIFVICESIGNEDITION
45			ı	1	İ	WLSMSMGK
45			1	(		THE PROPERTY AND A POST OF THE PROPERTY AND A PROPE
	1204	A	900	<del></del>	366	TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL
45	1396	A	900	1	366	TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR VFLFHQLNIT**CLHFFTMTTFIAIPFSFLFLGR

				Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D-Acceptic Acid E=Glutamic Acid,
O; of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in USSN	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
q-	uence		1	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence	[		914	amino acid	of peptide	T=Threonine V=Valine, W=Tryptophan,
	1				sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		)	ļ	residue of	Sequence	/=possible nucleotide deletion, \=possible
	1	1		peptide	Ì	nucleotide insertion
			l	sequence		DASI AMI PRI VSNSWPOVILPP
						QLQNLASRGCL*SQLLRRLRRENRLNPGGGG
<del>7</del>	1397	A	944	162	2	CSEIAP\CTPAWVTQRDFFRKKK
•		1			1	HFTPDRIAIVKNTRDSHCWRGC*EEGAPARC
8	1398	A	963	216	308	PRKRESWWGERLP/PRGFPPAAEDAPAPGWK
9	1399	A	967	466	1	GRKHASRTARAHVFHPIRQSIRSPVRGRPGDP
• •	1377			{		GRKHASKI AKAHVI HPIKQSIKSI VKOIG ODI
	1	1	ì	,	`	RAAHTRSAGTRLQCKASRGG*GKGPAPTR*E
		1	1	1	j	GGPGSAPAPLPASSGCSLFPDSSPWTPPPPAPG
		ì	1		{	AAAAQP**TPRCPAALRAGAHIGRVGRPY
	1	<del> </del>	973	45	421	EKCIQALDVFVFCYIDHSSHCLMSCD*E/DQA
50	1400	Α	9/3	1 43	]	I NEMPLEMEPKMSKLAFGCQRSS1SDDDSGC
		1				AT REVAWVPPGLRPEOIOLYFACLPEEK VP Y
	1	Ì		ì		VNSPGEKHRIKQLLYQLPPHDNEVRYCQSLSI
	1	٠	1			l r
					104	IDIDHEA ARSCLGCAAGHVPAPGLRLLPTVRC
51	1401	Α	992	2095	194	DDGDDGDAAPGCVCY*SGESTFVSHVPQRMA
			1			WPGSAPPRGFHPLQSQTSPSDTVSSPQLSKEE
	İ	İ	1			DGPGWEHPLSSSL*SLGQAGGNH*QPEELAG
	l l		Į	1	}	WEPRGPPSLAPSSPT/TMWTALVLIWIFSLSLS
	i		-	Ì		ESHAASNDPRNFVPNKMWKGLVKRNASVET
		1	1			VDNKTSEDVTMAAASPVTLTKGTSAAHLNS
	j	}	}	1		MEVTTEDTSRTDVSEPATSGVAADGVTSIAP
			1	1		AVASSTTAASITTAASSMTVASSAPTTAASST
	1	1	1			AVASSTIAASITTAASSMIVASSATTAATOS
	}	}	ĺ	l		TVASIAPTTAASSMTAASSTPMTLALPAPTST
	Į.				į	STGRTPSTTATGHPSLSTALAQVPKSSALPRT
	1		1	1		ATLATLATRAQTVATTANTSSPMSTRPSPSKI
	1	1	ł			MPSDTAASPVPPMRPQAQGPISQVSVDQPVV
			1			NITNKSTPMPSNTTPEPAPTPTVVTTTKAQAI
	1	1	1			EPTASPVPVPHTSPIPEMEAMSPTTQPSPMPY
	ł		ł	1		ODAAGPGTSOAPEOVETEATPGTDSTGPTPK
		ļ	1	1		SGGTKMPATDSCOPSTOGOYMV/DHH*APHI
	İ	l	1			GRGRONSPSGGAVTRGDPFHHSLGFVCPAGI
	}	1	1			*FLOFEGLHPGGLLNORDVCGLKNVKGAGA
	ļ	i	1			WREAWPLPRPFLLPLRPNQVLPNSFGAIEEIC
		1	1	1		OMIKHI
•		-			160	ESCEET VSFTLKKPTNVFHHINGMKFFNK/LL
52	1402	A	994	1	462	*SHTDIAFYKIQHPFMLKALTKWA*EGT*PDI
	1	1	!	1	1	RYLH*SLRLNGEQLKTFPLRSGMR*G/CAILP
		1		1		VLNAMLSIVPAVVPAGKTRHEKEITCPLIGQI
	1					EK*FS*FVGDMNTCVENKKESKKLLE
		1		1		EK-12-1 ADDAN TO CALVET A NOEDDY
63	1403	A	1011	1	630	PEVIQOSAYDSKADIWSLGITAIELAKGEPPN PEVIQOSAYDSKADIWSLGITAIELAKGEPPN
53	1403	^	1	} -		DMHPMRVLFLIPKNNPPTHCWRRLLESFKE'
		{		1		*LMLA*TKDPSNRPTAKELLKHKFIVKNSKK
[	1	-				SVI TELIDREKRWKAEGHSDDESDSEGSDSE
1		1	1	1	]	TODENNTHPEWSFTTVRKKPDPKKVQNGAL
l			1	1		DLVOTLSCLSMIITPAFAELKQQDENNASKN
1	1		- 1	1	1	AIRELEKSIAVAEAAGPG
		l				ISIDA*KAFDKIOH/CFMITTLKKLGIDGKYLI
54	1404	A	1016	1	222	TIKAIDDRHTVSTILNVEKLKAFL*RSGTRQF
			1	1	1	DISCISCARI
		- }				HASVDGDEGSDDVYYYYTPAILRELQALNT
55	1405	A	1033	3	366	EAAEHRPEEDRMLSEDPWRPAHMIKGYMP
1 22	1403	1				EAAEHRPEEDRMLSEDFWRFAITING TIME
1						HNIPHTEVIDVTGLNQSHLYQHLNKGTPMK
			1			QKRAALYTWHVLEQLEILRQINQQSHGPG
			1044		429	SVI TI OTRSPSKPLS\RKLMDWEVVSRNSISI
56	1406	A	1044	1,	727	DDIETOSRASRSPPVTPNOSOETPVDGKPLA
			1			DDNOSOKNIR VHIHYLHLOYYLDRHISATLP
1	l l	-				SSSGIPTPIAVITDALTDLVELILGQPCSEESG
1		1			1	
	ł	ţ	Y		1	APGTLFLLAL

	000 ID	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,	
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D-Accordic Acid E=Glutamic Acid,	
10: of	NO: of	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,	
ucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,	
otide	seq-	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,	
eq-	uence			ng to first	acid residue	O-Glutamine R=Arginine, S=Serine,	
ence	1	1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,	
	}	}		residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,	
	1	}	1		sequence	/=possible nucleotide deletion, \=possible	
	}	}	1	peptide		nucleotide insertion	
	\		1	sequence	122	GAYAFETNGFPIMLVLTTDKIEGDVGIAGLYD	
57	1407	A	1050	11	430	MHISLPMAFLLRTLVRCTSYIIPVTHVLSTPV	
	Ì		1	1		TCLRRREKDGVIVDVLSDTASNHNGFPVEEH	
	ł		İ	1	ł	1	ADDTHPARLQGPTLRSQPMGPLKHKAFEERA
	l .		1	1		ADDITION DIED	
	i	1	1	ļ		NLGLVQRRLRLED LKHRDTPVVGANNRALSCTPLTSLTLCALCPI	
58	1408	A	1058	258	419	LKHRDTPVVGANNKALSCIPLISETECABELL	
38	1400	1	1030			PCLGCPTXATCRLYQTTVAVVF	
	1400	<del>                                     </del>	1064	3	425	KAFSFTTSLIGHQRMHTGERPYKCKECGKTF	
59 1409	1409	A	1004	"		L'OSSOI NNHORTHTGEKPYKCNECGKALSQC	
		1	1		•	SSLIOHHRIHTGEKPYECTOCGKAF1SISKLSK	
	1	}	1	1	}	HHRIHTGEKPFHCNECGKVFSYHSALIIHQRII	
	1	i	ļ	1		TGEKPYACKDVGK	
		1			419	CCDDCDEL AHTHAGLOAPGPLLAPAGDEGDL	
60	1410	Ā	1065	204	419	LLLAVQSCLADHLLTASWGGK/DPIPTKAL	
		1	ţ	ì		EGQEGLPLTV	
	Ì		1	ļ	<u> </u>	RHSRAHLCQPFHLVMRDLLQLGQDIPQGCH	
61	1411	A	1079	3	383	LEENHLIHRDIAARNCLLSCAAPTRAATIGDE	
0.			1			GMARYTYRTRYYQLGDRAL/LPRK WMPPEA	
	\	1	1	1		LEGIFTYNTDSWTFGVLLWEIFSLGYMPYPG	
	1		1	1			
	1			1		TN TN	
	1412	A	1080	1	859	VVEFLWSRRPSGSSDPRPRRPASKCQMMEEF	
62   1412	A	1000	1.		ANLMHMMKLSIKVLLQSALSLGRSLDADHA		
			Į.	1		PLQQFFVVMEHCLKHGLKVKKSFIGQNKSFI	
		}	}	1	1	GPLELVEKLCPEASDIATSVRNLPELKTAVGI	
	.		- 1		1	GD AWI VI AI MOKKLADYLKVLIDNKHLLSI	
,	`	-		l l	ļ	LEVEREAT MMEEEGMVIVGLLVGLNVLDANL	
	- {	1	1			CLKGEDLDSOVGVIDFSLYLKDVQDLDGGK	
	1	- {	- {	Ì	{	HERITOVI DOKNYVEELNRHLSCTVGDLQ11	
	1		l			IDGLEKTNSKLQERVSAATDRICSLQEEQQQ	
	1	1	Ì			DEONEL IR	
						CCEAKHKRIHTGEKPFICLECGKAFTSSTILL	
63	1413	A	1083	2	615	HRRIHTGEKPYTCEECGKAFRQSAILYVHRR	
			1	1		HTGEKPYTCGECGKTFRQSANLYAHKKIHT	
	1		l l	-	İ	EKPYTCGDCGKTFRQSANLYAHKKIHTG\Ek	
	1			1		YKCKECGKAFKSYYSILKHKRTHTRGMSYE	
		- 1		j	Ì	YKCKECGKAFKS1 ISILKHKIIII KOM512	
	1	- 1			ļ	DEC/QRSLN/RSSILSNHKIIHNEEK/PLKCEKO	
		,	1	100	)	KAFNHTSICCRHKKN	
	1414	+-	1084	946	1	KKQDLSSSLTDDSKNAQAPLALTESHLATL	
64	1414	Α	1004	740	-	SSSOSPEATKOLLDSGLPSLLVRSLASFCFSH	
		1	ļ		1	L constancinisonklarhhvpoocnkmpij P	
		1		[		I WADTI RET TEVGNSHIMKDWLGGSEVNPLY	
		1		}	}	TALLELL CHSGSTSGS\HNLG\AOODQCKISH	
				1		FESWI TTGI TTOORTAIE\NATVAFF\LQCI\S	
		1	İ			LIDNINGKI MAOVI.CELFOTSPORGNLP15GP	
		1	1			S\GFIR\RLFLQLMLEDEK\TMFLQSPCPLYK	
		1	1	1	1	RINATSHVIQHP\MYGAGHKFRTLHLPVSTT	
			}	Ì		KINA I SH VIQHENNI I GAGHAI KI DILLI YOTT	
	Ì	1	1		Į	SDVLDRVSDTPSITAKLISKQKDDKKKK	
	1415	A	1087	103	324	PRAFEFVHTEMIVG/RVQNIHLFTLQVLEDR	
65	1415	A	1,007	1.55		LFTMSVGSSLWSTYLIHVMALP/DRELLKPN	
03	ł	- 1				SVALHKLSNALV	
l	1				493	HETCSVTHIVSESLPFLNPSHPASTPGHTENE	
		A	1095	3	473	DOI VWFDRGKFYLTFEGSSRGPSPLTMGAQ	
66	1416		1	-		TLPVAAAFTETVNAYFKGADPSKCIVKITGI	
66	1416		ļ			I ILEVANALIDITIATITATI	
66	1416					AGU CEDA GITDUE ANNIPSPA AI TERVINESR	
66	1416					MOVI SEPAGITRHEANNPSPAALTERVINESK	
66	1416					MVLSFPAGITRHFANNPSPAALTFRVINFSR HVLPNPQLLCCDNTQNDANTK\EFWVNMP	
66	1416					MVLSFPAGITRHFANNPSPAALTFRVINFSK HVLPNPQLLCCDNTQNDANTK\EFWVNMP	
			1000	57	356	MVLSFPAGITRHFANNPSPAALTFRVINFSKI HVLPNPQLLCCDNTQNDANTK\EFWVNMPI MTHLK	
66	1416	A	1098	57	356	MVLSFPAGITRHFANNPSPAALTFRVINFSKI HVLPNPQLLCCDNTQNDANTK\EFWVNMPI	

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	<b>\</b>	in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	иепсе	(	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1		}	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
		1	1	peptide	1	nucleotide insertion
	1	1	1	sequence		
	1			1		RYL
68	1418	A	1106	1	1326	MGKISATGINMGTKCSWALVWHLESYDPKH
		1	1	·	1	YEREGMQDWKTASGQSEEATQQSSQKPQPH
			i			YTTYQSSSFLKYSSESHLLAWRENSSEGSFQF
	į.	ì	ł		ļ	PGRSRARPPRTRQQRRGAAAGPGRGAVRLG
	1	1	1		1	HPQSAAQPQLRAAARIPESPAAFPAQPRPGSA
	1	1		j ·		RNSDASGPASLSRTLGRASSPRPPQAPDVTAP
	1	1	1			SPAALAPRAARGGSRAAALAGAEAEEPLRTL
	1	i	1	{		APRPTRAAAPPPPPPPPPPPPLPPGAPPPPVRCVSR
		1		}		RARAPPWR/PAATGPPP\RPVAPSRKLGSARAP
						APALQIRKGTSSGLPGRGGGSGPGNNLSSVA
		1	1	1	}	GNWRGSSFAVERPGMAKYOGEVOSLKLDDD
		1	1	1		SVIEGVSDQVLVAVVVSFALIATLVYALFRNV
		1		1	1	HQNIHPENQELVRVLREQLQTEQDAPAATRQ
	ļ	}	į.	1	i e	OFYTDMYCPICLHQASFPVETNCGHLFCGSLT
	}	}	1			PNSIW
				1	466	FDTARLHEFGTSITQIFAVDNREDLQKWMEA
69	1419	Α	1107	2	400	FWQHFFDLSQWKHCCEELMKIEIMSPRKPPLF
}	{		{		1	LTKEATSVYHDMSIDSPMKLESLTDIIQKKIEE
	1	1	İ			TNGQFLIGQREESLP/SS/CGPHSLMVTIKWSS
	1		1			RKRY/SYPASEPLHDEKGKKRQAPLPPSDK
		<u> </u>		<u> </u>		ALRRLHYVRATKVFLSFRRPFWREEHIEGGH
70	1420	A	1111	698	23	SNTDRPSRMIFYPPPREGALLLASYTWSDAAA
		1	1	1		AFAGLSREEALRLALDDVAALHGPVVRQLW
		-	Į		1	DGTGVVKRWAEDQHSQGGFVVQPPALWQT
	Ì	1	1	}		EKDDWTVPYGRIYFAGEHTAYPHGWVETAV
	j	-	ļ			EKDDWIVPYGKITAGERIATING WYLIAV
1	1	1	1	1		KSALRAAIKINSRKGPASDTASPEGHASDMEG
	ł		1			QGHVHGVASSPSHDLAKEEGSHPPVQGQLSL
	}	1		1		QNTTHTRTSH COLDEN OVER DE
71	1421	A	1119	2	385	QKQTLQNGYLDSSMDILYLGSLPPELQVSSDE
' '	. }	-	1		1	PPGPPEQAGLSQFHLEPETQNPETTEEIQSS/LQ
1	1		ı	1		QEAAAQLPQLPEVVELSSTKA\EAPALPSQSL
ŀ	ŀ	ł	İ	1	1	EGVHSSTEQKAPAQQLPAFEEILAPLLIHHE
72	1422	A	1127	1	906	HAQYVGPYRLEKTLGKGQTGLVKLGVHCIT
12	1422	1.	1	1		GQKVAIKIVNREKLSESVLMKVEREIAIL\RLI
		.	}		ļ	EHPHVLKLHGVYENKKYFPPDELTSGPSMLA
(	[	1			į	QVSPHGKLSARRSWDLLSGFPRYLVLEHVSG
		-	Į.			GELFDYLVKKGRLTPKEARKFFRQIVSALDFC
		ı		{	}	WOLLDEN THE THE TANK THE THE TANK THE T
	į	ì	i			HSYSICHRULKPENLLLDERNAIRIADI GIVAS
		-			ł	HSYSICHRDLKPENLLLDEKNNIRIADFGMAS LQVGDSLLETSCGSPHYACPEVIKGEKYDGR
						LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE
						LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE
						LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEOIOKHPWYLGGNFIS
			1120		802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEOIOKHPWYLGGNFIS
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS LRNALDVLHREVPRVLVNLVDFLNPTIMRQV
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVOQA/MLEPLGSKTETLDLRAE
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA
73	1423	A	1128	1	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HIATEYVOHIQQALDILSE
			1128	60	802	LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HLATEYVQHIQQALDILSE FREPCLLVPGDHQPLREASWLA/LPPIGLWGT
73	1423	A				LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HLATEYVQHIQQALDILSE FREPCLLVPGDHQPLREASWLA/LPPIGLWGT DSPLCCYEVAIPCNKGAHSVGLKGWLLAQG
						LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HLATEYVQHIQQALDILSE FREPCLLVPGDHQPLREASWLA/LPPIGLWGT DSPLCCYEVALPCNKGAHSVGLKGWLLAQG VLGMRDTIPQEHPWESTPDLCFCRDPEEIEVE
						LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HLATEYVQHIQQALDILSE FREPCLLVPGDHQPLREASWLA/LPPIGLWGT DSPLCCVEVAIPCNKGAHSVGLKGWLLAQG VLGMRDTIPQEHPWESTPDLCFCRDPEEIEVE EQPAADAAVAKGEF/QGEQIAPVPA\IIAAHPE
						LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HLATEYVQHIQQALDILSE FREPCLLVPGDHQPLREASWLA/LPPIGLWGT DSPLCCVEVAIPCNKGAHSVGLKGWLLAQG VLGMRDTIPQEHPWESTPDLCFCRDPEEIEVE EQPAADAAVAKGEF/QGEQIAPVPAUIAAHPE AAPPAPVHTTAHPKGA
						LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS  LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQAMLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTLPNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HLATEYVQHIQQALDILSE FREPCLLVPGDHQPLREASWLA/LPPIGLWGT DSPLCCVEVAIPCNKGAHSVGLKGWLLAQG VLGMRDTIPQEHPWESTPDLCFCRDPEEIEVE EQPAADAAVAKGEF/QGEQIAPVPA\IIAAHPE

6F 6 TO	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		Ì	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
201100	}	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide		/=possible nucleotide deletion, \=possible
	İ	}	1	sequence		nucleotide insertion  RFDNFSSLSIQWESTRPVLASIEPELPMQLVSQ
						DDESGQKKLHGLQAILVHEASGTTAITATAT
	1	}			1	GYQESHLSSAR
		l	<u> </u>		ļ	PIISAPAQDDPILLSFIHCLHANLLCVWRRDVK
76	1426	A	1155	38	410	PDCKEIWIFWWGDEPNLV/VQYIMNCMLWK
		1				KDSGKMAFPMNVGRC/FFKEIHNLLERCLMD
	}		1	{	İ	KNFVLIGKWFVRPYYKDEKPVNKSEHLSCAF
				1	1	T
				506	350	RFPQGLEDVSTYPVLIEELLSRGWSEEELQGV
77	1427	A	1162	526	330	LRGNLLRVFRQVEKVQEENKWQSPLED
			1	\ ,	1293	MAFSASPPSSSAAAPAAEPGVTTEQPGPRSPP
78	1428	A	1171	I	1293	SSPEGLEEPLDGADPHVPHPDLAPIAFFCLRQT
	1	1				TSPRNWCIKMVCNPWFECVSMLVILLNCVTL
	i		1			GMYOPCDDMDCLSDRCKILQVFDDFIFIFFA
	1	1	ì	ľ		MEMVLKMVALGIFGKKCYLGDTWNRLDFFI
			1	ł		VMAGMVEYSLDLONINLSAIRTVRVLRPLKA
					1	INRVPSMRILVNLLLDTLPMLGNVLLLCFFVF
		1				FIFGIIGVQLWAGLLRNRCFLEENFTIQGDVAL
		1	}	,		PP\YYOPEEDDEMPFICSLSGDNGIMGCHEIPP
	1		Ì	}		LKEQGRECCLSKDDVYDFGAERQDLNASGL
						CVNWNRYYNVCRTGSANPHKGAINFDNIGY
	į			į	1	AWIVIFQVITLEGWVEIMYYVMDAHSFYNFI
		1	1	1	(	YFILLIIVSVREPGLLGGSFSTAQSPKCQGDSFP
l	1	-				GVAAESLLLRGWVLWLPGGG
79	1429	A	1175	1	405	PNDFFKDMFPDLPGGPLGPIKAENDYGAYLN
13	1427	1.				FLSATHLGGLFPPWPLVEERKLKPKASQQCPI
	1				1	CHKVIMGAGKLPRHMRTHTGEKPYMCTICE
		]				VRFTRQDKLKIHMRKHTGERPYLCIHCNAKF
	1	1				VHNYDLKNHMR EMNELSQQLSQQGGRGASQCPSPPAPTLPNPT
80	1430	A	1182	25	198	PLCQLQRVNTGLPTPPCHPGAGAA
		1	_			KTVLDVGAGTGILSIFCAQAGARRVYAVEAS
81	1431	A	1186	254	583	AIWQQAREVVRFNGLEDRVHVLPGPVETVEL
	ł		Ì	1		PEQVDAIVSEWMGYGLLHESMLSSVLHARTK
	Ì	1	ļ	1		VVKDGGFFLPXSSELFM
				<del></del>	716	DEVDAARNI.PLESTKSPAEPSKSVPSLE\DPRA
82	1432	Α	1187	2	/10	SSOGLPSOGPVONOGRRGEORPKKF/TVIQHT
		1	1			SSFEKSDSLEOPSGLEGEDKPLAQFPSPPFAPH
		}		1		GRSAHSLOPKLVRQPNIQVPEILVTEEPDRPD
1	1	1				TEPEPPPKEPEKTEEFOWPQGSQTLAQFPVEK
1						L PPKKKRLGLAKMAOSSGESSFESSVPLFRSP
i	1		-	{	ļ	SQESNVSLSGSSRSALFERDDHGKAEAPSPSF
1				1		DMGPKPLGTHMLTV
1-00-			1188	517	804	ESPGLSKVLRTGAFAYPFLFDNLPLFYRLGLC
83	1433	A	1199	311	30.	WGRGHGCGOEALSTSHGYHLFCALLTGFLFA
1						SHLPERLAPGRFDYIGHSHQLFHICAVLGTHF
			}	}	1	0
-	1222		1192	45	476	I GDVGFWVERTPVHEAAORGESLQLQQLIES
84	1434	A	1172	33	1	GACVNOVTVDSITPLHAASLQGQARCVQLLL
• .	1					AAGAOVDARNIDGSTPLCECLRLGOHRVCEA
1		1				LAVLRGQGQPSPVHSVPPARGLHXREFRMC*
	- [	1	1	1		GFLFDVGXNLEAHEFHFGEP
			}			THE REPORT COTTON AND ACT DECIT I PR
95	1125		1104	69	410	KRSEEASAPPFPLGGTGAAPTRASLPEQILLPR
85	1435	A	1194	69	410	SCLEARKSOPDEKLLSALHNSRTWN*EPRRSQ
85	1435	Á	1194	69	410	SCLEARKSQPDEKLLSALHNSRTWN*EPRRSQ HRLVSPEVHPGRRGSSPGVAECKLTSAYFRT
85	1435	A	1194	69	410	SCLEARKSQPDEKLLSALHNSRTWN*EPRRSQ HRLVSPEVHPGRRGSSPGVAECKLTSAYFRT GRSPCPSLPGTTRTNSLL
						SCLEARKSQPDEKLLSALHNSRTWN*EPRRSQ HRLVSPEVHPGRRGSSPGVAECKLTSAYFRT GRSPCPSLPGTTRTNSLL LPSHTCGNPGRLPNGIOOGSTFNLGDKVRYSQ
85	1435	A	1194	69	410	SCLEARKSQPDEKLLSALHNSRTWN*EPRRSQ HRLVSPEVHPGRRGSSPGVAECKLTSAYFRT GRSPCPSLPGTTRTNSLL

			Cono	D 11.4.1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		ì	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	ì	}	į.	amino acid	of peptide	1=1 hreonine, v=vaine, w=11yptophan,
	i	ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	{	1	peptide	j	/-possible nucleotide deletion, \-possible
	Ì	ĺ	1	sequence	_	nucleotide insertion
	<del> </del>	+	<del> </del>	·		NADCTWTILAELGDTIALVFIDFQLEDGYDFL
		ł		ł	1	EVTGTEGSSLW
07	1437	A	1216	226	964	GTARFGPMVGFGANRRAGRLPSLVLGVLLV
87	1437	^	1210	-20	,	VIVVLAFNYWSISSRHVLLQEEVAELQGQVQ
ł	1	1	1		1	RTEVARGRIEKRNSDLFAVVGHAQETDRPEG
l	ł	1	i	1		GRIRPPOOPAAGORGPREEMEDDKVKLQNN
	ì	1	1	1	1	ISYOMADIHHLKEOLAELRQEFLRQEDQLQD
]	}	}	1	}		YRKNNTYLVKRLEYESFQCGQQMKELRAQH
ļ	Į.	1				EENIKKLADQFLEEQKQETQKIQSNDGKELDI
	1	1	ļ	1		NNQVVPKNIPKVAENVADKNEEPSSNHIPHG
			<b>⊥</b>		<del> </del>	PEFGTTISCGYLMATDVSRRPSVHKAVEIEQE
88	1438	A	1218	1	534	RVKSAGAWIIHPYSDFRFYWDLIMLLLMVGN
		1		1	1	LIVLPVGITFFKEENSPPWIVFNVLSDTFFLLD
			}	1	}	LVLNFRTGIVVEEGAEILLAPRAIRTRYLRTW
[	1	1		1		FLVDLISSIPVDYIFLVVELEPRLDAEVYKTAR
	1	1				
		1	·	l		ALRIVRFTKILSLLRL MGFDEVFMINLRRRQDRRERMLRALQAQEIE
89	1439	A	1223	1	743	CRLVEAVDGKVGMLTRSNAAPGRHLAMLET
			1	Į		CRLVEAVDGKVGMEI KSNAAFGKILAMEET
	1	1	1	}	1	LVVVAPRFVDADNLILNPDTLSLLIAENKTVV
1	1		1			APMLDSRAAYSNFWCGMTSQGYYKRTPAYI
	1		Į	1		PIRKRDRRGCFAVPMVHSTFLIDLRKAASRNL
}	1	}		ł	1	VAFYPPHPDYTWSFDDIIVFAFSCKQVAEVQMY
	1	1	1	ł	•	VCNKEEYGFLPVPLRAHSTLQDEAESFMHVQ
1		1		1		LEVMVPSSPSSAQSMAVVSADHIGLVISYL
90	1440	A	1227	2	349	NKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGF
1 30	1	1	1	1		GPWDFKFILCRYTSVLFYANMDTSIVVLGLIT/
	1	1	}		1	YDRY/WKVVRHL/WDSWMTGI/SFTRVYLLG
j	ļ	1		1	}	LGARLVWFGKLILAKGGHGGISWL
91	1441	A	1245	3	1937	LGSSDVRAPQRSELGAESPSRMVASQAYNLT
الع	1441	^	1213	-	1	SALTPILTRSRVLNEEPLTLAGF\SRAPANLSD
	1	1			}	VVQLIFLVDSNPFPFGYISNYTVSTKVASMAF
1	1	1	- {			OTOAGAOIPIERLASERAITVKVPNNSDWAAR
						GHRSSANSVVOPOAFVGAVVTLDSSNPAAV
	1	}		\	1	LHLOLNYTLLDGRYLSEEPEPYLAVYLHSEPR
	]	1		}		PNEHNCSASRRIRPESLQGADHRPYTFFISPGT
	1		1			RDPVGSYRLNLSSHFRWSALEVSVGLYTSLC
		1	1	1		QYFSEEDVVWRTEGLLPLEETSPRQAVCLTR
1	1	1		ſ		HLTAFGTSLFVPPSHIRFVFPEPTADVNYIVML
		1	1	1		TCAVCI VTYMVMAAILHKLDOLDASRGRAIP
1			ļ	j .		FCGQRGRFKYEILVKTGWGRGSGTTAHVGIM
	]	1	]	1	1	LYGVDSRSGHRHLDGDRAFHRNSLDIFQLATP
			Į.			HSLGSMWKIRVWHDNKGLSPAWFLQHIIVRD
		-		ļ		LQTARSTFFLVNDWLSVETEANGGLVEKEVL
1		ł		1		AASKASFRVPTPS\AALLRFRRLLVAELQRGF
		Į.		1		FDKHIWLSIWDRPPRSCFTRIQRATCCVLLICL
					1	FLGANAVWYGAVGDSAYSTGRVSRLNPLSV
1		- [		}		PERMANAL MOST DE L'ANGUERE DE L
Ì		1		}		DTVAVGLVSSVVVYPVYLAILFLFRMSRSKV
				1		GWGWGPGSTGNGAWASAPCPEPPLSSAAAR
1						GKGVHQRLLGKGQHT
92	1442	A	1246	5	562	VFDEENILNELNDPLREEIVNFNCRKLVATMP
12	1774	1	1	l		LFANADPNFVTAMLSKLRFEVFQPGDYIREG
		-	1	1		AVGKKMYFIQHGVAGVITKSSKEMKLTDGS
			1	1	!	VEGEICLLTKGRRTASVRADTYCRLYSLSVD
	1	-		1	į	NENEVLEEYPMMRRAFETVAIDRLDRIGKKN
1			}	1	ļ	SILLOKFOKDLNTGVFNNQENEILKQIVKH
		<del>-  </del>	1240	180	901	TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL
93	1443	Α	1249	100	701	PGRKASCSTAGSGSRGLPP\SSPMVSSAHNPN
		1	}	1	į	KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT
		}	1	1	1	ERPGAERPSLLPNGKENSSGTPRVPPASPSSHS
1	1	1	i	1		Did 0, mid 00011.010.

			1000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN 09/496	1	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		1	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	ì	1	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		residue of	sequence	/=possible nucleotide deletion, \=possible
	1	1		peptide	1	nucleotide insertion
	·	1		sequence		LAPPSGERSRLARGSTIRSTFHGGQVRDRRAG
		T	1	1		GGGGGVQNGPPASPTLAHEAAPLPAGRPRP
	ì		<b>,</b>			TTNLFTKLTSKLTRRVADEPERIGGPEVTRRP
	1		1	1		ROEDHLSPGGRGCSEL
	1	1	1			KFSQWGLTKPKLSNASP/WISLVKKLMKKWS
94	1444	A	1261	3	385	VTQNLTFREQLEAGIRYFDLRVSSKPGDADQ
		1	j		)	VIQNLIFREQLEAGIR I FOLK VSSRI ODADQ
	1	1	1			EIYFIHGLFGIKVWDGLMEIDSFLTQHPQEIIFL
	1	1	1	1		DFNHFYAMDETHHKCLVLRIQEAFGNKLCPA
	ļ	ì				CR
95	1445	A	1282	2	550	GPRDNPG\EDPRFEIVEHFGIAWFTFELVARFA
	1,775	1		1	1	VAPDFLKFFKNALNLIDLMSIVPFYITLVVNL
	1		1	-	1	VVESTPTLANLGRVAQVLRLMRIFRILKLARH
		}	1			STGLRSLGATLKYSYKEVGLLLLYLSVGISIFS
		ļ	}	1		VVAYTIEKEEN\EGLATIPACWWWATVSMTT
						VGYGDVVPGTTAGKLTASACILA
96	1446	A	1294	1	1456	QLLPPSNRENAGLLVGRCLCSAALRPVGDLIT
) 90	1440	1.	1257	} -		SSGQVAVRNAPQAGSAKAGKGKFQDNFEFIQ
	ĺ		j			YFKKFFDANCNEKDYNPVAAGQGQETEVAP
	1		- (			SIVAPVLNKPNQCPEGYICVKAGRNPNYGYT
	1	1	ĺ			SFDTFSWAFLSLFRLMTQDYWENLYQLTLRA
		1	ļ	4		AETTYMIF/LV/LVILLGSLYLVTLILAV/VAMA
	1	Ì	1	ļ		YEEQNQATLEEAEQKEAEFQQMLEQLKKQQ
		1	1	ì		EAAQQAATATASEHSREPSAAGRLSDSSSEAS
	1	-{	1	ļ	1	KLSSKSAKERRNRRKKRKQKEQSGGEEKDED
	]				1	EFQKSESEDSIRRKGFRFSIEGNRLTYEKRYSS
				}	)	PHQSLLSIRGSLFSPRRNSRTSLFSFRGRAKDV
		1		1		GSENDFADDEHSTFEDNESRRDSLFVPRRHGE
	1	- [		Ì		RRNSNLSQTSRSSRMLAVFPANGKMHSTVDC
]	}	1	- 1	1		NGVVSLVGGPSVPTSPVGQLLPEVIIDKPATD
			]			DNGTTTETEMRKRRSSSFHVSMDFLEDPSQR
	ì	1	l		]	QRAMSIASILTNTVE
	1447	A	1295	2	2057	IQTQLPTKSSQQLRKGGNCVRCKMQMNFLAE
97	1447	Δ.	1275	1		EVLLKYRITFYNNNKGPNMLYIEIKAFVHFMI
		-				NRYLSYGSGPKRFPLVDVLQYALEFASSKPV
	1	)	Ì	1	1	CTSPVDDIDASSPPSGSIPSQTLPSTTEQQGALS
	1	į	1	[		SELPSTSPSSVAAISSRSVIHKPFTQSRIPPDLP
		- 1	1	}		MHPAPRHITEEELSVLESCLHRWRTEIENDTR
		1	1		]	DLQESISRIHRTIELMYSDKSMIQVPYRLHAV
	1 .	1	1	1	Ì	LVHEGOANAGHYWAYIFDHRESRWMKYNDI
		- (	1	1		AVTKSSWEELVRDSFGGYRNASAYCLMYIN
		1	1	1		DK AOFLIOE\DLIKTGQPLVGIETLPPDLRDFV
		1		}	}	FEDNORFEKELEEWDAOLAOKALQEKLLAS
		ĺ		1		OKLRESETSVTTAOAAGDPKYLEQPSRSDFSK
1	}	1		1	{	HIKEETIOIITKASHEHEDKSPETVLQSAIKLE
}	1	1		ļ	1	VARLVKLAOEDTPPETDYRLHHVVVYFIQNQ
1		- [	İ	1		APKKIJEKTLLEOFGDRNLSFDERCHNIMKVA
	i	1		1	1	OAKLEMIKPEEVNLEEYEEWHQDYRKFRETT
1	1	1		1	(	MYLLIGLENFORESYIDSLLFLICAYONNKELL
1	1	1	1		}	SKGLYRGHDEELISHYRRECLLKLNEQAAELF
			1	1	1	ESGEDREVNNGLIMNEFIVPFLPLLLVDEMEE
1	1					KDILAVEDMRNRWCSYLGQEMEPHLQEKLT
		}				DFLPKLLDCSMEIKSFHEPPKLPSYSTHELCER
1						FARIMLSLSRTPADGR
			_			SGPSSRAIYLHRKEYSQNLTSEPTLLQHRVEH
98	1448	A	1304	118	453	LMTCKQGSQRVQGPEDALQKLFEMDAHGRV
	1			1		WSQDLILQVRDGWLQLLDIETKEELDSYRLD
		- 1				WOODLILQ VKDOWLQLLDIE I KEELDO I KLD
i	- 1	1	1			SIQAMNVALNTCSYNSILS
	1					
99	1449	A	1306	3	1660	CGYFCHTTCAPQAPPCPVPPDLLRTALGVHPE TGTGTAYEGFLSVPRPSGVRRGWQRVFAALS

			1 050	D4!e4-4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spertic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	Ì	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1		sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	Ì	ļ	1	residue of	Sequence	/-possible nucleotide deletion, \-possible
	ì	1	i	peptide		nucleotide insertion
	ì	l	l	sequence	ļ	DODI LI EDAPDI RI SPPSGALLOVLDLRDPQF
				Į	ļ	SATPVLASDVIHAQSRDLPRIFRVTTSQLAVPP
	1	}	Ì	1		TTCTVLLLAESEGERERWLQVLGELQRLLLD
	1		1		1	ARPRPRPVYTLKEAYDNGLPLLPHTLCAAILD
	i		Ì	ì		QDRLALGTEEGLFVIHLRSNDIFQVGECRRVQ
	1		1			QLTLSPSAGLLVVLCGRGPSVRLFALAELENI
	ļ	1	Ì	1	1	EVEVPKIPESRGCQVLAAGSILQARTPVLCVA
	1		4	į		VKRQVLCYQLGPGPGPWQRRIRELQAPATVQ
		1	ł	1		SLGLLGDRLCVGAAGGFALYPLLNEAAPLAL
	1	}	}	}	Į.	GAGLVPEELPPSRGGLGEALGAVELSLSEFLL
	1	1	1	1		LFTTAGIYVDGAGRKSRGHELLWPAAPMGW
		}	}	1	j	GYAAPYLTVFSENSIDVFDVRRAEWVQTVPL
	1	1	1			KK\VRPLNPEGSLFLYGTEKVRLTYLRNQLAE
	1	-	į			KDEFDIPDLTDNSRRQLFRTKSKRRFFFRVSE
	1	1	į		1	EQQKQQRREMLKDPFVRSKLISPPTNFNHLV
	ł	Ì	ŀ	1	1	HVGPANGRPGARDKSP
		1			<u> </u>	SLCVPGPVDTGTFAVMSVMVGSVTESLAPQA
100	1450	A	1318	918	190	LNDSMINETARDAARVQVASTLSVLVGLFQV
100		1			}	GLGLIHFGFVVTYLSEPLVRGYTTAAAVQVF
	ł		(	{	1	VSQLKYVFGLHLSSHSGPLSLIYTVLEVCWKL
	ļ			1		PQSKVGTVVTAAVAGVVLVVVKLLNDKLQQ
	1		ł	1		QLPMPIPGELLTLIGATGISYGMGLKHRFEAG\
	1	}	}		1	PPVAPNTQLFSKLVGSAFTIAVVGFAIAISLGK
	i	Ì	-		ł	IFALRHGYRVDSNQVWVMRDV
1			ł			DWPDLFTYPLIGSPKCFQSARPERMYRRTVR
101	1451	Ā	1353	220	445	SSHGNHALQEVLPRSGHGTEFTKQKHLEAAD
10.				ì		SSHGNHALQEVERSONOTELTIQUEEZ
	ì	j				HGHPPARMSIFSR AHLLMLNLAL\TDLL\YLTSLPFLIHYYASGEN
102	1452	A	1363	542	2	WIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRY
102	1				}	CVIIHPMSCFSIHKTRCAVVACAVVWIISLVA
	- 1	1	ì	Ì		VIPMTFLITSTNRTNRSACLDLTSSDELNTIKW
		1	}	}	ł	YNLILTAULCLPLVIVTLCYTTIIHTLTHGHAN
		ļ	l l	-		YNLILIAULCLPLYIVILCI I IIIII BIII GIA
ļ	Ì					\DSCLKQKARRLTILLL CHSTESSSDFILPGDYLLGGLCPLHSGCLQV\C
103	1453	A	1371	2	410	SFNEHGYHLFQAMRLAVEEINNSTALLPNITL
103	1433	1	1	l l		GYQLYDVCSDSANVYATLRVLSLPGQHHIEL
1	1	}		ļ		QGDLLHYSPTVLAVIGPDSTNRAATTAALLSP
	Į.		ļ	Ì		QGDLLHYSPIVLAVIGPDSTNRAATTATEEDI
	<b>,</b>	ì	l	1		FLVPMLLEQ
104	1454	A	1376	3	432	NSRVEDRS/NMSLWTQNITVCPVRNVTRDGG
104	1434	1	1			FGPWSPWQPCEHLDGDNSGSCLCRARSCDSP
1	1			}	1	RPRCGGLDCLGPAIHIANCSRNGAWTPWSSW
İ		ì	ì	Ĭ	1	ALCSTSCGIGFQVRQRSCSNPAPRHGGRICVG
	1		1	1		KSREERFCNENTPCPVPIF
100	1455	$-\frac{1}{A}$	1379	2	396	GLGLLYLIFAAVEGVMRVIGGSNHLAVVLDD
105	1433	A	13/3	1-		IILAVIDSIFVWFIFISLAQTMKTLRLRKNTVKF
		1	1			ST VEHEKNTI IFAVLASIVEMGWITKITKIAK
]				1	}	CQSDWMERWVDDAFWSFLF\SLILIVIMFLW
			1	ļ		RPSA
			1202	<del>   </del>	432	EDGHGGWSSRCLVDHAEEGHREPWKRLCIW
106	1456	_ A	1383	1	7,72	ORGGHEIRFAFYFPGHPLLSPQICLAPETPPRG
1		-				CPPVSSI HFISLO/RLPRDCOELFQVGERQSGL
1	1	1	l	1		FEIQPQGSPPFLVNCKMTSGTFWTCRTDSRVF
1			1	- (		ONANPSNAAHSEDOPTP
					650	FFFVTRSHSVAQAECSGVFTAHRSLDLVGSSN
107	1457	A	1386	719	558	VPAI SLOSSWDHRHTWLIFAFL
						RVAISLLCAAIFISFMVQSAGKRWPTGVMLM
	1458	A	1397	631	2	VVVLFAFLYSWPIQALLPTYLKTDLAYNPHT
108	1 100	- 1	1		1	A A A DI LAT DI MITATION IN THE COMPANY
108	1,150	l	1	ĺ	í	VANDE SESCEGA A VGCCV/GGFLGDWLGTRK
108	1.50					VANVLSFSGFGAAVGCCVÆGFLGDWLGTRK AYVCSLLASQLLIIPVFAIGGANVWVLGLLLF

T	0FQ ID 1	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of		noa	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	ì	{	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ì	(		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	į			sequence	/=possible nucleotide deletion, \=possible
	l	}		peptide	Ì	nucleotide insertion
	<u> </u>			sequence	<del> </del>	FOOML GOGIAGILPKLIGGYFDTDQRAAGLG
						FTYNVGALGGALAPIIGALIAQRLDLGTALAS
			}	Ì	]	LSFSLTFVVILRNRRPGKSLVR
	ľ	i	Ĺ			VLVALPDT\VTSETVVTEVLGHRVTLPCLYSS
109	1459	A	1402	15	387	WSHNSNSMCWGKDQCPYSGCKEALIRTDGM
					1	RVTSRKSAKYRLQGTIPRGDVSLTILNPSESDS
	1	}	1	l		GVYCCRIEVPGWFNDVKINVRLNLQRASTT
		1	l	<u> </u>		HEDLSSLLTRGSGNQERERQLKKLISLRDWM
110	1460	A	1421	3	350	LAELAFPVGVLATCA*SLLSC*YCVILFPCSCF
		1				FFHSPDALFSLLLLSCYFPSYCFFYYLFFSSSPL
			Ì		ļ	FFHSPDALFSLELLSC IFFS ICIT I I BIT GOOD E
	1	1	}			CLLLASSPFPLFILLASL
111	1461	1 A	1426	2	344	FTSTMTKPFEKESEQPA*ATLAFGAQTSTTAD
111	1401	1.			ì	QCALKPDLSYLNNSSSSSSTPATSAGGGIFGSS
		1	1	1	1	TSSSNPPVATFVFGQSSDPVSSYGFVNTAESST
	1	1	1			SDSLLFSQDSKLATTS
	1462	A	1434	46	372	TTSWTTSCTRSCT*SGASSGPGWTPRTTWWR
112	1462	1^	1434	1.0		SRRSSQRTCSRACSGAWSRTW*RSS*TSSSSC
						STSCSSSSSRSCGRPGGPLGARGVHITSCLNSC
	1	1		1	}	MSSSTTSSTTSTF
		<del></del>	1439	3	292	HEDIMTHYDRI.VDE*ALNAGKORYEKMISG
113 .	1463	Α	1439	3	272	MVI GEIVENII IDETKKGFLLRGOISEMLKIK
	1	i		Ì		GIFLTFLLSNFLIVCVLLFYVSFYLFQSCINFVL
				<b>_</b>	396	KOOAVPEPHSSTTTPOEQEQNWYGQDLLNLQ
114	1464	Α	1463	1	390	QRTKVHLPGHKTGPAVAKDTPEPVKKEFTVP
	1	1		l	j	ATSQGP*SPFSEEPPLPPSNEEVPPTLPP*EPQS
l	İ	1	į.	}	1	EDP*KNA*LKQMHAATTHWQQHQQHQVGC
İ		-				OVEGIMO
1	Į.					AGSYPSMVWSCHWGVTQKRRAL*VYSFEEG
115	1465	A	1464	291	2	GRRKCGQYWPLEKDSRIRFGFLTVSNLGVEN
	1		1			MNHYKKSTLEILNPEVNPGFFFLTLWKQGEN
1		1	}	1		NYCN
1	1	1				LPPQRPA*TDSYSTCNVSSGFLAGQSHNIHLQ
116	1466	A	1465	667	337	YWTKYQVWEWLQHFLDTNQLDANCIPFQEF
	į	1	l	i		DINGEHLCSMSLQEFTRAAGTAGQLLYSNLQ
ł	1	1	Ì	1		DINGEHLCOMOLOGIC CI SI PC
1	]	-		_		HLKWNGDSLFLCLSLPC GTSGGPKRVLVTERFPWQNPLPVNRGQAQR
117	1467	A	1479	1	381	VLGPSNSFQRVPLQAQKLVSSHKPGQNQKHK
111/	1107	1				VLGPSNSFQRVPLQAQKLVSSHKFQQIQALI
]	Į.					QLQATSVPHPVCMPLNNTQKSKQPLPSAPEN
	ì		1	1		NPEEELASDPNNEESL*RPWALEDFEIGRPLG
}		1	1			KGK
110	1468	A	1485	3	385	TYLWL*GNPPFYEKNDGGLFELILRAKDEFNS
118	1408	^	1,403	•		PYWDDMSDSAKHFIRPLTGRDP*KPFPCDQPL
	{					OHPWIEGHTCL DNNIHOAASEPINNNFAESKR
	1			Į.		NLAFLATGVVRHMRKLFMGANLEGPGPTVS
1	1		1	i	[	н
				<del></del>	398	GTTSKHH*LARSLIRGPFDHDLKPNAATRDQL
119	1469	Α	1486	1	370	NITUSYPPTKOLTYEEODLGWKFRYYLINQE
1				)		VALTUEL KWYNWDI POEAKOALELLUKWK
1		ļ				PMDVKDSLELLSSHYTNPTVRRYAVARLRQA
1		1				DDEDLLMYL
		1				MGESPAV*GYFVLAGMNSAGLSFGGGAGKY
120	1470	A	1497	3	999	LAEWMVHGYPSENVWELDLKRFGALQSSRT
		1		)		FLRHRVMEVMPLMYDLKVPHWDFQTGRQL
,		(	1			FERNING DAY OF A DAY VENT GEED BY A LINE OF A
				1	1	RTSPLYDRLDAQGARWMEKHGFERPKYFVP
			1	1		
						PDKDLLALEQSKTFYKPDWFDIVESEVKCCK
						FAVCVIDMSSFTEFEITSTGDQALEVLQYLFS
						EAVCVIDMSSFTEFEITSTGDQALEVLQYLFS NDI DVPVGHIVHTGMLNEGGGYENDCSIARL
						FAVCVIDMSSFTEFEITSTGDQALEVLQYLFS

SEQ ID   SEQ ID			B P. J	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl- peptide		in USSN	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
eotide seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence		914	ng to first	acid residue	O=Ghitamine, R=Arginine, S=Serine,
uence		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
]			peptide		/=possible nucleotide deletion, \-possible
			sequence		nucleotide insertion
		<del> </del>	3043		MTPDHFPSLFCKEMSVGYANGIRVMSMTHT
					GEPGFMLYIPIEYRWGFTMLSTLVSNS
121 1471	A	1498	3	306	AQFLLVGWDHIL*LIVL*TNLTELGRTTCDQN
121 14/1	Λ.	1470	-		WPNSPDVLNHGCFYMQCLSKDCTIGYVSRE
	l		1		MLVAHTHTVEEHTGTHLQYVSWPDHSVPDD
	ļ		[	1	SSDFVEFEN
122 1472	A	1533	121	329	LGLFSFVWTEVLEEPKDFSCETEDFKTLHCT
122	1	1.500			WDPGTDTALGWSKQPSQSYTLFES*VGSGYII
		}			DNFFLA
123 1473	A	1547	111	408	DARTTWKPRNGSSGIWPGDGAK*PPAVEQAE
123	1		· ·	1	RGHVEMIEKLTFLNLHTSEKDKGGNTALHLA
	1	1			AKHGHSPAVQVLLAQWQDINEMNEKQQTPL
	l .		}		HVAADRG
124 1474	A	1555	1	745	MTFDDDDKNTYGVALVWKKFQTQSLRLSDL
127 177	1				HRKSHLWRGIVSITLIEGRDLKAMDSNGLSDP
					YVKFRLGHQKYKSKIMPKTLNPQWREQFDF
}	1				HLYEERGGVIDITAWDKDAGKRDDFIGRCQV
] ]	1				DLSALSREQTHKLELQLEEGEGHLVLLVTLT
	ļ				ASATVSISDLSVNSLEDQKEREEILKRYSPLRI FHNLKDVGFLQVKVIRAEGLMAADVTGKSD
	}	1		]	PFCVVELNNDRLLTHTVYKNLNPEWNKVFTL
	1		ł		*VALVWKKFQTQSLRLSDLHRKSHLWRGIVS
	1				ITLIEGRDLKAMDSNGLSDPYVKFRLGHQKY
1	1			1	KSKIMPKTLNPQWREQFDFHLYEERGGVIDIT
	1				AWDKDAGKRDDFIGRCQVDLSALSREQTHK
1					LELQLEEGEGHLVLLVTLTASATVSISDLSVN
	1		ļ		SLEDQKEREEILKRYSPLRIFHNLKDVGFLQV
	İ				KVIRAEGLMAADVTGKSDPFCVVELNNDRLL
	i	İ	1		THTVYKNI.NPEWNKVFTL
		1.55		509	GGPAPNSRYAEP*KNSLAMT*AHADCENYVA
125 1475	A	1556	57	303	CGGLDNICSIYNLKTREGNVRVSRELPGHTGY
	1	1	l		LSCCRFLDDSOIVTSSGDTTCALWDIETAQQI
	1				TTFTGHSGDVMSLSLSPDMRTFVSGACDASS
					KI WDIRDGMCROSFTGHVSDINAVS
	<del></del>	1592	13	178	KSEKSCVSSLAHFGTSCORDYDAMVKLVETL
126 1476	A	1392	13	1,70	EMILPTCDLADOHNIKFHYAFALNR*ER
100	<del> </del>	1612		497	TESPI I VRPYLPYITKSELHAIMTAGFSTIAGS
127   1477	A	1012	1 *		VI GAYISFGVPSSHLLTASVMSAPASLAAAKL
	1	- [	1		FWPETEKPKITLKNAMKMESGDSGNLL*AAT
			1		OGASSSISLVANIAVNLIAFLALLSFMNSALA
			1		WVGNMFDYPQLSFELICSYIFMPFSFMMGVE
}	}	1	1		WPDSFM
100		1619	286	486	CCMNSKAOESVFKNVLCNPPALSEMPDVKA
128 1478	A	1013	200		EDEVDFRASSISEEVAVGSIAATLKMKQGPM
					TOAINR
100	<del>  </del>	1627	<del>                                     </del>	395	PTRGALRYWIFGRFLCNIWAAVDVRCCTATI
129 1479	A	1027	1.		MGLCUSIDRYVGVSYPLRYPTIVTQRRGLMA
	1				LI CVWALSLVIYIGPLLGWRHPAPEDETICQI
			1	i	NEEPGYVLFSTPGSFYLPLAIMLVMN*RVYRV
1 1	-		1	ł	AKTE
1	<del></del>	1638	2	466	DPRVRTKIVNRKTTIYEIQDKTGSMAVVGKG
120		1036	1-	1.50	FCHNIPCEKGDKLRLFCFRLRKRENMSKLMS
130 1480	A				FMHSFIOIOKNTNORSHDSRSMALPQEQSQHP
130 1480	A	Ì			
130 1480	A				KPSEASTTLPESHLKTPQMPPTTPSSSSFTKVT
130 1480	A				KDKDIK*LLFNLYSSVEILPEVLHLKT
		1651	407	3	KDKDIK*LLFNLYSSVEILPEVLHLKT LAEGGDVFDCVLNGGPLPESRAKALFRQMVE
130 1480 131 1481	A	1651	607	3	KDKDIK*LLFNLYSSVEILPEVLHLKT  LAEGGDVFDCVLNGGPLPESRAKALFRQMVE AIRYCHGCGVAHRDLKCENALLQGFNLKLTD
		1651	607	3	KDKDIK*LLFNLYSSVEILPEVLHLKT  LAEGGDVFDCVLNGGPLPESRAKALFRQMVE AIRYCHGCGVAHRDLKCENALLQGFNLKLTD FGFAKVLPKSHRELSOTFCGSTAYAAPEVLQ
		1651	607	3	KDKDIK*LLFNLYSSVEILPEVLHLKT LAEGGDVFDCVLNGGPLPESRAKALFRQMVE

SEQ ID No. of No		_					Amino acid sequence (A=Alanine C=Cysteine,
NO. of No. of lo No. in cleation mucl-code of the coation mucl-code of the coation of the coatio	SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Admine C-Cystolic,
muche official poptide contribution of the con			hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
Coulde Sequence 1944   1484   1656   150   48   1534   1484   A 1666   1276   466   1276   466   1276   1485   A 1673   1   417   1485   A 1673   1   417   4185   A 1673   1   417   4185   A 1678   325   9   A 1678   A 1678   1   417   4187   A 1680   1   417   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4187   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1680   1   4188   A 1673   1   4170   A 1680   A 1678   A					nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ence ence ence ence ence ence ence ence							I=Isoleucine, K=Lysine, L=Leucine,
sequence   14	eotide		l			to lost omino	M=Methionine N=Asparagine, P=Proline,
uence   914   ng to first anino acid residue of peptide sequence   victual of peptide sequence   victual of peptide sequence   victual of peptide sequence   victual of peptide sequence   victual of peptide sequence   victual of peptide sequence   victual of peptide sequence   victual of peptide   victu	seq-	uence		09/496			O Clataria Badeginine Sassine
antino acid residued peptide sequence peptide sequence peptide sequence peptide sequence sequ	-		i	914	ng to first		Q=Glutamine, K=Arguille, 3-Seriue,
	uchec	i	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptopnan,
		Ì	ļ	(	residue of		Y=Tyrosine, X=Unknown, *=Stop codon,
1482   A   1656   150   48		}	1	ļ		Joque	/=possible nucleotide deletion. \=possible
132	1	Ţ	ļ	1		ļ	
RILLEPOMILRSIEEVSWHPWLAST*KQWQV LSNXVGGESKPKKK     132		Į.		ì	sequence		nucleotide inscrion
132	·	+	1			Ţ	TDIPKMLWQQQKGVSFPIHLSISADCQDLLK
132	1	1	}	1			RLLEPDMILRPSIEEVSWHPWLAST**KQWQV
132	Ì	1	1	1		1	LSNKVGGESKPKKKK
133			1			<u> </u>	LUAVELL VCGCLEELL OLAKNVGNNSENDIM
133	132	1482	Α	1656	150	48	E AND TOPODY DEPOSIT AND THE TYPE CAWHY
133	ì		ļ	1	1		
KKEFKKKMDDQRFEKITEA*SKDKSPMEEK   TEMRSYIQEVGPYIKKLER.QKSKLEKLREK   HKERQPILDEKPKGEGSSSFLSETCHEDTSWF   TEMRSYIQEVGPYIKKLER.QKSKLEKLREK   HKERQPILDEKPKGEGSSSFLSETCHEDTSWF   PNFTP   PSTHASARITIV*L*III.SNATEVDNNFSKPP   FFFAGAPPASSSSSSSSPTVSTAPPLIPPGF   PPPFOAPPSLIPTIESGHSSQTDRRSARAFPYG   NVAFPILLPGSAPSSSPSSSSPRONDRER; RTRERERERDHS   SSSSSSSSSSSSSSSPRONDRER; RTRERERERDHS   PTFSVFNSDEERYRYREYAERGYERHRASE   KERHRERHREKETHRIKSSNSRRHESE   EGDSHRRHKHKSKRSKEGKEAGSFPAFGE   STEATPAE   EGDSHRRHKHKSKSKSKEGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKEGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKEGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSKSKSKSMISSMSMALGE   EGDSHRRHKHKKSKSKSKSKEGKEAGSFPAFGQE   STEATPAE   EGDSHRHKHKKSKSKSKSKSKSKSMISSMSMALGE   EGDSHRRHKHKKSKSKSKSKSKSKSMISSMSMALGE   EGDSHRFHKKKSKSKSKSKSKSKSKSKSKSKSKSKSKSKSKSKSKS	)	1	}			ł	VDAQ
KKEFKKKMDDQRFEKITEA*SKDKSPMEEK   TEMRSYIQEVGPYIKKLER.QKSKLEKLREK   HKERQPILDEKPKGEGSSSFLSETCHEDTSWF   TEMRSYIQEVGPYIKKLER.QKSKLEKLREK   HKERQPILDEKPKGEGSSSFLSETCHEDTSWF   PNFTP   PSTHASARITIV*L*III.SNATEVDNNFSKPP   FFFAGAPPASSSSSSSSPTVSTAPPLIPPGF   PPPFOAPPSLIPTIESGHSSQTDRRSARAFPYG   NVAFPILLPGSAPSSSPSSSSPRONDRER; RTRERERERDHS   SSSSSSSSSSSSSSSPRONDRER; RTRERERERDHS   PTFSVFNSDEERYRYREYAERGYERHRASE   KERHRERHREKETHRIKSSNSRRHESE   EGDSHRRHKHKSKRSKEGKEAGSFPAFGE   STEATPAE   EGDSHRRHKHKSKSKSKEGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKEGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKEGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSGKEAGSFPAFGQE   STEATPAE   EGDSHRRHKHKSKSKSKSKSKSKSMISSMSMALGE   EGDSHRRHKHKKSKSKSKSKEGKEAGSFPAFGQE   STEATPAE   EGDSHRHKHKKSKSKSKSKSKSKSMISSMSMALGE   EGDSHRRHKHKKSKSKSKSKSKSKSMISSMSMALGE   EGDSHRFHKKKSKSKSKSKSKSKSKSKSKSKSKSKSKSKSKSKSKS		1.400	<del>                                     </del>	1660	2	406	RKHIKLLIOKLSDVP*ECQNNQL*KLTEICEKE
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EVDHLREITEREMQLTSQKQTMEALKTTCT MLEEQVMDLEALNDELLEKERQWEAWRSVL GDEKSOFECR VRELQRMLDTEKQSRARADQ RITESRQVVELAVKEHKAEILALQQALKEQK LKAESLSDKLNDLEKKHAMLEMNARSLQQK LETERELKQRLLEEQAKLQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRKESST PEEFSRRLKERMHINIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSFGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	137	1487	A	1080	1	2777	DNAFI NNONFYLSKOLDEASGANDEIVOLRS
MLEQVMDLEALNDELLEKERQWEAWRSVL GDEKSQFECRVRELQRMLDTEKQSRARADQ RITESRQVVELAVKEHKAEILALQQALKEQK LKAESLSDKLNDLEKKHAMLEMNARSLQQK LETERELKQRLLEEQAKLQQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHFSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHINIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMK VPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRITLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCHFTNYSLIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	ı	1		}	1		EVIDITI PREFERENCI TSOKOTMEALKTTCT
GDEKSQFECRVRELQRMLDTEKQSRARADQ RITESRQVVELAVKEHKAEILALQQALKEQK LKAESLSDKLNDLEKKHAMLEMNARSLQQK LETERELKQRLLEEQAKLQQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGGLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQVTLEEFLDKNDHSLAPAVFAASS	1	Ĭ	1	- (			EADHEWELLEWING LOOK AMBONI
RITESRQVVELAVKEHKAEILALQQALKEQK LKAESLSDKLNDLEKKHAMLEMNARSLQQK LETERELKQRLLEEQAKLQQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWYTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS		1	1		1		MLEEQVMDLEALNDELLERERQWEAWRSVL
LKAESLSDKLNDLEKKHAMLEMNARSLQQK LETERELKQRLLEEQAKLQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHRFNVGLNMÄATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEFFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS		}		J	1		GDEKSQFECRVRELQRMLDTEKQSRAKADQ
LKAESLSDKLNDLEKKHAMLEMNARSLQQK LETERELKQRLLEEQAKLQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHRFNVGLNMÄATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEFFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS		1	- 1	1	1		RITESROVVELAVKEHKAEILALQQALKEQK
LETERELKQRLLEEQAKLQQQMDLQKNHIFR LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS		1	1	1		1	I KAESI SDKLNDLEKKHAMLEMNARSLOOK
LTQGLQEALDRADLLKTERSDLEYQLENIQV LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPPSAMSLLAPPSSRKESST PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	}	1	- 1	1	1	1	TETEDEL KORLLEFOAKLOOOMDI OKNHIFR
LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS		1	1	1	1		LETEVETVÁVETERÁVETÁÁÁINE ÁIRIUM
KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRKESST PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS	٠.				ļ		LIQGLQEALDRADLLK TERSDLE T QUEINIQV
KKKKVPLQYNELKLALEKEKARCAELEEALQ KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRKESST PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS	1	ľ		1	1		LYSHEKVKMEGTISQQTKLIDFLQAKMDQPA
KTRIELRSAREEAAHRKATDHPHPSTPATARQ QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS	1			- 1	1	[	KKKKVPLOYNELKLALEKEKARCAELEEALQ
QIAMSAIVRSPEHQPSAMSLLAPPSSRRKESST PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	1	İ	1	j	}	1	KTRIFI RSAREFAAHRKATDHPHPSTPATARO
PEEFSRRLKERMHHNIPHRFNVGLNMRATKC AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	-			1		1	OTANGA IND CDETTODS VIVET I VDDCCD BK ECCT
AVCLDTVHFGRQASKCLECQVMCHPKCSTC LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YIVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WVTALES VVAGGRVSREKAEADAKLLKLEGDD RLDMNCTLPFSDQVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS			l	i	1		QIAMSAIV KSFERQF SAMSLEAF I SSIGGLESSI
LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WYTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	!	1	1	1	[		PEEFSRRLKERMHHNIPHRENVGLNMKATKC
LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQR WYTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	1	1	1	1	1		AVCLDTVHFGRQASKCLECQVMCHPKCSTC
KEPSSSLHLEGWMKVPRNNKRGQQGWDRK YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS			ì	J	1	1	LPATCGLPAEYVTHFTEAFCRDKMNSPGLQT
YTVLEGSKVLIYDNEAREAGQRPVEEFELCLP DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	1	- 1	- 1		[	1	KERSSSI HI EGWMK VPRNNKRGOOGWORK
DGDVSIHGAVGASELANTAKADVPYILKMES HPHTTCWPGRTLYLLAPSFPDKQRWVTALES VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS	ļ	1	- 1		1	1	PELBOOTHER MANEY LEGISLICATION OF THE PERSON
HPHTTCWPGRTLYLLAPSFPDKQRWVTALES  VVAGGRVSREKAEADAKLLGNSLLKLEGDD  RLDMNCTLPFSDQVVLVGTEEGLYALNVLK  NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA  LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV  KGCHLFGAGKIENGLCICAAMPSKVVILRYN  ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK  FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS	Ì		1		1	į	YIVLEGS VLITUNEAREAUUR VEEFELCE
HPHTTCWPGRTLYLLAPSFPDKQRWVTALES  VVAGGRVSREKAEADAKLLGNSLLKLEGDD  RLDMNCTLPFSDQVVLVGTEEGLYALNVLK  NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA  LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV  KGCHLFGAGKIENGLCICAAMPSKVVILRYN  ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK  FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS		- 1	- 1		1	İ	DGDVSIHGAVGASELANTAKADVPYILKMES
VVAGGRVSREKAEADAKLLGNSLLKLEGDD RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS		1		1	[	¥.	HPHTTCWPGRTLYLLAPSFPDKQRWVTALES
RLDMNCTLPFSDQVVLVGTEEGLYALNVLK NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS		1	1	(	1		VVAGGRVSREKAEADAKLLGNSLLKLEGDD
NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS			1	1			DI DI DICTI PECDOVUI VCTEEGI VAI NVI K
LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS					1		KLDIMING I LELOUGY Y LYGI EBOD I ALLY DIX
KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS	i	1		(		:	NSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA
KGCHLFGAGKIENGLCICAAMPSKVVILRYN ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS	1	1	- [	- 1	1		LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV
ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS			-	)		1	KGCHLEGAGKIENGLCICAAMPSKVVILRYN
FYEIDMKOYTLEEFLDKNDHSLAPAVFAASS				1	1		ENI SKYCIRKEIETSEPCSCIHETNYSILIGTNK
NSFPVSIVQVNSAGQREEYLLCFHEFGVFVDS_	Į	Į.				!	ENDAROUT EEE DEMOUS ADAVEAACC
NSFPVSIVQVNSAGQREEYLLCFHEFGVFVDS_		i	į	1			FIELDWAY I LEEFLUNNUMSLAFA FRANSS
						!	NSFPVSIVQVNSAGQREEYLLCFHEFGVFVDS

	00010	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
NO: of	NO: of	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence	ı	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	delice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	}			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ļ	peptide		/=possible nucleotide deletion, \=possible
		1	}	sequence		nucleotide insertion
			<del> </del>			YGRRSRTDDLKWSRLPLAFAYREPYLFVTHF
	}					NSLEVIEIQARSSAGTPARAYLDIPNPRYLGPA
	i	1	1			ISSGAIYLASSYQDKLRVICCKGNLVKESGTE
		1		ĺ		HHRGPSTSRR*PASPLPQYQGQRAFLQGRRK
138	1488	A	1686	2	526	GRPQGPAPGAGSPPESGPGLWAALGCSLVWV
130	1400	1 .			ļ	PLCCLGGAAGRL*ARSGKSGLRRRRAHAGPP
			1			PGGPCNSCP*CSAPESGGRGPLPGPGTGGVCS
			1	i		CWTRGCQTTARTAAAAAAPGPAGRRPPGGA
		1	1	1		PONGSCAASASQEAAAPPPMCPPGRRWAVAS
	ļ		1	1		PPETRCPAAPGTRCRRLEAA
139	1489	A	1693	3	376	LPSMSNCTSCFRLQSRTES*IRQAGHLLGRNE
139	1402	1		į	į	FIETKALGCAWFSLCYYLVLYFESSHKVDFVF
	1	İ		i		IV*CFSTPPGAQMTIMSQACAERCNIMRLVDR
	1	1	1	1		RWAGIAKGVGTQKIIGRVHLGEQKALGL
140	1490	A	1704	3	376	ERTNKFIKELIMDGKNLIAATKSLSVAQRKFA
140	1420	'-				HSLRDFKFEFIGDAVTDDERCIDASLREFSNFL
			}		j	KNLEEQREIMVS*EGCKLISQLSRGKKIWIWK
						LVLVEVVKHLSLGTVVHCNGKMRFPEP
141	1491	A	1743	1	362	LITNKVFVARELSCLDVHLDSTGSTAVVADQ
171	147.	1		1	İ	DKLELELYLKGSYEDTQTSFLGTASAFRFHY
	ì	1	1		]	MAAL*TELSGRLRSSKSNGWNGDNSTGYLTV
	Ì					PLRPLTIVKEVTMDVPAPNVRGLNWMG
142	1492	A	1769	1	406	NNPSTLPRGS*PMSPRTTMGRRRQRRREHKSS
172	1.,,2	1				LSLASSTVGPGGQIVHTETTEVVLCGDPLSGF
		1				GLQLQGGIFATETLSSPPLVCFIEPDSPAERCG
	İ	1	1	}		LLQVGDRVLSINGIATEDGTMEEANQLLRDA
!	ł	1				ALAHKVV
143	1493	A	1789	1	447	QMLRNGGDQNTVPDYHFADRIRELL*PTEDQ
1.5	1	1				KNCIP*DTYLRPSALGNIVEEVTHPCSPGPCPA NELCEVNRKGCTSGDPCLPYFCVQGCKLGQA
	Ì	ì		1		SDFIARQGTLIQVPSSAGEVECYKICSCGQSGL
ļ		}		}		SDFIARQUILIQVESSAUEVECTRICSCOQUE
	.	ł		<u> </u>		LENCMEMHCMDLPTDTSALVR PGRRFRPRLSQAGTDSGS*VFPDSFPSAPAEPL
144	1494	A	1814	1	404	PYFLQEPQDAYIVKNKPVELRCRAFPATQIYF
	1	ŀ				KCNGEWVSQNDHVTQEGLDEATGLRVREVH
	ļ	ļ	}		}	IEVSRQQVEELFGLEDYWCQCVAWSSAGTTK
	Ì	1				SRRAYVRI
						XVEEKHADTWRSXCLSDFFFHAAKXLCXE*N
145	1495	A	1827	26	448	CGDAISLSVGDHFGKGNGLTWAEKFQCEGSE
	1	ĺ				THLALCPIVQHPEDTCIHSREVGVVCSRYTDV
	-	l l		1		RLVNGKSQCDGQVEINVLGHWGSLCDTHWD
	Í			-		PEDARVLCRQLNCGTAL
						QHEGGDLRRRQLGEIQLTVRYVCLRAASAC*
146	1496	A	1828	574	333	SMAAET*HHVPASGADPYVRVYLLPERKWA
1						CRKKTSVKRKTLEPLFDET
	1					ERLVLTSEHCLVLTLFWPSWTYHTLLLSRQH
147	1497	Α	1855	1	372	VRRLPKLTHAEHDHLASIMNKLLTNYDNLFE
	1	1		1		TSVTYSMG*HGAPTGSEAGANWNH**LHAH
						YYPPLLRSDTVRKFMVGSQMLAQAQRDLTPE
1		1		}		
i	1				<u> </u>	Q   LLSALDDKGGTQPSASFSNAPTIVCVTACPAG
148	1498	Α	1879	568	7	IAHTYMAAEYLEKAGRKLGVNVYVEKQGAN
						GIEGRLTADQLNSATACIFAAEVAIKESERFN
1	1	1				GIPALSVPVAEPIRHAEALMQQALTLKRSDET
						RTVQQDTQPVKSVKTELKQALLSGISFAVPLI
1		1				VAGGTQVA*AV*RQGISSLHDVQVRTWNS
						GLNSENALSNEAMERGWQCLRLFAERLQDIP
149	1499	A	1880	611	24	PSQIRVVATATLRLAVNAGDFIAKAQEILGCP
		1 '	1	ı	1	- PACIEV VATATEKLA VINAGDEMANA QEDUCE
1					i .	VQVISGEEEARLIYQGVAHTTGGADQRLVVD

PCT/US01/03800

			1000	6 3:3-4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence		}	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	residue of	sequence	/=possible nucleotide deletion, \=possible
		1	1	peptide		/=possible nucleotide deteriori, /-possible
	İ		}	sequence		nucleotide insertion
		<del> </del> -				IGGASTELVTGTGAQTT*LFSLSMGCVTWLER
	1	1	1	İ		YFADRNLGQENFDAAQKAAREVLRPVADEL
		Į				RYHSWKEVRGASVTVQALQEIMMAQGMDE
	1	1		ł	1	RITMEIWPVD
		<del>  </del>	1004	2	750	GRYDFEHTDYRPLIRDSNNYVLDEQTQQAPH
150	1500	A	1894	2	130	I MPPPFI VDVDGNPHPTKYQRLVPGRENSAU
	1	İ	Į.	İ		FHI IPOL GYVATSDGEVIEQIISLQTNDNDERS
1	İ	·	1			PESSILDGMIRQLQQQQDQRMGADQDTIPRG
	ł		1	1		LSNGEETPRRGFRRLSLDIQSPPNIGLRRSGQV
	1	1	1	1		EGVRQMHQNAPRSQIATERDLQAWKRRVVV
	1	1		1		PEVPLGIFRKLEDFRLEKGEEERNLYIIGRKRK
ì	1		ł	Į.		PEVPLGIFKKLEDFKLEKGEBERGET HORGAGE
ì	1		į.			TLQLSHKSDSVGLVSQSRPRTCRRKYP
	1501	A	1900	141	785	GKTIQIQTTMQNKYKTVQKQYKTIPKNKKA
151	1201	1 ^	1,000	1		MEMQIKKQFQDTCKVQTKQYKALKNHQLEV
				ì		TPKNEHKTILKTLKDEQTRKLAILAEQYEQSI
}	1	1	1	i	1	NEMMASOALRLDEAOEAECOALRLQLQCEM
1	1	1	1	1	<b>\</b>	FILNAVOSKIKMOTEAOHERELQKLEQRVSL
Ì	l		}	1	-	RRAHLEOKIEEELAALQKERSERIKNLLERQE
ļ	1	1	1	1		REIETEDMESLRMGFGNLVTLDFPKEDYK
Į.					200	LVRLLDTQRDGLQNYEALLGLTNLSGRSDKL
152	1502	Α	1915	2	377	ROKIFKERALPDIENYMFENHDOLROAATEC
			1		j	MCNMVLHKEVQERFLADGNDRLKLVVLLCG
	i	Ì	- {			EDDDK VQNAAAGALAMLTAAHKKLCLKMT
l	- {		Į.			
1	- 1					QVTT ACVITS A VOI
153	1503	A	1921	1	237	AYQSLRLEYLQIPPVSRAYTTACVLTSAAVQL
123	1505	11	1,72.	1		ELITPFQLYFIPELIFKHFQIWRLITNFLFFVPFG
		i	Ì			FNFLLYMIFLYT
1	1504	- A	1928	12	354	EMVEGGEGKMCINTEWGGFGDNGCIDDIRTR
154	1504	\ A	1920	-		YDTEVDEGSLNPGKQRYEKMTSGMYLGEIV
	Ì	1	1	[		RQILIDLTKQGLLFRGQISERLRTRGIFETKFLS
į.	1	1	Į.			OTESTRE AT LOVERILOOLGLD
				<del></del>	369	TETAKIKMEAKKKYEKELTMFONDFEKACQA
155	1505	A	1929	2	309	LYSEAT VI REKSTLERIHKHOEIETKELYAURU
1	i		- 1	}		LLLKDMDLLRGREAELKQRVEAFESYQLELK
		i	ì	}		DDYIIRTYRLIEDDRINIQISGHWQESP
	ļ	- }	i	<u> </u>		VTRKLPIFIVDAFTARAFRGSPAADCLLENEL
156	1506	A	1935	1	270	DEDMHQKIAREMNLSETAFIRKLHPTDNFAQ
1	1		İ	1		DEDMINUALARENINGS IN THE TOTAL
1		1		1		RSCFGLIWFTPTTDLQILTSSILPSIL
157	1507	A	1936	584	305	ESKVNNEKFRTKSPKPAESPQSATKQLDQPTA
137	1507	10	1			AYEYYDAGNHWCKDCNTICGTMFDFFTHMH
		j	1	1		NKKHTQGQFQKSSDFQKEELQQTFLPPERQG
<u></u>	1500		1939	1	423	TTHRLNVTAEPPCTSMPIYWMPDVPHRCTTA
158	1508	Α	1737	1.	1	NTCDVDI TDVCAONGFYCLVYGFLPYGSLED
Ì	1	1			İ	DI HOOTOACPPI SWPORLDILLGTAKAIQFLH
		1	1	1	· ·	QDSPSLIHGDIKSSNVLLDERLTPKLGDFGLA
}		1			1	RESREAGSSPIOSSM
	1	L			<del></del>	HTSTARLLHRGAGKEAVTSDGYTALHLAAR
159	1509	A	1974	3	401	NGHLATVKLLVEEKADVLARGPLNQTALHL
1				1		AAAHGHSEVVEELVSADVIDLFDEQGLSALH
	1	1				LAAQGRHAQTVETLLRHGAHINLQSLKFQGG
						LAAQGRHAQIVETLLKHGAHIIALQSLKIQGG
-	1		1			HGPAATLLR
1	1510		1982	2	417	KFLKDLEKQYNKEEPHLSEIGSCFLQNQEGFA
160	1510	A	1702	1 -	1	IVSEYCNNHPGACLELANLMKQGKYKHFFEA
1	,	-		İ		CPLI COMIDIAIDGELL TPVOKICKYPLQLAEL
	1	1		)		LKYTTQEHGDYSNIKAAYEAMKNVACLINER
1	1	1		1		KRKI ESIDKIA
	1	1				RETGSVSLSPSGLEGAESYAVSPILYSSPDVKE
161	1511	A	1984	4	770	LWLETLQGQRHSHTGVKSTPGQSAAILMKLR
1 ' ' '	1					SSHNASKTLNANNMETLIECQSEGDIKEHPLL

			1.000	Dudiand	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ł	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	i		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	1		residue of	sequence	Y=1yrosine, X=Unknown,Stop codon,
	l	i		peptide	{	/-possible nucleotide deletion, \-possible
	<b>{</b>	1	l	sequence		nucleotide insertion
	<del> </del>	<del>                                     </del>				ASCESEDSICQLIEVKKRKKVLSWPFLMRRLS
	ļ	]				PASDFSGALETDLKASLFDQPLSIICGDSDTLP
	1	1	1			RPIQDILTILCLKGPSTEGIFRRAANEKARKEL
}	1	}	1			KEELNSGDAVDLERLPVHLLAVVFKDFLRSIP
ļ	1	1	1	}		RKLLSSDLFEEWMGALEMQDEEDRIEALK
		<del> </del>	1000	864	501	LLNSGLFSAPDGSNLEMRLTRGGNMCSGRIEI
162	1512	A	1986	804	301	KFQGRWGTVCDDNFNIDHASVICRQLECGSA
	1	1	1	ì		VSFSGSSNFGEGSGPIWFDDLICNGNESALWN
ł	1		l			CKHQGWGKHNCDHAEDAGVICSSKD
	}	1	i	l		AVDLSIDESSLTGETTPCSKVTAPQPAATNGD
163	1513	A	2001	419	187	AVDESIDESSETGET PCSKVTAPQPAATNOD
	1	}		1		LASRSNIAFMGTLVRCGKAKGVVIGTGENSE
	1	1	1			FGDIINLSTFVVHS
164	1514	A	2012	284	597	SLLCLFPGTSTVVCKPIVIETQLYVIVAQLFGG
104	1314	1 ^	1 20.2	1 -0.	1	SHIYKRDSFANKFIKIQAIEILKIRKPNDIETFKI
ĺ			1			ENNWYFVVADSSKAGFTTIYKWERETGFYSH
1						OSFTR
	<del></del> _		2013	12	403	EDPEELGHFYDYPMALFSTFELFLTIIDGPANY
165	1515	Α	2013	4	703	NVDLPFMYSITYAAFAIIATLLMLNLLIAMMG
1			1	i		DTHWRVAHERDELWRAQIVATTVMLERKLP
	1	1	1	ļ		RCLWPRSGICGREYGLGDRWILRVEDRQDLN
}	ł	1	ł	{		RORIORYA
					<del></del>	CCOREGLGLKAVVQILLSHGRNGLPGEPASS
166	1516	A	2019	2	927	QGLSAASSTPVFHLALQIDSAPDNIDWVEMLF
İ			1	1		NKNMVTERLQNVMVLEQCFSDSSSLYRFLTY
1	1		l	1		SYLLAFNVWLLLAPVTLCYDWQVGSIPLVETI
1	ł	1	1	1	[	SYLLAFNYWLLLAPVILCIDWQVOSILEVEIT
-	1		i	1		WDMRNLATIFLAVVMALLSLHCLAAFKRLE
1	Į.		ł		1	HKEVLVGLLFLVFPFIPASNLFFRVGFVVAER
}	}			}	1	VLYMPSMGYCILFVHGLSKLCTWLNRCGATT
		į.	i		1	LIVSTVLLLLLFSWKTVKQNEIWLSRESLFRS
1	1					GVQTLPHNAKVHYNYANFLKDQGRNKEAIY
1	1	- {				HYRTALNNNKAWDYLCWRFRKTLTDLP
167	1517	Ā	2025	696	71	AAASAASSLTVTLGRLASACSHSILRPSGPGA
167	1517	A	2023	1 000	1	ASLWSASRRFNSQSTSYLPGYVPKTSLSSPPW
	<b>\</b>	1	ļ			PEVVLPDPVEETRHHAEVVKKVNEMIVTGQY
1		- 1	l l	Į		GRLFAVVHFASRQWKVTSEDLILIGNELDLA
	ľ		- (	1		CGERIRLEKVLLVGADNFTLLGKPLLGKDLV
1						RVEATVIEKTESWPRIIMRFRKRKNFKKKRIV
1	1	1	l		1	
ļ					1266	TTPQTVLRINSIEIAPCLL HLQVAARVFMPLQAVDSAPKPLKGQAQAPQ
168	1518	A	2046	2	366	RLQGAARVFMPLQAQVKAKASKPLQMQIKA
		1		1		PPRLRRAARVLMPLQAQVRAPRLLQVQSQVS
1	1	l	1	1		YEAR A OF OTERPORT DOMPETER CONTOUR P
}			1	1		KKQQAQTQTSEPQDLDQVPEEFQGQDQVLR
169	1519	A	2049	1	945	QNLEDREVLNGVQTELLTSPRTKDTLSDMTR
107	1317	1.		1		TVEISGEGGPLGIHVVPFFSSLSGRILGLFIRGI
1			}	1	}	EDNSRSKREGLFHENECIVKINNVDLVDKTFA
1	1	1		1		OAODVFROAMKSPSVLLHVLPPQNREQYEKS
				1	i	VIGSLNIFGNNDGVLKTKVPPPVHGKSGLKTA
1			1	1		NLTGTDSPETDASASLQQNKSPRVPRLGGKPS
1						SPSLSPLMGFGSNKNAKKIKIDLKKGPEGLGF
			}	1	1	TVVTRDSSIHGPGPIFVKNILPKGAAIKDGRLQ
				1	1	SGDRILEVNGRDVTGRTQEELVAMLRSTKQG
		1				ETASLVIARQEGHFLPRELVMFRSQSH
	1					PVATHLTKILNSDEHAVVISSAKTLCETVKDF
170	1520	A	2050	363	1	PVAIHLIKILNSDEHAVVISSAKILUEIVKDE
1		1		1	1	VAKVEKTYDKTLENAVVADAVASKCSVLNE
				1	1	KLEQLLQALHTDSQAAPVLPGLSPLIVEEDAV
						ESSSEESLGESKEOLGDDVTKPSSQKA
101	1531	<del></del>	2055	139	675	IPSRPWLGRITGLDPAGPLFNGKPHQDRLDPS
171	1521	Α	2033	133	1 3.3	DAOFVDVIHSDTDALGYKEPLGNIDFYPNGG
ı	1				1	LDQPGCPKTILGGFQYFKCDHQRSVYLYLSSL

		->	CCO T	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	1 — 1	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	ĺ		914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	l	l		amino acid	or peptide	V=Tyrosine, X=Unknown, *=Stop codon,
			Į.	residue of	sequence	/=possible nucleotide deletion, \=possible
		}	1	peptide		nucleotide insertion
	1		1	sequence		RESCTITAYPCDSYQDYRNGKCVSCGTSQKE
	<del>                                     </del>				1	SCPLLGYYADNWKDHLRGKDPPMTKAFFDT
	1	1		ļ	1	SCPLLGY YADNWADHLAGADI WITA
	Į.		}	ļ	_	AEESPFCMYHYFVDIITWNKNVR
172	1522	A	2056	3	361	LIQHKSAVEYAQSHLSLVSMCKESHKCSEPK
172	1322	1.	2000	1	1	MEWKVKIRSDGTRYITKRPVRDRILKERALKI
	1	1	1	1		KEERSGLTTDDDTMSEMKMGRYWSKEERKQ
	}	1		}		HLVRGKEQRRRREFMMRIRLKCLKES
		<del> </del>	2060	1	387	GTRILSMQIPFVGFQPIRTSEHMAAAGVFALL
173	1523	Α	2060	1	307	OAVAFLOYLEDRITKOEFOTLFFLGVSLAAG
	Ì	Į	· I			AVFLSVIYLTYTGYIAPWSGRFYSLWDTGYA
			1		l	KIHIPIIASVSEHQPTTWVSFFFDLHILGCTFPA
	ł	1	1		1	G
		1		<u> </u>		LLMGPKAKKSGSKKKKVTKAERLKLLQEEEE
174	1524	A	2071	74	443	RRLKEEEEARLKYEKEEMERLEIQRIEKEKW
• • •	1		1	1	l	HRLEAKDLERRNEELEELYLLERCFPEAEKLK
		1		1		HRLEAKULEKKNEELEEL I LLEKCT FEAERLK
	1			1		QETKLLSQWKHYIQCDGSPDPSVAQEMNT
175	1525	+A	2083	139	486	AALTWSQPQEFWPMEMQPIVTDMVTVHWV
1/5	1323	1	2000	1		AESSTVGWLCALFRVTHVGVGATGHGVVCG
	1	1	ì			RRVLCGLPLPSPAPMPIMSLPEGESRKEREVQ
	ļ	1	1	1		RLQFPYLEPGHELPATTLLAFLAAV
			2092	3	587	EGSVNFKFGVLFAKDGQLTDDEMFSNEIGSEF
176	1526	A	2092	13	1 307	FORFINILGDTITLKGWTGYRGGLDTKNDTT
		-	Į.	1	1	GIHSVYTVYOGHEIMFHVSTMLPYSKENKQQ
	1	1	Ì	1	Ì	VERKRHIGNDIVTIVFOEGEESSPAFKPSMIRS
1		1	1	1		HETHIEALVRYNOONDNYRLKIFSEESVPLFG
		1	-		1	PPLPTPPVFTDHQEFRDFLLVKLINGEKATLET
	1	ŀ	l		Ì	PCI
)	ì	·			100	GKGQVSLEGRPHRGPLCLGSWWPGSRVPGC
177	1527	A	2103	44	427	CDGAWLAWACWVFGNDFPSPASAACSALLO
		- [	ì	ľ		CSVSTACLCVPLCSGSPLAPFRRTAALQEGLR
		1	1	1		RAVSVPLTLAETVASLWPALQELARCGNLAC
}	1	- (	ł	1		
ì				1		RSDLQ
178	1528	A	2104	12	409	ALQSTLGAVWLGLLLNSLWKVAESKDQVFQ
176	1320	1	1			PSTAASSEGAVVEIFCNHSVSNAYNFFWYLHI
}	j	1	Į.		į	PGCAPRLLVKGSKPSQQGRYNMTYERFSSSL
	1	- 1				LILQVREADAAVYYCAVEVPNTDKLIFGTGT
		}	)	1		DI OVERNIONED
			<del>-  </del>	<del>-                                    </del>	312	PTRSSTRPPSLFVHASAKGGEKEEGDDGHYL
179	1529	A	2111	1	312	MRTESHTGLKKGGNANLVFMLKRNTEPKKG
}		1	Į.		1	SYHFDLERLRAAHILFEREQEHLAPGGISMPL
}	1	- {			1	PPPI PI PACLG
		[				TSIKRAIETTDVTRSFGWDSSEAWQQHDVQE
180	1530	A	2116	3	366	LCRVMFDALEQKWKQTEQADLINELYQGKL
1.55						KDYVRSLECGYEGWRIDTYLDIPLVIRPYGSS
		- 1		Į		KDYVKSLECUTEUWKIDITEDIRETINI
1		1.		1		QAFASVVCTFHLTACVSLHRIHNSTVV
101	1621	A	2117	2	386	YGLGAHFGRLFIQAGINENDFYDGAWCAGR
181	1531	Ι Δ	211/	-		NIDI OOWIEVDARRLTRFTGVITOGRNSLWLS
}	ł	}				DWVTSYKVMVSNDSHTWVTGKNGSGDMIF.
	1	Ì				GNSEKEIPVLNELPVPMVARYIRINPQSWFDN
				1		GSICI
1		L			402	RTKTDVYILNLAVADLLLLFTLPFWAVNAVI
182	1532	Ā	2123	1	493	GWVLGKIMCKITSALYTLNFVSGMQFLACIS
1						DRYVAVTKVPSQSGVGKPCWIICFCVWMAA
		1				DKI VAVIA VISQSO VOLICODVI CTEME A
						LLSIPQLVFYTVNDNARCIPIFPRYLGTSMKA
		}				IQMLEICIGFVVPFLIMGVCYFITARTLMKMP
		1		1		NIKIS
	1	<b></b>			561	RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ
183	1533	A	2140	3	201	RSGNYFVTMFDDYSATLPLLIVVILENIAVCF VYGIDKFMEDLKDMLGFAPSRYYYYMWKY

PCT/US01/03800 WO 01/57188

						Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-A martic Acid E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		in	nucleotide	corresponding	Introducing K=Lysing, L=Leucing,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	j	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T-Threonine V=Valine W=Tryptophan,
	ľ		1	amino acid residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
					sequence	/=possible nucleotide deletion, \=possible
1				peptide sequence	l .	lestide insertion
				sequence		SPI MI I SI LIASVVNMGLSPPGYNAWIEDKAS
		·	1		1	FEELSYPTWGLAVCASLDVFAILPYPVAFIGR
	İ	<b>\</b>	1		1	DESCIDENCAGPECSAAYTTTGCRTPYL
			21.45	3	538	LUCI TVA A ADRGOPPOSSVVPVTVTVLDVND
184	1534	A	2145	3	750	NIDDI/CTD ASVRVTVPEDTPVGAELLHVEASU
					1	ADDODLICI VRETVSSGDPSGLFELDESSGILK
	ļ	t	ì	1		I ATTAL DOCTOARHOLVVOAADPAGAHFALA
		1	\	į		PUTIEVODVNDHGPAFPLNLLSTSVAENQPPG
			}	1		THE VITTE HAIDGDAGAFGRURYHL
		<del></del>	2161	2	671	LOVILDEMENYNIFNEYILKOVAATYIKLUW
185	1535	A	2151	12	"	DENDIENGSI VOASYOHEELRREVIMLACSI'U
	1	1		1		NICHOLOGA STI ISDWISSNRNRIPLNYKUIV I
		•	1			1 OTCVCI I DEDUWEFIWMKEHSI IAVSEKKIL
		1	İ			LEALTCSDDRNLLNRLLNLSLNSEVVLDQDAI
	1	1		1	Ì	DVIIHVARNPHGRDLAWKFFRDKWKILNTRI
						ROKTLEFDFAEPLILAFPIILYTAIDNPPLVREH
		1				E CEIDVIA DEIDVIA DE WETWA
106	1536	- A	2153	2	400	GPMCDKHSAFAEKFHAGFIDYIVHPLWETWA
186	1530	\^	21.55			HLALPDAQDILYTLEDNRNWVDSMIPQSPSPP
	1	1 .,				LDEONROWOGLLENLHVELTLDEEDSEGPEK
	1	1 '		1		EGEGQTYFTSSKTLCGIVPQNTDSLGETGIHIC
				1		AHDKSP FNCFRVASDSFLENSSLLIMILPLRNATQEFIIR
187	1537	A	2158	227	442	PGAVAYTCNPSTLGGWGGWITRSGVRDQPG
107	133,	1				PGAVAYICNPSILOGWOGWINGOVIA
Ì						QHGGTPS AHLGGAWLTQRSLGSWAAPGPARAAKEVVA
188	1538	A	2167	3	486	CIPQNQKMNIWRMKTSKHLQLLSFVLGAVSP
100	1330	1		1	į	AVVVPYMMVLQENGYGVEGIPTLLMAASS
1	1					MDDILAITGFNTCLSIVFSSGCARSSGSRNSKS
		1	}			LRTPLGTICEGCDDSSIFSHLDHSSKWSSTYG
		ł		İ		HSGA
		L			412	TEL SSNOTTOL PNTTERPMPNLRSVDLSYNKL
189	1539	A	2168	2	412	OALAPDI FHGI RKI TTLHMRANAIQF VP VRIF
		ì		1		ODCDEL VELDICYNOLKSLARNSFAGLIKLIE
1		1	}	1		LHLEHNDLVKVNFAHFPRLISLHSLCLRRNKV
	· I	-	1	1		AIVUSSI DW
					399	ARL MONITLL LESEGX XRPYTSEHAPTYHQW
190	1540	A	2179	64	333	LAW ADEL I DWTTSEPLILEHE I AMURI WEED
		1	1			AVECTFIVLDAEKRHAQPGATEESCMVGDVF
	1		1			TELEPTICAL TO LEGAL T
		_		1	469	CLDB A A CIRHERNVIYINETHTRHRGWLAKK
191	1541	_ A	2190	1 1	1.05	I COULTIOERD VHKGMFATNVTEN VLNSSKV
			}	1		DEALARYAAFI NPDGSAOOOSKAYNKYKKA
	1	1	1			AVDIT OF ACCUATOS PAMIRLI GWYLLKLINST
-	<b>\</b>		1			FWNIQIHKGQLEMVKAATETNLPLLFLPVHR
	1	1	}	ļ		1 011
L				26	157	PSKXGGIRLLLTGTQLYGRFGSAIAPLGDLDR
192	1542	A	2197	20	13.	LDCVNGFGREEPY
		_ +	2226	- 2	383	FVEDNETURS FSTMDLGDIGFYTYRILUALS
193	1543	A	2236	1	1 505	VTHSKGIMHRDVKPLNILCNSPKNKVILADW
!	-	1	ļ			CLAFFVHPMRKYSVHVATRYYKSPEILLDIG
						YYDYSLDIWAVGVILLELLTLKLHVFEGGDN
	)	1				FO.
				105	409	PKGVGKMPTSEGRPGOERSDWVTSYKVMG
194	1544	A	2241	103	100	NOCHTWYTYKNGSGDMIFEGNSEKEIPYLNE
		Ì	}	- 1		LPVPMGARYIRINPQSWFDNGSICMRMEILG
	1	1		1		DI PIDPNNY
L				<del></del>	672	MGVASDWTKRIEYOPGSGSMPLFPSIHLEIC
195	1545	Α	2245	1	0,2	GAVSSLQIVTELQTNYIGKGCDRETYSEKSLO
133	1					

IO: of I ucl- I otide	NO: of peptide seq-	Met hod	SEQ ID NO: in	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
ucl- otide eq-	peptide seq-	hod	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide eq-	seq-					
eq-	. ,			location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
~4			USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
ence	uence		09/496		acid residue	O=Glutamine R=Arginine, S=Serine,
	}		914	ng to first amino acid	of peptide	T-Threonine V=Valine, W=Tryptophan,
1	!		ļ [		sequence	V=Tyrosine, X=Unknown, *=Stop codon,
ł			1 1	residue of	Sequence	/=possible nucleotide deletion, \=possible
. \			1 1	peptide		nucleotide insertion
1		_		sequence		VI CGASSGUDLL PSPSAATNWTAGLLVDSSE
+						MEKEDGROGAKIPDGIVPKNLTDQFITIMW
1			ļ i			MKHGPSPGVRAEKETILCYSDKTEMNRHHY
1	'		}			ALYVHNCRLVFLLRKDFDQADTFRPAEFHW
1			1			KLDQQALAKVDGQPGKSITRQLQEMPVTIQG
Ì			1	Ì		ISLKPS
			1		<u> </u>	FRGTPVSGLTNRDTLAVIRHFREPIRLKTVKP
196	1546	A	2256	1	396	GKVINKDLRHYLSLQFQKGSIDHKLQQVIRD
170	10.0		l		1	NLYLRTIPCTTRAPRDGEVPGVDYNFISVEQF
1		İ	1	ļ	ì	KALEESGALLESGTYDGNFYGTPKPPAEPSPF
1		ĺ	1			
į		ļ	1			QPDPV CONTROL DREODVIOREE
197	1547	A	2259	43	594	QLAIEIGVRALLFGVFVFTEFLDPFQRVIQPEEI
17/	1577	1.,				WLYKNPLGQSDNIPTRLMFAISFLTPLAVICV
		}		1		VKIIRRTDKTEIKEAFLAVSLALALNGVCTNTI
	]	}	-	1		KLIVGRPRPDFFYRCFPDGVMNSEMHCTGDP
	1	1	1			DLVSEGRKSFPSIHSSFAFSGLGFTTFYLAGKL
				1		HCFTESGRGKSWRLCAAILPL
100	1548	A	2275	3	404	TCTTVVVIPRMLVDFLSESKTISLPECATQMFF
198	1348	Α.	2213	1		FLGFASNNCFIMAAMSYDRYTAIHNPLQYHT
	1					LMTRKICLQMMMASWMVGFLFSLCIIVTVFN
	1.5	1	1	1		LSLCDLNTIQHYFCDISPVVSLACNYTFYHEM
		1	i			AIFVLSA
	1.640	A	2315	1	375	LTOMFFIHALSAIESTILLAMAFDRYVAICHPL
199	1549	A	2313	1.		RHAAVLNNTVTAQIGIVAVVRGSLFFFPLPLL
	1	1	1	ì		KRLAFCHSNVLSHSYCVHQDVMKLAYADTL
	1	1	Ì			PNVVYGLTAILLVMGXDRMFISLSYFLII
	1.77		2334	- 2	409	PRVRPQQRKMSFFFKTELGEKLVTKFLFETDF
200	1550	Α	2334	2	100	CDDDMI PSPDOLKKKAPFINKKLKAHQIPVI
	1		1	}	1	ILKQKAHQLASMQVQAYNGGNANPRPANNE
	1	Ì	}		}	EEEDEEDEYDYDYESLSDDNILEDRPENKSCH
			i	į		DQLQFEYKEEM
i		<del></del>	- 2350	+3	512	ISWEAQIAEIIQWVSDEKDARGYLQALASKM
201	1551	Α	2350	) 3	312	TEELEVI BOSSI GSRTI DPLWK VKRSQKLDM
	l	- 1	Į.	1		CADI FLOSAL FAFIRAKOLVOEELKKVKDAN
ļ	1		Ì	1		I TO TOKE KOSEAKNRELLEEMELLKKKMEEK
		l	1	ļ		FRADTGKLMLCDSALFEYKYFSNECFYFLFD
ì	1	1	1		Ì	LIVIL FAPTEFOIOY
					1003	DSSVSSDELSPGEPLTSPPWAPLGAPERPEHLI
202	1552	Α	2351	1	1003	LADATEDI AGGATRDSAASDILLDDIVLIHSLI
		1	ļ.	ì		I DTEKET OF LHOYEVRAGGMEGPEGLGRKQ
	1			1		CLAMITHELDTYOGLLOEEEGAGHIKULYL
	-		l			I IMVDEST VOGLREDTLRLHOLVETVELKIPI
İ		ļ				ENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGS
		l		}	1	DETECTATION THIS TRIBLES AS VOLUMES V
1	1	1	1			TEKLQYSEPAGREDSLILVAVSSSGEKVLLC
1	1		-			PTEDCVFTALGINSHLFACTRDSYEALVPLPE
		1		ļ		EIQVSPGDTEIHR VEPEDVANHLTAFHWELF
		i	(		!	FIGASACHIENKAELEDAWIMIDIA
				Ì		CVHELEFVDYVFHGE
202	1553	A	2361	2	403	NNLNCAEPLFEQNNSLNVNFNTQKKTVWLII NNLNCAEPLFEQNNSLNVNFNTQKKTVWLII
203	1223	1	230.			GYRPVGSIPLWLQNFVRILLNEEDMNVIVVD
ļ					1	WSRGATTFIYNRAVKNTRKVAVSLSVHIKN
1		1			ļ	LKHGASLDNFHFIGGSLGAHISGFVGKIFHGG
1		-	}	{		I CRITCI DP
		+-	2390	280	476	SPSLLPQCLMSLSDLSLSPAPPSHLSPRCPSPC
. 204	1554	Α	2390	200		AGSRLGAMRRCAREMDATPMPPAPSCPSER
204	1		1	1	;	Τ
204	- 1					the second secon
				5/2	745	AAVALRDISWQQPYPMDFYAGSSLGPWIVE
205	1555	A	2400	543	745	AAVALRDISWQQPYPMDFYAGSSLGPWTVI HGQDRRPHAPGRPARGKVQEGSARPPSAVA

					- 1: - 1 d	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-Agnertic Acid E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	I=Isoleucine K=Lysine L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	of peptide	T=Threonine V=Valine, W=Tryptophan,
		1		amino acid	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	}	1	\	residue of	sequence	/=possible nucleotide deletion, \=possible
		j	}	peptide		-valentide insertion
		l		sequence	105	DLSPDSREDHPQGHRRLLPKRPVRGSLMPGH
206	1556	Α	2406	122	485	THHPCPVSSTTNDTPDQIWVSVGSLRMGTGG
	ì				·	MGANASTSPRCWDLSSGNKKWIIQVPILASIV
	Ì	ĺ	1		Į.	ESRGGLLATGVGGMCACVPRNQPLTGT
		1				LWTLYRHKQQVQHNHSNRLSCRPSQEDRAT
207	1557	A	2409	289	418	HTIMVLDKENTLS
			i		<u> </u>	VQGTGXXFIAFTEAMTHFPASPVWAGMFFL
208	1558	A	2413	64	492	MLINLGLGSMIGTMAGITTPIIDTFKVPKEMFT
200	1.000					GGCCVFAFLVGLLFVQRSGNYFVTMFDDYSA
	1	1		1		TLPLTLIVILENIAVAWIYGTKKFMQELTEML
			l l		ļ	TEPETETY OF THE THE THE THE THE THE THE THE THE THE
	1	1		<u> </u>		GFRPYRFYFYMWKFVSP EKERLLDEWFTLDEVPKGKLHLRLEWLTLMP
209	1559	A	2417	3	877	EKERLLDEWFILDEVPROANDGI SSALLILY
209	1337	1	1			NASNLDKVLTDIKADKDQANDGLSSALLILY
	)				ì	LDSARNLPIRYKTNEPVWEENFTFFIHNPKRQ
	1	}				DLEVEVRDEQHQCPLGNLKVPLSQLLTSEDM
	1		-	1		TVSQRFQLGNSGPNSTIKMKIALRVLHLEKRE
	İ	1	1			RPPDHQHSAQVKRPSVSKEGRKTSIKSHMSG
		1				SPGPGGSNTAPSTPVIGGSDKPGMEEKAQPPE
		ļ				AGPQGLHDLGRSSSSLLASPGHISVKEPTPSIA
	ı	1	1			SDISLPIATQELRQRLRQLENGTTLGQSPLGQI
	,		1	1		QLTIP
	1560	- A	2422	35	456	REFAASDLEPFTPTDQPISPEATTQPSCIKRQRA
210	1360	1^	2-722			AGNPGSLAATIDHKPCSAPLEPKIQASRNQRW
		1	þ	1		GAVRAAESLTDIAEPASPQVHETPIDASQTQK
		i	<b>\</b>			VEPASKSRFTPELQAKVSHSRERALSTMDATE
	- 1		l	Į.		HHAQPQRGEG
	1561	- A	2431	1	764	RRYSQKLIQHTACQLLRTYPAATRIDSSNPNP
211	1301	A	2431			LMFWLHGIQLVALNYQTDDLPLHLNAAMFE
	]	j	ì	ì	1	ANGGCGYVLKPPVLWDKNCPMYQKFSPLER
ĺ			ļ			DLDSMDPAVYSLTIVSGQNVCPSNSMGSPCIE
1	1				1	VDVI GMPLDSCHFRTKPIHKNI LNPM WNEQ
ì		- }			1	I FHYHFEDI VFLRFAVVENNSSAVI AQKIIPL
}	1	- (			1	KALKRGYRHLQLRNLHNEVLEISSLFINSRRM
1	İ				1	EENSSGNTMSASSMFNTEERKCLQTHRVTVH
İ	1	- {	ľ			GVPG
L			2426		411	GIRGTTGHLGCPINDDPSLTLTVSWVMEDKP
212	1562	Α	2436	1	1	VICNOTEKEDDSLTIFAVAKRDHVSDTCGAC
		1	1	1		TOT DUNT DEGYT TVI GEORT PINKLUALEN
	1	Ì		l l		RANRTRDLELTYLAERIVRLTWIPGDANNRP
		1		1		TDYDCOIEEHO
1					1294	MSSIGCI WVSRSSOIDGLTAEKSGPEKPHGT
213	1563	A	2445	1	1274	WI MPEL HPKEOTLELLVLEOFLSILPEELQIW
		1		1		OOHNDESGEESVTLLEDLEREFDDPGQQVPA
1	1		1		1	DOGDAVDWKDI TCI RASOESTDIHLUPLKI Q
1			- 1			I POWEDCI SPESDCENSETATKEGISEEKSQU
	1				{	T DOEDCED CICEHESM VWKOGSATGERERS
		Ì		İ		SQGGSFSQVIFTNKSLGKRDLYDEAERCLILT
		1	ì	1	1	TDSIMCQKVPPEERPYRCDVCGHSFKQHSSL
		- 1			}	QHQRIHTGEKPYKCNQCGKAFSLRSYLIIHQI
1	ļ		- 1	1		IHSGEKAYECSECGKAFNQSSALIRHRKIHTC
1		]		1		EKACKCNECGKAFSQSSYLIIHQRIHTGEKPY
[		1		1	1	ECNECGKTFSQSSKLIRHQRIHTGERPYECNE
		1		1	1	ECNECCK I PSOSSKLIKHOKUT GERT I ECH
	1					CGKAFRQSSELITHQRIHSGEKPYECSECGKA
		l	{		1	FSLSSNLIRHQRIHSG
1	1564	A	2461	-+1	615	GIPGSTISSSRNIFLEDDLAWQSLIHPDSSNTP
214	1564	A	2401	•		STRLVSVQEDAGKSPARNRSASITNLSLDRS
	ì			1	1	SPMVPSVETSVSPOANRTYVRTETTEDERKI
}	1					
	{			ì	}	LDSVQLKDLWKKICHHSSGMEFQDHRYWLITHPNCIVGKELVNWLIRNGHIATRAQAIAIG

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutarnic Acid,
IO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	ļ	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	!	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	}	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence		}	914	ng to first		T=Threonine V=Valine W=Tryptophan,
	Į.	ì	1	amino acid residue of	of peptide sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	ĺ	Ì		1	Sequence	/=possible nucleotide deletion, \=possible
			1	peptide		leatide insertion
	1	<u> </u>	<u> </u>	sequence		AMVDGRWLDCVSHHDQLFRDEYALYRPLQV
						LEGUNCOLECSKLIL
			0164	1 3	2932	GPGVRSSODGMADVFVHLRTAWPRCSFISGQ
215	1565	A	2464	)	2752	UCPGRHGRRVCSSODSMADVFVHLKTAWP1
		1		i		CSLISCOHGPGESVSYEDDDIPAPASLLHVNA
	Í	1	1			A A DAT TNIPT A PVI. CTAPNNTA OKEK VPSGMK
	•			}		OPPAGVRISSRTPDLTCAVSTHSTVPGVRISSC
	1	1		}		TODI TOAVSIHSTVPSVCISSCIPULICAVSIH
	1			1	•	STVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
		ļ		1		TPDLTCAVSIHATVPGVRISSCTPDLTCAVSIH
		}		ł		ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
						TPDLTCAVSIHSTVPGVRISSCTPDLTCAVSIH
		1				ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
		l	Ì	Į.		TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH ATVPGVRISSCTPDLTCAVSIHATVPGVRISSC
	1	ļ	1	1		TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH
		ì				ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSE
		l	ļ	1		TPDLTCAVSIHATVPGVRISSCTPDLTCAVSTI
		1				STVPGVRISSRTPDLTCAVSIHATVPGVHISSC
		1	1			TPDLTCAVSTHSTVPGVRISSRTPDLTCAVSIF
	1	1	<b>[</b>		7.4	STVPGVCISSRTPDLTCAVSIHSTVPSVHISSCT
	1	İ		ŀ		PDLTCAVSIHSTVPGVRISSRTPDLTCAVSTHS
		-		ļ		TVPGVHISSCTTDLTCAVSIHATVPGVHISSCT
	1	i		ţ		PDLTCAVSTHTTVPGVRISSRTPDLTCAVSIHS
		1				TVPGVRISSCTPDLTCAVSTHSTVPGVRISSKT
				1		PDI TCAVSTHI TVPGVRISSRTPDLTCAVSILL
	{					TVPGVHISSCTPDLTCAVSIHATVPGVRISSKI
				1		PDI TCAVSIHATVPGVHISSCTPDLTCAVSTH
	}	1	}	}		TVPGVRISSRTPDLTCAVSIHSTVPGVHISSCI
	ŀ	i				DDI TCAVSTHSTVPGVHISSCTPDLTCAVS I H
					Ì	STVPGVHISSRTPDLTCAVSIHATVPSVHISSC
			1	ł		TPDI TCAVSIHSTVPGLLTSVSQTSTG
	1266		2477	1	414	FRIKSYRKGSYRCIVSEWIAEQGNWQEIQEK
216	1566	A	2477	1 *	1	AVEVATVVIQPTVLRAAVPKNVSVAEGKELI
ł		- (		•		LTCNITTDRADDVRPEVTWSFSRMPDSTLPG
1						RVLARLDRDFLVHSSPHVALSHVDARSYHLI
		- 1	- }	1		VRDVSKENSGYYY
	1000	A	2480	2	460	CRTLCEGPQRFEEYEYLGYKAGLYEAIADHY
217	1567	^	2400	1		MQVLVCQHECVRELATRPGRLSPIENFLPLH
ì	1	1	}	]	1	DYLQFAYYRVGEYVKALECAKAYLLCHPDI
İ	İ	1				EDVLDNVDYYESLLDDSIDPASIEAREDLTM
ì						VKRHKLESELIKSAAEGLGXSYTEPNYW
212	1568	A	2483	140	383	AFSSPHPSPAPQFPECGFYGLYDKILLFKHDP
218	1300	^	1 2 705			SANLLQLVRSSGDIQEGDLVEVVLSASATFE
1						LQIRPHALTVHSYRAP
210	1569	-	2489	- 3	428	SSRLVLLAGAAALASGSQGDREPVYRDCVL
219	1309	^	12,00			CEEQNCSGGALNHFRSRQFIYMSLAGWTCR
1		1		1	İ	DCKYECMWVTVGLYLQEGHKVPQFHGKW
						FSRFLFFQEPASAVASFLNGLASLVMLCRYR
						FVPASSPMYHTCVAFAWVS
220	1570	A	2498	1	1297	MDGEAVRFCTDNQCVSLHPQEVDSVAMAP
220	13/0	^	1 21,75			APKIPRLVQATPAFMAVTLVFSLVTLFVVDI
		ĺ				HHFGREAEMRELIQTFKGHMENSSAWVVEI
1						MLKCRVDNVNSQLQVLGDHLGNTNADIQM
1		1	1	1		KGVLKDATTLSLQTQMLRSSLEGTNAEIQR
		1	-	1		KEDLEKADALTFQTLNFLKSSLENTSIELHV KEDLEKADALTFQTLNFLKSSLENTSIELHV
1				1		SRGLENANSEIQMLNASLETANTQAQLANS
j	]		1	1	[	LKNANAEIYVLRGHLDSVNDLRTQNQVLR
	1		L L	l l	(	LEGANAEIQGLKENLQNTNALNSQTQAFIK

PCT/US01/03800

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine K=Lysine L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	<b>)</b> 1		914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	] -		1	amino acid		V=Tyrosine, X=Unknown, *=Stop codon,
	1			residue of	sequence	/=possible nucleotide deletion, \=possible
	1			peptide		nucleotide insertion
	ļ	}		sequence		FDNTSAEIQFLRGHLERAGDEIHVLKRDLKM
	<del>                                     </del>					VTAQTQKANGRLDQTDTQIQVFKSEMENVN
]	1		1			TLNAQIQVLNGHMKNASREIQTLKQGMKNA
1	l				}	SALTSQTQMLDSNLQKASAEIQRLRGDLENT
	[	[	}			KALTMEIQQEQSRLKTLHVVITSQEQLQRTQ
]	1	ļ				RVRLNNDGLSPLMMAAKTGKIGIFQHIIRREV
221	1571	A	2501	3	500	TDEDTRHLSRKFKDWAYGPVYSSLYDLSSLD
221	1 .3/1	1		1		TCGEEASVLEILVYNSKIENRHEMLAVEPINE
ļ	1	}	1	1		LLRDKWRKFGAVSFYINVVSYLCAMVIFTLT
1	1	ł	-	İ		LLRDKWRKFGAVSF HINVVSTLCAMVITTET
1	1	ł	1			AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFT
		1				GVLFFFTN
	1.670	+	2508	3	395	DAHCQRKLAMQEFMEINERLTELHTQKQKL
222	1572	A	2500	"	1	ARHVRDKEEEVDLVMQKVESLRQELRRTER
	1	1	1	ì	1	AKKELEVHTEALAAEASKDRKLREQSEHYSK
1	1	ł	1	1		QLENELEGLKQKQISYSPGVCSIEHQQEITKL
	l	1	1			KTDLEKKS
		<del></del>	2544	2	412	NDPAIISNESAAVVHTIVNETLESMTSLEVTK
223	1573	A	2544	12	,	MVDERTDYLTKSLKEKTPPFSHCDQAVLQC3
}	1	1	ļ			EASSNKDMFADRLSKSIIKHSIDKSKSVIPNID
ì	ì	1	ĺ			KNAVYKESLPVSGEESQLTPEKSPKFPDSQNQ
1						I TUCSI SAA
				401	+1	CAST CEISTAFTVI TELIDSCRFSYPERPIIFLSM
224	1574	A	2552	401	1	CVNIVSIAVIVRLTVGRERISCDFEEAAEPVLI
ļ	Į.					OFGI KNTGCAIIFI LMYFFGMASSI WW VILIL
	1	l l	i	1		TWFLAAGLKWGHEAIEMHSSYFHIAAWAIPA
	}	1	}	ł		W
	1	<u> </u>			1	MCADKERREKGEEEGEGEKDGDEDEKEEEKE
225	1575	A	2563	724	1	CI CEEEEKEACKKKKKOEEKEKEKGAVYSK
1		,		ļ		LVADICKNDMGGSORVLEKHWISFLKARLNU
						CVPGDSFFYFDVLOSITDIIOINGIPIVVGVF11
1	1	}	1		i	LOT NEIDGE AVCAFSMDDIEKVFKGRFKEUK I
1	1	1	ļ	}	į	DSVWTAVPEDKVPKPRPGCCAKHGLAŁAYK
1	- 1	1	1			TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFT
	- [		1	ł	ì	V TO VR VRI TAISVDHSAGPYH
	1					EGVLFVYGNYVGDVMNFEMAAEMAQEVAIP
226	1576	A	2571	449	3	TRTVLTTDDISSSPIEDRDGRRGVAGNFFIFKV
~~~		1		1		A CAACDROMSI FACEAVTRKANKKI Y IMG
İ	[	1				VALEPCSLPQTRRHNFEIGAEEMEIGMGIHGE
	1	1		1		RGVIREKMMPADAIVDHIMDRIFS
						VLSDLCLFYYRDEKEEGILGSILLPSFQIALLTS
227	1577	A	2575	3	1197	EDHINRKYAFKAAHPNMRTYYFCTDTGKEM
421	13,7	1 1				EDHINKA JAFAAAFI WATEDVEDVETVETVAP
		1	-			ELWMKAMLDAALVQTEPVKRVDKITSENAP
		- (	ĺ			TKETNNIPNHRVLIKPEIQNNQKNKEMSKIEE  TKETNNIPNHRVLIKPEIQNNQKNKEMSKIEE
	}	- [	1	1		KKALEAEKYGFQKDGQDRPLTKINSVKLNSL
		{		1		PSEYESGSACPAQTVHYRPINLSSSENKIVNVS
		1		1		I A DI DOGNIR PNTGPLY LEADRY LUKI NOMYY
		- [				LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS
-		l		-		LID A OIM ARY PEGYRTLPRNSK I RPESICSV IP
				Į.		STUDETI GPGAFFKRRSMRDDIMWQLYEW
			1	- [		OOD OF VNKOSTI PRHSTLSSPKTM VNISDQI
		1	1			MHSIPTSPSHGSIAAYQGYSPQRIYRSEVSSPI
1		-		1		OPCDATIDERHEAHHEKAK
					330	I PELGLGSVLPOGMVMASPEMNPTICSVFEA
228	1578	A	2583	3	330	TITURE I ELLATTER ROFOVTVLVGNVKULAV VE
		Ì				KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD
		1	1			DTMCIKPHI WWVAA
1	1	- 1	- 1		_	I INOIN THE WAR TO THE THE THE THE THE THE THE THE THE THE
1	1	- 1	1			DDVNAOGIKRHVKYLSGNAFIICKITCURDV
229	1579	A	2589	1	448	DDKNAQGIKRHVKPTSGNAFTICKYPCGKSR EGVAPNICKCKPGYIGSNCOTALCDPDCKNH
229	1579	A	2589	1	448	DDKNAQGIKRHVKPTSGNAFTICKTFCGRSK ECVAPNICKCKPGYIGSNCQTALCDPDCKNH GKCIKPNICQCLPGHGGATCDEEHCNPPCQH

			-050	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=4 enertic Acid E=Glutamic Acid,
VO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	<b>\</b>			amino acid	of peptide	1=1 hreonine, v=vaille, w=1 typiophan,
	,	}	ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ł	peptide		/=possible nucleotide deletion, \=possible
	l .	ļ	ì	sequence		nucleotide insertion
	ļ	<del></del>	<del> </del>	Sequence		GGTCLAGNLCTCPYGFVGPRCETMVCNRHC
	1	1				ENGGOCLTPDICOCKPGWYGPTCSTA
					138	AVTFSVVFAYVADITQEHERSMAYGLVCMFI
230	1580	A	2593	2	130	LYLLYLLRNAFFLR
		1			<u> </u>	SGPYTDFTPWPTEEQKLLEQALKTYPVNPPER
231	1581	A	2595	185	2	WEKIAEAVPGRTKKACIKRYKVADLRISK
				1		WEKIAEA VPGKTKKACIKKTK VALERISK
232	1582	A	2596	1	391	STVTGQPRRLLDTAGHQQPFLELKIRANEPGA
232	1302	1 11	120,0	1		GRARRTPTCEPATPLCCRRDHYVNFQELGW
	į.	1	Į.			RDWILLPEGYQLNYCSGQCPTHLAGSPGIAAS
	}	]	1	ì	1	FHSAVFSLLKANNPWPGRTSWCVPTARRPLS
	1	1	l			LLVI.
					102	LLFSDEIIMAAPLRIADVTSGLIGGEDGRVYV
233	1583	A	2601	184	403	YNGKETTLGDMTGKCKSWITPCPEEKVNVLQ
		1	1			NSIPYWERIT
		1				PLTLCLPENNKPPQADAVPDKELTLPVDSTTL
234	1584	Ā	2614	178	335	PLTLCLPENNKPPQADAVPDRELIEI VDSITE
254	1	1	1			DGSKSSDDQKIISYLWEKTQ
225	1585	A	2616	2	896	DVLEVYGTGVASTRHEMGTLDKHKELEDLV
235	1383	1 ^	2010	1 -		AKFLNVEAAMVFGMGFATNSMNIPALVGKG
		1	1			CLILRDEVNHTSLVLGARLLGATIGIFKHNYA
		1			. [	OSLEKLLRDAVIYGOPRTRRAWKKILILVEGV
			Į.	1		YSMEGSIVHLPQIIALKKKYKAYLYIDEAHSI
	]			}		GAVGPTGRGVTEFFGLDPHEVDVLMGTFTKS
				1		FGASGGYIAGRKARILSPPACLVPNTGSHSLH
	ļ		]	}		RLTRDLQMNEAMVALVTDRLQGWNSGEGN
	[		i			WDRADKFGDLVDYLRVHSHSAVYASSMSPP
	1	ì	1		1	WDRADKIGDLYD IERVIISIOAV I IIGEMET I
	1					AEQIIRSLKLIMGLDGTTQ
236	1586	A	2621	11	392	NTSSFPAQPSSPARPSLPHLSQHPSNPLLPLAS
230	1500	1 '	2020			ADHPQCGRFLPLHEPEPLCPSPSLSYPTLVSS
ì	1		j			WSSPFSSHHGCPPGLYPFPTSPKTIQPPGLAQL
İ	1					KMLCIPPGRQQLRGAQSMPGHGALSPLLLPP
	- 1	1			l l	l A
				200	+1	DI VCKISGEGRGPRDRSEAVYTTMSGRSPAL
237	1587	Α	2628	398	1	WAAPETLOFGHESSASDVWSFGIIMWEVMAL
i	1	}	- 1	ł	1	GERPYWDMSGQDVIKAVEDGFRLPPPRNCPN
		1	- }	į		LMHRLMLDCWQKDPGERPRFSQIHSILSKMV
	1	}	}	1		
		1		1		QDPEPPNV
238	1588	A	2631	1	1104	WSPCSLTCGVGLQTRDVFCSHLLSREMNETV
ەت ا	1,200	^		1		ILADELCROPKPSTVQACNRFNCPPAWYPAQ
]	- }	1				WQPCSRTCGGGVQKREVLCKQRMADGSFLE
1	1	1	1			1 PETECSASKPACOOACKKDDCPSEWLLSDW
1	1	- 1		1	}	TECSTSCGEGTOTRSAICRKMLKTGLSTVVN
1	[	[	İ	Į.	ì	TLCPPLPFSSSIRPCMLATCARPGRPSTKHSPH
	1	- 1				AAARKVYIQTRRQRKLHFVGGGFAYLLPKTA
1	1			{		VVLRCPARRVRKPLITWEKDGQHLISSTHVT
ł					l	VAPFGYLKIHRLKPSDAGVYTCSAGPAREHF
		1	}		i	VAPPOYLKIHKLKPSDAUVIICSAUPAKEHP
		1				VIKLIGGNRKLVARPLSPRSEEEVLAGRKGGF
1					1	KEALQTHKHQNGIFSNGSKAEKRGLAANPGS
İ	(					RYDDLVSRLLEOGAPCSSSKKKN
			- 1 2000	<del></del>	678	MK PDNILLDEHGHVHITDFNIAAMLPRETQI'I
239	1589	A	2636	1	078	TMAGTKPYMAPEMFSSRKGAGYSFAVDWW
1	1		}	1	1	SLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET
	1	i	1	}	· !	TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSC
				1		I A A I I LOW MODERN A OPPLY THE LAIL THE DOLD THE
	1	ļ				LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK
		ì	1	l		GRUNCDPTFELEEMILESKPLHKKKKRLAKK
1	l				İ	EKDMRKCDSSQTCLLQEHLDSVQKEFIIINRE
	1					KVNRDCI
		1		1200	13	FILDPTTPMRTKCIELLYAALTSSSTDQPKAL
240	1590	A	2639	389	3	I WONEAREIEEHVETLYSKNIKKYKTCIRSKY
240	1590	A	2639	389	3	LWQNFAREIEEHVFTLYSKNIKKYKTCIRSKY ANLKNPRNSHLQQNLLSGTTSPREFAEMTVN

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ì	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, r=rionic,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1		1	amino acid	of peptide	T-Threonine, V=Valine, W=Tryptophan,
		l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ì	1	1	peptide	1	/=possible nucleotide deletion, \=possible
	1	}	1	sequence		nucleotide insertion
	<del> </del>	├──	+	<del></del>		EMANKELKQLRASYTESCIQEHYLPQVIDGTL
		1			ļ	Υ
	1501	A	2640	392	3	IRLTILRCVFMRLATICVLVFTLGSKITSCDDD
241	1591	A	2040	1372		TCDLCGYNOKLYPCWETOVGQEMYKLMIFD
		1	ļ	}	ļ	FIIILAVTLEVDEPRKLLVTYCSSCKLIQCWGQ
	1	ĺ				QEFAIPDNVLGIVYGQTICWIGAFFSPLLPAM
		1	1	1		Y
		<del> </del>	10010	405	1	YFKNTTLLLVGVICVAAAVEKWNLHKRIALR
242	1592	A	2642	405	\	MVLMAGAKPGMLLLCFMCCTTLLSMWLSNT
	1		ì			STTAMVMPIVEAVLQELVSAEDEQLVAGNSN
	Ì	1	j		}	TEEAEPISLDVKNSQPSVELIFVNEDILDFLMK
	1		}	l	i	SPLMISQACI
					<del></del>	CLAMIKGIQSSGKIIYFSSLFPYVVLICFLIRAF
243	1593	A	2646	412	2	LLNGSIDGIRHMFTPKLEIMLEPKVWREAATQ
				1		VFFALGLGFGGVIAFSSYNKRDNNCHFDAVL
	1	ì	1	ł .		VFFALGLGFGGVIAFSSTNRRDINGIT DAVE VSFINFFTSVLATLVVFAVLGFKANVINEKCIT
	ļ	1	1	ļ		
	1			_		QNSETV
244	1594	A	2650	1	1271	MTTTLIGLLKTARLLRLVRVARKLDRYSEYG
			i		ţ	AAVLMLLMCIFALIAHWLACIWYAIGNVERP
	- {	i	1	<b>\</b>		YLTDKIGWLDSLGQQIGKRYNDSDSSSGPSIK
,	1	ł	1	1		DKYVTALYFTFSSLTSVGFGNVSPNTNSEKIF
	1		1		-	SICVMLIGSLMYASIFGNVSAIIQRLYSGTARY
	1		1	ĺ		HMQMLRVKEFIRFHQIPNPLRQRLEEYFQHA
	1	-	l l		ļ.	WTYTNGIDMNMVTNGTCSSCTSDDGHFILVS
						NHHQGGLIYSWNDAASMQRPFNHIKSSLLGS
	ľ			Í		TSDSNLNKYSTINKIPQLTLNPSEVKTEKKNSS
	į					PPSSDKTIIAPKVKDRTHNVTEKVTQVLSLGA
	1		1	ļ	1	DVLPEYKLQAPRINKFTILHYSPFKAVWDWLI
	ì	- {	l	ĺ	1	LLLVIYTAIFTPYSAAFLLNDREEQKRRECGY
1	ļ.	1	İ	İ		SCSPLNVVDLIVDIMFIIDILINFRTTYVNQNEE
1	-	1	l l	}	1	VVSDPASV
-	1595	A	2656	385	2	NLTWWPLFRDVSFYIVDLIMLIIFFLDNVIMW
245	1393	A	2030	303	1	WESLLLLTAYFCYVVFMKFNVQVEKWVKQ
	1		Ì	1		MINRNKVVKVTAPEAQAKPSAARDKDEPTLP
	{		į		{	AKPRLQRGGSSASLHNSLMRNSIFQNKIHTLD
	i	ļ.	- }	1		PHV
			2660	200	506	VI VI OMNYYOMI IIYYVLFFKVNEFLAFEGPI
246	1596	Α	2660	200	300	LLDMRIKHLIKTNQLSQATALAKLCSDHPEIG
	\					IKGSFKQTYLVCLCTSSPNGKLIEEVSMFSFIS
		1			}	NYFLS
					267	DAWYKNDIIFNQTERKQKISENLKHLASVRV
247	1597	Α	2678	3	267	VOKNLVFVVGLSQRLADPEVSPLVFFVILIFF
	- 1		ļ		1	VSLSYLEIIFDPAQLCDSSEHIIS
1					<del></del>	DFTTLAAMMRTLFSLFGDVRSDVHRFSVTLF
248	1598	A	2687	1	404	GAAIKSVKNPDKKSIENQVLDSLVPLLLYSQD
				1		ENDAVAEESRQVLTICAQFLKWKLPREVYSK
		- 1				ENDAVALESACYL HCACILA WALLALY TOR
						DPWHIKPTEAGTICRFFEKKCKGKINILEQTL
			İ			MYSKNPKL ARCHIVATERIUM
249	1599	A	2692	1	440	FRRRRRERDCAAQGARRHCRHLAECKLV
1		1				SFPIGIYKVLRNVSGQIHLITLANNELKSLTSK
		-	1	ļ	1	FMTTFSQLRELHLEGNFLHRLPSEVSALQHLK
1			1	1	1	AIDLSRNQFQDFPEQLTALPALETINLEENEIV
Ĩ						DVPVEKLAAMPALRSINL
1	1	<del></del>	2693	459	21	LLPGSLGVPILHSOPWDPSPQCPHRAPSTPRRL
250	1.000			1 707	ı ~•	THE CALL OF A TANK OF A AVAILAGE DECK CTV DED
250	1600	Α	2073		i	PPLGALSQALIFLSKAAKNHSQDFGKGIKITI
250	1600	A	2073			PPLGALSQALTFLSRAAKNHSQDPGKGTKPFP AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF
250	1600	A	2073			AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF
250	1600	A	2073			AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF NSPWHPATLPGALGPQLSQAAPSPIPPPCLMG
250	1600	A	2694	2	404	AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF

				Deadlesed	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	1	residue of	sequence	/=possible nucleotide deletion, \=possible
	1			peptide	ļ	nucleotide insertion
		<u> </u>		sequence	ļ	OKRKKAPDHSSGRKEELVTTHTVDKLETKK
			Į			PVGRVLCGLSGELLHSLLLPRRKTEKRALGSH
	1	İ	l	1	j	RKAGFPEHPVAPEPLSNSCQISKEGREQVLSEI
	Ì	1	1	İ	1	GAGDCL
						POKSHSGAYQCFATRKAQTAQDFAIIALEDG
252	1602	Α	2697	421	1	TPRIVSSFSEKVVNPGEQFSLMCAAKGAPPPT
		1		İ		VTWALDDEPIVRDGSHRTNQYTMSDGTTISH
		1	1	1	{	MNVTGPQIRDGGVYRCTARNLVGSAEYQARI
		i	1			MNV I GPOIR AMPAIR
						NVRGPPSIRAMRNIT ACCQWRRTLIPAKSTTVSCTISTPHHPFRGSYS
253	1603	A	2698	65	401	ACCOMRRILIPARSI I VSC I ST FILLI ROSTO
233	1005	1			1	FDDHITDSEALSRSSHVFTSHPRMLKRQPAIEL
	1	ì	1		1	PLGGEYSSDVPRPLSTQLSSSLLGYFSTLMTG
		•				AAFTNNIASSTIIL
254	1604	A	2699	438	301	GQIHSQDDPPFIDQLGFGVAPGFQTFVACQEQ
254	1004	1 11	20,,			RVRGPWEAGPGVGY
255	1605	A	2700	1	842	LONREDSSEGIRKKLVEAEELEEKHREAQVS
255	1005	1 ^	2.00	-		AQHLEVHLKQKEQHYEEKIKVLDNQIKKDLA
		Ì				DKETLENMMQRHEEEAHEKGKILSEQKAMIN
						AMDSKIRSLEQRIVELSEANKLAANSSLFTQR
		İ	1		Į.	NMKAQEEMISELRQQKFYLETQAGKLEAQN
	1					RKLEEQLEKISHQDHSDKNRLLELETRLREVS
						LEHEEQKLELKRQLTELQLSLQERESQLTALQ
		1	ì		1	AARAALESQLRQAKTELEETTAEAEEEIQALT
		Ì				VGLGSNIFRLLKASARMSVELALSILAHP
-	1,000	A	2701	2	405	FVGGPGADPPVAVMWDPRAARMDLTAYAE
256	1606	A	2/01	1	1	LLKESGNQVLKNGNFSLAIRKYDEAIQILLQL
		İ	1	ļ		VOWGVPPRDLAVLLCNKSNAFFSLGKWNEA
ļ	1		ł	{		FVAAKECLQWDPTYVKGYYRAGYSLLRLHQ
}	1	1	i	1		DVEAARMFFEGLR
<u></u>			2702	12	399	FVESASSRPPGCFSGDGRFWLVSEGSRRGWD
257	1607	A	2/02	1 2	333	ENPSESEL DPRYSVGGDENIGTVTTLANILREF
Ì		-	1			NPSLKGFSVGTGKETSPNAFLNQAVAGGRAE
<b></b>	1	1	1			DLPVQARRLVDLMKNDTRIHFQEDWKIITLFI
ļ	ì		l	]	ļ	GGNDI.
			2700	+,	1097	SVGARQGEARDRIRRFFPKGDLEVLQAQVERI
258	1608	Α	2709	1 1	100,	MTRKELLTVYSSEDGSEEFETIVLKALVKACG
		.		1		SCEASAVI DELRI AVAWNRVDIAOSELI KODI
1	l l	.	1			OWNSEHI FASI MDALLNDRPEF VRLLISHULS
		į.	ļ			I GHELTPMRLAOLYSAAPSNSLIRNLLDQASH
1		1	}	1	1	SAGTKAPALKGGAAELRPPDVGHVLRMLLG
	1		Ì	ļ .		KMCAPRYPSGGAWDPHPGQGFGESMYLLSD
				1	}	KATSPLSLDAGLGOAPWSDLLLWALLLNKA
1		İ	[	ĺ		OMAMYEWEMGSNAVSSALGACLLLRVMAR
	1			1	1	LEPDAEEAARRKDLAFKFEGMGVDLFGECYR
1		1	'	{	1	SSEVRAARLLLRRCPLWGDATCLQLAMQAD
-		- 1			i	ARAFFAQDGVQSLPTQKWWGDMARR
		1_				VYLGAGPGLFFSNEGAKEGEKANIPKLMLPR
259	1609	A	2721	1	403	GGFSQREMVTGERSPSPEEEEEEEEGFGERA
			}	1	. [	GUISQKEMY I GEROFOFEEEEEEEEEG GEGDA A
[						SCRRGLFRVRLTRVGLAAPSKASRGQEGDAA
	1		J	1		PKSPVREKSPKFRFPRVSLSPKARSGSGDQEE
			1			GGLRVRLP
	1610	A	2728	1	477	LLGGDLRYHLQQNVHFTEGTVKLYICELALA
260		1 1	1 2,20			LEYLORYHIIHRDIKPDNILLDEHGHVHITDFN
260	1610	1			i	IATVVKGAERASSMAGTKPYMAPEVFQVYM
260	1610			1		IAT V KOMBIG IDENTITION TO THE TOTAL TOTAL
260	1610					DRGPGYSYPVDWWSLGITAYELLRGWRPYEI
260	1610					DRGPGYSYPVDWWSLGITAYELLRGWRPYEI HSVTPIDEILNMFKVERVHYSSTWCKGMVAL
260	1610					DRGPGYSYPVDWWSLGITAYELLRGWRPYEI HSVTPIDEILNMFKVERVHYSSTWCKGMVAL
260	1611	A	2730	3	547	DRGPGYSYPVDWWSLGITAYELLRGWRPYEI HSVTPIDEILNMFKVERVHYSSTWCKGMVAL

				D 11	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l I	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	ļ	}	peptide	004	/=possible nucleotide deletion, \=possible
		1		sequence	1	nucleotide insertion
	<u> </u>		<del> </del>	Sequence		RLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLP
	1	1		ļ	ļ	RPSFLYRTIQDLGIGTFRDLAVVLETAPILTAL
		1	1			DIFVDRRVSALAVVNECGTHPQDERLGLGW
	ļ	ĺ	ł		{	GLGEPGSEERLFPAAITSR
260	1612	A	2733	3	431	GPEFPGSAKLVFLDLSYNNLTQLGAGAFRSA
262	1012	^	2133			GRLVKLSLANNNLVGVHEDAFETLESLQVLE
	1			]		LNDNNLRSLSVAALAALPALRSLRLDGNPWL
						CDCDFAHLFSWIQENASKLPKGLDEIQCSLPM
	1			}	{	ESRRISLRACRRPASRV
0.62	1613	A	2736	2	343	PARISGVDPPVRKATKGGENCSFEDNKNWQF
263	1013	A	2730	1		LWGLNGNFNFFKEPWGGRNNHAKGFRTTW
		1	1			ARSSSQNNRTFQNNRNFLRLQRDSQKKGQFA
	İ					RLISPLVNLPQSPGGLEFQYQAT
264	1614	A	2738	2	245	RAMLKCLREGQPPPSYNWTRLDGPLPSGVRV
264	1014	Α	2/30	1		DGDTLGFPPLTTEHSGIYVRHDTNEFSSRDSH
}		1	1	1	Ì	DTVDVLDPPEDSGKQVDL
265	1615	A	2752	2	388	AAGDAPLRSLEQANRTRFPFFSDVKGDHRLV
265	1013	1	2752			LAAVETTVLVLIFAVSLLGNVCALVLVARRR
1	-	1		Ì	1	RRGATACLVLNLFCADLLFISAIPLVLAVRWT
l		1		1		EAWLLGPVACHLLFYVMTLSGSVTILTLAAV
	1	1	1	1		SLER
266	1616	A	2755	192	1	AFREVGGYWGLLCEHLYAIPSKTSEGNWTAK
200	1010	1"	-,			LQGYLPLQDAFHIFQDPLTGDLPWPELILGLP
1		ŀ				V V V V V V V V V V V V V V V V V V V
267	1617	A	2760	434	714	ASRLEKONSTPESDYDNTPNDMEPDGMGYM
207	1017	1	1		Í	HRTSVPGEGLPRARDLAGLGQQKQFTTHTPF
1					L	LYFQTHKGLKDSSIRSEVTCLGISQCWRKGFF
268	1618	A	2762	1	405	IACTFCGQDEWSPERSTRCFRRSRFLAWGEP
200	10.0	1				AVLLLLLLSLALGLVLAALGLFVHHRDSPL VQASGGPLACFGLVCLGLVCLSVLLFPGQPSP
1		1		ì		ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESE
		1		į.		
		1				LPLSWAE TRPAEKIQYLVLFFVMSHPSQAYDKLSLSDHL
269	1619	A	2772	3	243	LIAVLNLLRREVSEHGRHLQQYFNLFVMYAN
20,						LSKNLSFSEFCFDVSY
1		-				ELQSQQACTHTKETEQLRSQLQTLKQQHQQA
270	1620	A	2789	1	486	VEQIAKAEETHSSLSQELQARLQTVTREKEEL
	}					LQLSIERGKVLQNKQAEICQLEEKLEIANEDR
	1	]		1		KHALERFEQEAVAVDSNLRVRELQRKVDGIQ
				)	}	KAYDELRLQSEAFKKHSLDLLSKERELNGKL
	1	1	ļ			
						RHLSP KEKRVIVQLPTESIQKNQEDKLKMVPRKQRE
271	1621	A	2795	1	568	FSGSDRGKLPGSEEKNQGPSMIGRKEERLITE
	[	į		1		RKHEHLKNKSAPKVVKQKVIDAHLDSQTQN
						FQQTQIQTAESKAEHKKLPQPYNSLQEEKCLE
		1		ì	1	VKGIQEKQVFSNTKDSKQEITQNKSFFSSVKE
			1	1	1	SQRDDGKGALNIVEFLRKREELHQILSTVKQP
		-				KCMQGKYAGAMESEPCVCTEADFDCDYGYE
272	1622	A	2797	8	523	RHSNGQCLPAFWFNPSSLSKDCSLGQSYLNST
1	Ì	1				GYRKVVSNNCTDGVREQYTAKPQKCPGKAP
1	1	i		- [		RGLRIVTADGKLTAEQGHNVTLMVQLEEGD
1						VQRTLIQVDFGDGIAVSYVNLSSMEDGIXHV
1	1	1				YQNXGIXRXTVQVDNSLGS
		!				HPSRSNVGPRQLTVWNTSNLSHDNRRKYIFS
273	1623	A	2801	72	395	DEEGQNQLGIRIHQDIPLPPRRRELPALRTTNG
1	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \					DEEGGNGLGIKINGDIPLITAKKELI ABKI ING
1			}			KADSLNVSRNSVMQELSELEKQIQVIRQELQL
	1	J				AVSRKTELEEYH ILWLYFETGTWVYPVFAKLSLLGLAALFSLRE
ļ	1624	A	2805	168	320	ILWLYFETGTWVYPVFAKISLEGLAALFSEKE IFIARNGVVGETLTHCKRV
274						

EO II)	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
10: of		под	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	l	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ience		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ		peptide	Sequence	/=possible nucleotide deletion, \=possible
	1			sequence		nucleotide insertion
		<del> </del>		208	321	GSLATCQLSEPLLWFILRVLDTSDALKAFHD
275	1625	A	2812	208	321	MGKIIFO
276	1626	A	2813	41	266	AGRSLHGAGDRAWVGISPTDWSPKVVELCK
270	1020	^	1 2015	1.7	İ	KYQQQTVVAIDLAGDETIPGSSLLPGHVQAY
		1		ł	1	QVGPVRRNGEAGPG
000	1627	A	2817	3	410	VLQERLDNFQRKCIQLASSTEGKVDKLLMRN
277	1027	A	2017	\ \ \	1	L FISYLHTPKHKOHEVLQAMGSILGITGEEME
	Į.	1			}	PI FOREHGTATRWMTGWLEGGSKSVPKTPL
	ĺ	1	1	1	<b>\</b>	GLNQQPALNGSFSELFVKFLKTESLSSTLPTX
			· I			T PPHNSPGKIK
		<del> </del>	2821	238	457	GLSGPSCSCPHSPLPTIISRAQLETALKWRNYE
278	1628	A	2821	230	13'	VKLRLLLHLEELQMEHDIRHYDLESVPMTWD
	1	1	1			PVDONPRLV
	J			1212	1	PLIPANLPAHSNPLQPLPSLPHPFLPATHKFPT
279	1629	Α	2822	342	1	TPPTFSSVPPPLPSLSSILHHSPLHSELNPHLQS
		1	1	}		CRLPSRPSVSRELPPQSGPASSVPLAPTPLPDS
	1	į	- \		}	VPSQRHPTXPPPAS
					<del> </del>	PSMVWSYHWGVKQKRLALCVFSFEEGGRRK
280	1630	Α	2825	307	77	CGQYWPLEKDSRIRFGFLTVTNLTGAVGEPG
	1	ľ	1		}	VAFQCDGQRREPTC
		l			ļ	KMGTAVWVPKEKEKRDKASQEGGDVLGAR
281	1631	A	2827	81	381	QDCTPSLKSLVATGNLLDLEETAKAPLSTVSA
			- {	1	1	NTTNMDEVPRPQALSGSSVVWVSGCVASRS
	1	Į.	1			
	ļ	-	<u> </u>			VILSLTSG KLPXDKYELEPSPLTQYILERKSPHTCWQVFV
282	1632	A	2830	471	160	TSSGKYNELGYPFGYLKASTTLTCVNLFVMP
		1				YNYPVLLPLLDDLFKVHKLKPNLKWRQAFDS
		-	1	1	1	
		}	_			YLKTLPPYYL VSPALSLTPTIFSYSPSPGLSPFTSSSCFSFNPEE
283	1633	A	2835	462	148	MKHYLHSQACSVFNYHLSPRTFPRYPGLMVP
		1		1		MKHYLHSQACSVINIALSFRITTRII GENTI
	ł					PLQCQMHPEESTQFSIKLQPPPVGRKNRERVE
						SSEESAP
284	1634	A	2836	2	384	KTLPRTLLDILADGTILKVGVGCSEDASKLLQ
20.	1	-		1		DYGLVVRGCLDLRYLAMRQRNNLLCNGLSL
	ļ	-	}	i		KSLAETVLNFPLDKSLLLRCSNWDAETLTED
	1				1	QVTYAARDAQISVALFLHLLGYPFSRNSPGEK
	i					KR PDID (II
285	1635	A	2843	20	271	PIRPYYSYSGLDRDCSWLPLAKAWLPDVMIL
263	1 1035	' '				VCDRVSEDGINRQQAQEWCIKHGFELVELSP
	1	- 1				EELPEEDGKCLCVRRKYGTYI
286	1636	A	2845	197	278	TAEDVLTVAYEHGVNLFDTAEVYAAGK
	1637	$\frac{\Lambda}{\Lambda}$	2851	2	427	FVAEVRREWAKYMEVHEKASFTNSELHRAM
287	103/	1^	2051	1 -		NI HVGNLRLLSGPLDOVRAALPTPALSPKDK
1	1	1		1		AVLONLKRILAKVQEMRDQRVSLEQQLRELI
1	[	- [		l .		OKDDITGSLVTTDHSQMKKLFEEQLKKYDQL
		1		1		KVYLEONLAAODRVLCALT
		<del>-   -  </del>	2859	12	469	FVNLGILTCIECSGIHREMGAHISRIQSLELDK
288	1638	A	2839	[ *		LGTSELLPAKNYGNNSFNDIMEANLPSPSPKP
		1		1		TPSSDMTVRKEYITAKYVDHRFSRKTCSTSSA
				<b>\</b>		KLNELLEAIKSRDLLALIQVYAEGVELMEPLL
1	ł	1				EPGOELAETALHLAVRTADQTSLHLVE
			<del></del>	1.	454	FVASGGPATARMSDSQFFCVAEERSGHCAV
289	1639	A	2861	2	454	DGNFLYVWGGYVSIEDNEVYLPNDEIWTYD
		1	1		ļ	DSGLWRMHLMEGELPASMSGSCGACINGKL
1	[	1			:	YIFGGYDDKGYSNRLYFVNLRTRDETYIWEK
ł		1	İ		1	TTDFEGQPPTPRDKLSCWVYKDRLIYFG
						IIDLEGOLATOR TOCOCOMATICO A LEGITA O
L	1640	TA	2868	1	378	FRQGQLYKVFLHGSQGQVYHSQQVGPPGSA SPDLLLDSSGSHLYVLTAHQVDRIPVAACPQI
290	1040					
290	1040		}	<b>.</b>		PDCASCLQAQDPLCGWCVLQGRCTRKGQCC

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1		ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł	Ì		Sequence	/=possible nucleotide deletion, \=possible
	ì	Į	Ì	peptide	1	nucleotide insertion
	L		<u> </u>	sequence		RAGQLNQWLWSYEEDSHCLHIQSLLPGHHPR
		ł	1	1		OE
		<u> </u>			385	FRYMPNNRQQLLRKRHIGNDIVTIVFQEPGAL
291	1641	A.	2870	1	363	PFTPKSIRSHFQHVFVIVKVHNPCTENVCYSV
		1	į		Í	GVSRSKDVPPFGPPIPKGVTFPKSAVFRDFLL
	1	1	1	l		AKVINAENAAHKSEKFRAMATRTRQEYLKD
	1	Ì	1	1	ļ	LA
		<u> </u>		<u> </u>	100	RPTRPPPATTQSPESTMDTSLKKEKSAILDLYI
292	1642	Α	2877	3	188	PPPPAVPYSPRYVAVHCHGMLVSCWCHL
			1		<u> </u>	REKEEEVEEEDKVVKETEKEAEQEKEEDSL
293	1643	A	2878	1	427	GAGTHPDAAIPSGERTCGSEGSRSVLDLVNYF
	1	1	ł			LSPEKLTAENRYYCESCASLQDAEKVVELSQ
	į	1				GPCYLILTLLRFSFDLRTMRRRKILDDVSIPLL
		ŀ	1			LRLPLAGGRGQAYDL
		1		1		QLCCFCFRQTTLIVYILSFIGMVIFTFTLDLRYI
294	1644	A	2879	109	245	IVFVTGGVLG
				L		LASSQHGILNNLSLLFSICKTCIRTMDHHCPRA
295	1645	A	2880	3	320	NNCVGEQNHRFFCALHCKSKHFCIEFTLNTNF
	i	1		[		FNCFLPGAEKSTIDAPFSLQPFLQDSKYNTALS
	- <b>.</b> .	1	l	1	ļ	
					J	LSESISQ SQYSHSLDYHLLQVTKNPFTLGDSSNPGQTE
296	1646	A	2892	209	363	RLQEFSQKMDQVRGHWPVST
						SPXTLXLDTFILLGIQDNILVLILATPPFMAGG
297	1647	A	2893	8	424	KLYSTMGRFLRDRKNPACREMAVVLLANLA
		1				QGDSLAARAIAVQKGSIGHLLGFLEDSLAAT
	ì		ľ	1	1	QIQQSQASLLHMHNPPFEPTSVDMMRRACRA
	1	1	1	1		LLALAKVDDNHSEF
			1			FWIYFPSFFMTGYLPLGFEFAVEITYPESEGTS
298	1648	A	2894	310	445	SGLLNASAQVNL
		i				KIKAKNLTNYDLCSIFLGTSTLLVWVGVIRYL
299	1649	A	2898	1	492	GYFQAYNVLILTMQASLPKVLRFCACAGMIY
			Ì			LGYTFCGWIVLGPYHDKFENLNTVAECLFSL
	Į.	1			ļ	VNGDDMFATFAQIQQKSILVWLFSRLYLYSFI
ł	į.	1	ĺ	(		SLFIYMILSLFIALITDSYDTIKKFQQNGFPETD
	İ		1	1		
						LQEF   PVWWNSLNGASEVTFSVHVKDGGSFPKTDST
300	1650	A	2901	[ 1	445	TVTVRFVNKADFPKVRAKEQTFMFPENQPVS
		1	)	İ		SLVTTITGSSLRGEPMSYYIASGNLGNTFQIDQ
Į	1	1				LTGQVSISQPLDFEKIQKYVVWIEARDGGVPP
1			- 1			FSSYEKLDITVLDVNDNAPIF
	1					THFICLPLGYCFPLLDKDLQLPSGFNCNFDFLE
301	1651	A	2902	162	433	EPCGWMYDHAKWLRTTWASSSSPNDRTFPG
1				1		KPAVSEDMKELRPACSTYFNPRFPYKL
1				_l		GPOMLCKKIYFIWVTRSQCQFEWLADIMQEV
302	1652	A	2909	2	412	EENDHQDLVSVHIYVTQLAEKFDLRTTMLYI
1				j	1	CERHFQKVLNRSLFTGLRSITHFGRPPFEPFFN
	İ	- 1	j	1		SLQEVHPQVRKIGVFSCGPPGMTKNVEKACQ
1			1	1		SLOEANDOAKIOALSCOLLOMINIAA SIGNO
				L		LVNRQDRAHFM KLNRWLCFFYSWSFGILLYEMVTLGAPPYPE
303	1653	A	2914	291	453	KLNKWLCFF 15 W5FULL IEMV 1 LUAFF ITE
	1				_ :	VPPTSILEHLQRRKIMKRPSSCS
304	1654	- A	2926	179	354	PGVPSQALRKAESLKKCLSVMEAKVKAQTAP
1 304	1054	11				NKDVQREIADLGEVGAASLPPSSGPGA
305	1655	- <del> </del> _	2938	135	438	GMGYLHAKGILHKDLKSKNVFYDNGKVVIT
دند	1033	1	-,50			DFGLFSISGVLQAGRREDKLRIQNGWLCHLA
		1			Ī	PEIIRQLSPDTEEDKLPFSKHSDVFALGTIWYE
1	1	{				LHAREWP
				2	329	VRWNSCVNCSCAFGNGASLSTSLGESSGCLW
206	1666	- A	1 / 1/1/1/			1 1 T T T T T T T T T T T T T T T T T T
306	1656	Α	2944	2	323	EIGKWLSCSLLSFPSPLAVLITTFCIVTVLGREA LTKGALWAVFLLAGSALLCAEVTGVIWRQPE

						A-Alenine C=Cysteine
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	{			peptide	Sequence	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
	ļ	<b>↓</b>	<del></del>	sequence	<del> </del>	SKTKLSEKVSSSA
	1652	A	2950	2	411	NYLCIAKNSAGSAMGKTRLVVQVPPVIENGL
307	1657	^	2730	-	1	PDLSTTEGSHAFLPCKARGSPEPNITWDKDGQ
		1			1	PVSGAEGKFTIQPSGELLVKNLEGQDAGTYT
		1		1	1	CTAENAVGRARRRVHLTILVLPVFTTLPGDRS
	1	1.				LRLGDRLWLR
308	1658	A	2951	1	407	PTRPPRVRFDNEFDAESQRKRTTSVSKMERM
300	1050	1				DSSLPEEEEDEDKEAINGSGNAENRERHSESS
	1	1	1	j		DWMKTVPSYNQTNSSMDFRNYMMRDETLER LPKNWEMAYTDTGMIYFIDHNTKTTTWLDP
	1			}	1	
						RLCKKAKAPEDC QDFLTLTLTEPTGLLYVGAREALFAFSMEALE
309	1659	A	2954	2	179	LQGAVRGGAVGGSRACQRARPRGAVLG
	-			ļ	<del></del>	ODMMERAIDTFVGHDVVEPGSYVQMFPYPC
310	1660	Α	2959	1	419	YTRDDFLFVIEHMMPLCMVISWVYSVAMTIQ
		Ì	Ì	1		HIVAEKEHRLKEVMKTMGLNNAVHWVAWF
	Ì	1		1	[	TGFVQLSISVTALTAILKYGQVLMHSHVVIIW
	}	}			}	I FI AVYAVATIMFCF
		+	2963	3	465	MKPOMPGLGAPNGYGPGRGRAGVPGGPERR
311	1661	A	2903	3	1 403	PWVPHILPFSSPGYLGVMKAQKPGAGEGMK
		)	1	1	1.	POKPGLRGTLKPOKSGHGHENGPWPGPCNA
		Ì		1		RVAPMLLPRLPTPGVPSDKEGGWGLKSQPPS
		1				AVQNGKLPGHQPPNGYGPGAEPGFNGGLEPC
		1				KI CIDLINGN
312	1662	1 A	2967	3	405	WLAQEWSPCTVTCGQGLRYRVVLCIDHRGM
3.2				1		HTGGCSPKTKPHIKEECIVPTPCYKPKEKLPV EAKLPWFKQAQELEEGAAVSEEPSFIPEAWS
	1	-	ł			ACTVTCGVGTQVRIVRCQVLLSFSQSVADLP
		ſ		<b>\</b>	}	DECEGPKPA
ļ					1.50	VVADNCRQGYLDALRFLERRGLTKEPVLWT
313	1663	A	2969	2	430	IVSKEPPAPADGNWDAGCDQRRKGGLSLNV
!		į			ļ	KVPHVOVKDVPNFEOLSPELEAALKKACTRI
			}	}	ļ	PSRWARFWHSGPGQVLTYLLLPCTLPFEYIYI
		1		1	1	RSRRLVVWLPDVPADLWWMQ
	1001		2971	422	33	LDXSHNALORLRPGWLAPLFQLRALHLDHN
314	1664	A	29/1	722		I DAT GROVEVNASGLELLDLSSNTLRALGER
			ļ			DLDGLGALEKLLLFNNRLVHLDEHAFHGLRA
1		- {	-			LSHLYLGCNELASFSFDHLHGLSATHLLTLDI
						SSNRM
315	1665	+A	2973	1	525	ITVSTHASGSPFGLEPQSGWLWVRAALDREA
1 313	1005	1 : 1	/-			QELYILKVMAVSGSKAELGQQTGTATVRVSI
		1				LNONEHSPRLSEDPTFLAVAENOPPGTSVGR
				]		FATDRDSGPNGRLTYSLQQLSEDSKAFRIHPO TGEVTTLQTLDREQQSSYQLLVQVQDGGSPF
				-		TGEALLT OLD MENT
						RSTTGTVHVAVLDLNDNT ELVVELVSAGKSGPERNTYEVQVVTGNVPK
316	1666	A	2978	2	400	GTDANVYLTIYGEEYGDTGERPLKKSDKSN
-		1				FEQGQTDTFTIYAIDLGALTKIRIRHDNTGNR
	1					AGWFLDRIDITDMNNEITYYFPCQRWLAVER
}		1			}	DDGQLSRE
					140	VLNCQGRPTRPVRINGDGQEVLYLAESDNVI
317	1667	A	2981	3	440	I GCPYVLDPDDYGPNGLDIEWMQVNSNPAF
1 317				1		HRENVELSYODKRINHGSLPHLQHRVRFAAS
317		1				DPSQYDASINLMNLQVSDTATYECRVKKTTI
317					1	2.04.00.00
317						ATRKVIVTVQARPAVPMCWTEGQ
		1.	2005	110	414	ATRKVIVTVQARPAVPMCWTEGQ  LPEKEFPIIRKSSSLKVTKCLFTEQPKPIIILRFA
318	1668	A	2995	119	414	LPEKEFPIIRKSSSLKVTKCLFTEQPKPIILRFA FNYDARLLRIDIANTLREOVQELFNKTYGKQ
	1668	A	2995	119	414	ATRKVIVTVQARPAVPMCWTEGQ  LPEKEFPIIRKSSSLKVTKCLFTEQPKPIIILRFA ENYDARLLRIDIANTLREQVQELFNKTYGKQ RRTPGEGHVAAVDREVAGFPVPAEGISGETI GFFAYTYGRLVVVEDLHSGAQQHWSGHSAI

PCT/US01/03800 WO 01/57188

			CCCO T	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	, ,	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
otide	seq-		USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience		l	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	)			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ì	1	1	residue of	sequence	Y=1 yrosinc, A=0 iikilowii, —stop sociolis
	ļ		l	peptide		/=possible nucleotide deletion, \=possible
	<b>!</b>		ļ	sequence		nucleotide insertion
	ļ	ļ	<del> </del>	004		STLALSHSAQVLASASGRSSTTAHCQIRVWD
		ł	1	{		VSGGLCOHLIFPHSTTVLALAFSPDDRLLVIL
	ł	1	1			GDHDGRTLALWGTGHL
	l			-	322	IDESTGLUTVNYLDYETKTSYMMNVSATDQA
320	1670	A	3000	693	322	PRENIOGE CSVVITI I NELDEAVOFSNASYŁAA
	1					ILENLALGTEIVRVQAYSIDNLNQITYRFDAY
	l	ł		[		TSTQAKALFKIDAITVRGWGQGAPFFPI
		1	1	1		ISTUARALIFRIDATIVE OF SEASON PROPO
321	1671	A	3001	6	383	RIPRGKACXTVLGRSTGELEGFASSRLPPQPC
321	10/1	ΙΛ.	300.	1		GWGQSSDLLSRIDLDELMKKDEPPLDFPDTLE
	1	1	1		)	GFEYAFNEKGQLRHIKTGEPFVFNYREHLHR
	1		Ţ.		ì	UNION DATE AT GETTKYVYELLEKDCNSKKVS
	l			1.02	447	EDVENCE FEGREDSOCACCESSPVWVFLETGE
322	1672	A	3007	192	447	LFPWLFLQVEVIKKAYMQGEVEFEDGENGK
			1	1	}	DGAASPRNVGHNIYILAHQLARH
	Į.	Ì	i	1	<del> </del>	KELLFYHLIVNNINFFNTRYAKIHIPIIASVSEH
323	1673	A	3019	18	245	QPTTWVSFFFDLHILVCTFPAGLWFCIKNIND
723	1.0,5	1	1			Oblimazettoruracitiyorar
		ì	i			ERVFGKRGF
204	1674	A	3020	523	797 .	LCYFSARYHQRKIFGILYIFTLSAINRKEPNLFI
324	1674 A	3020	1 22		YLFIFFEMESHSVTHAGVQRHNLNSLQPLPPG	
	1		ļ	}	FKRFSCLCFLSSWNYRGAPPGPANF	
			2000	12	156	NDFLPLYFGWVLTKKSSETLRKAGQVFLEEL
325	1675	Α	3022	2	150	CNIHKAFKKELROCRWOVGAL
	1				122	KMVRGSKKLISFFPGGPYGILAGRDPSKGLAT
326	1676	Α	3023	38	172	DOLNIKE ALK DEFE
	1					LTLEFLLLPAASELAHGKRLACCIVDHKLPEC
327	1677	A	3027	1	385	GFYGLYDKILLFKHDPTSANLLQLVRSSGDIQ
321	10//	1				GFYGLYDKILLFKHDF1SANLLQLYRSBODSQ
	]	- 1				EGDLVEVVLSASATFEDFQIRPHALTVHSYRA
	ļ	- 1	(			PAFCDHCGEMLFGLVRQGLKCDGCGLNYHK
	Ì	1	Į	İ		RC
			2020	13	569	ITRPTISCQRPGPGLAAGMLPYTVNFKVSART
328	1678	Α	3030	13	307	I TO A I NAHNK A AVOWGWOGLIAY GCHSLV
		1	ì		1	VVIDSITAOTI OVI EKHKADVVKVKWAREN
		1	l			YHHNIGSPYCLRLASADVNGKIIVWDVAAGV
1	i	ì	1	1		AQCEIQEHAKPIQDVQWLWNQDASRDLLLAI
1	i	i				HPPNYIVLWNADTGTKLWKKSYADNILSFSF
}	1	ì	ļ			1 _
1				}		D DOTTO THE A POST OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
200	1670	A	3038	90	744	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAED
329	1679	A	0.00	1.		GNIEYKKLVNPSQYRFEHLVTQMKWRLQEG
1						P CE A VYOIG VEDNGLL VGLAEEEMRASLK II
ì		1		,		HDMAFKVGADITVLREREVDYDSDMPRKITI
	}		1	j		VI VRKVPDNOOFLDLRVAVLGNVDSGKSTL
1	l		(			LGVLTQGELDNGRGRARLNLFRHLHEIQSGR
					1	TSSISFEILGFNSKGEVHGINGTQWGQTLRMC
1	1	1	1	1		
İ		1		1		W CONTRACTOR AND THE
		<del></del>	3040	3	397	LCSTLLLLTIPSWVLSQITLKESGPTLMKPTE
330	1680	A	3040	1		I TI TOTESGESI NTSGVGVAWIRQPPGKALE
		1		i		WI ALLYWDDDKRYSPSLNDRLTIAKUTSKNO
1				Ĭ		VVLTMTNMGPVDTATYYCAQFARGARGSN
1	ŀ			1		WFDPWGQ
1	,	}				AGIRHEAPPTTSNRHRRQIDRGVTHLNISGLK
331	1681	A	3043	3	1509	MPRGIAIDWVAGNVYWTDSGRDVIEVAQMI
551	1,001	1				MPKGIAIDWYAGNY I W IDSOID TETAQUE
1						GENRKTLISGMIDEPHAIVVDPLRGTMYWSI
		i	ı	1		WGNHPKIETAAMDGTLRETLVQDNIQWPTG
1		}		}		I AVDVHNERI YWADAKLSVIGSIRLNGTDPI
1		l	1	1		VAADSKRGLSHPFSIDVFEDYIYGVTYINNK
1	1	1			ł	EVILLEGUSPI VNI TGGLSHASDVVLYHQHI
	1	1		1		QPEVTNPCDRKKCEWLCLLSPSGPVCTCPNC
F	1			1		KRLDNGTCVPVPSPTPPPDAPRPGTCNLQCF
1			1	1	1	KKTDMQICALALPITITIDGIG CICLDGOL
	1	ļ	l l	1	(	GGSCFLNARRQPKCRCQPRYTGDKCELDQC

EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
10: of	NO: of	hod	ID NO:	beginning	nucleotide	D-Aspartic Acid, E-Glutamic Acid,
ucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	1 !		'''	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	[		!	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ļ	peptide	1 004	/=possible nucleotide deletion, \=possible
	1		ļ	,	}	nucleotide insertion
			<u> </u>	sequence	<u> </u>	WEHCRNGGTCAASPSGMPTCRCPTGFTGPKC
			ļ	Į		TQQVCAGYCANNSTCTVNQGNQPQCRCLPG
	}	ì	1			FLGDRCQYRQCSGYCENFGTCQMAADGSRQ
	1	Ì	1	}	}	CRCTAYFEGSRCEVNKCSRCLEGACVVNKQS
	(		1	Ì		CRCTAYFEGSRCEVNRCSRCEEGACVITAGO
		1	1	1		GDVTCNCTDGRVAPSCLTCVGHCSNGGSCT
		1		1	Ì	MNSKMMPECQCPPHMTGPRCEEHVFSQQQP
	]	}	1	Ì		GHIASILIP
	1.00		3045	3	952	TTTISNFHTQVNRTYCCGTYRAGPMRQISLVG
332	1682	A	3043	١٦	752	AVDEEVGDYFPEFLDMLEESPFLKMTLPWGT
	1	1	1			I SSURLOCRSOSDDGPIMWVRPGEQMIPTAD
	1	1	1			MPKSPFKRRRSMNEIKNLOYLPRTSEPREVLF
	}	}	1	}	1	FORTRAHADHVGOGFDWOSTAAVGVLKAV
		1	1	1		QFGEWSDQPRITKDVICFHAEDFTDVVQRLQ
	1	1		1		LDLHEPPVSQCVQWVDEAKLNQMRREGIRY
	1	1				ARIQLCDNDIYFIPRNVIHQFKTVSAVCSLAW
		ł	1	Ţ		HIRLKQYHPVVEATQNTESNSNMDCGLTGKR
			1		ļ	HIRLKQYHPVVEATQNTESINSNVIDCGETGRI
	ì		1	}	1	ELEVDSQCVRIKTESEEACTEIQLLTTASSSFP
	1	}	i	}		PASE
222	1683	A	3046	497	167	SACSTGPELPGRATRSLTRPANQKGCDGDRL
333	1083	^	3040	1 '''	1	YYDGCAMIAMNGSVFAQGSQFSLDDVEVLT
	ł	1	i	Ì	1	ATLDLEDVRSYRAEISSRNLAVSAPVDTCVG
		1	- [			CSSKTWKVAPFVRAWWRP
				<del></del>	276	VITDLEFOLNOLTEDNAELNNONFYLSKQLD
334	334 1684	Α	3053	37	270	EASGANDEIVQLRSEVDHLRREITEREMQLTS
	1	}				QKQVRRVNKVVRSLEDF
	l .				<del></del>	WDAWGDWSDCSRTCGGGASYSLRRCLTGR
335	1685	A	3054	2	846	NCEGONIRYKTCSNHDCPPDAEDFRAQQCSA
	1		l l	1		YNDVQYQGHYYEWLPRYNDPAAPCALKCH
	1		ł			YNDVQYQGHI IEWLFRINDI AM CALICON
	ı	1		1		AQGQNLVVELAPKVLDGTRCNTDSLDMCISC
		ļ		1	1	ICQAVGCDRQLGSNAKEDNCGVCAGDGSTC
	j		1	j	1	RLVRGQSKSHVSPEKREENVIAVPLGSRSVRI
	٠ .	1				TVKGPAHLFIESKTLQGSKGEHSFNSPGVFVV
	ŀ	į.	Į.			ENTIVEFORGSERQTFKIPGPLMADFIFKTRY
1	l l			1		TAAKDSVVQFFFYQPISHQWRQTDFFPCTVT
	}	}		ļ	i	CGGG
			10000		347	VVGKOEAGAHSDSCCLLHTPPRLTPAHSRKA
336	1686	Α	3058	54	341	I RNSRIVSOKDDVHVCIMCLRAIMNYQVSKG
		l		1	1	AWDWRLGSPACPHWGLHKLPRLWDPLSLYF
1	1					
İ	1			l		VLCWGT  ILTSLVELTRFETLTPRFSATVPPCWVEVQQE
337	1687	A	3059	2	709	ILISLVELIKTEILITATSAIVITCH VEVQO
1 33 '	1 2007	1		1		QQQRRHPQHLHQQHHGDAAQHTRTWKLQT
	1	-		1		DSNSWDEHVFELVLPKACMVGHVDFKFVLN
]		j				SNITNIPQIQVTLLKNKAPGLGKVNGLRLCPF
1		-	1	1		I EDHKEDILCGPVWLASGLDLSGHAGMLTLI
		- }	1	1		SPKLVKGMAGGKYRSFLIHVKAVNERGTEEI
1		İ		1		CNGGMRPVVRLPSLKHQSNKGYSLASLLAK
	1					VAAGKEKSSNVKNENTSGTRK
					<del></del>	KAFYNYHVLELLQMLVTGGVSSQLEQHLDK
338	1688	A	3060	85	384	DKVYGVADSCTSLLSGRNRCKLGLLSLHETII
		- {		1		SDVNPRNTFGQLFCGSLDLFGILCVGLYRIIDI
1	1	1	1		Į.	
						EELNP
225	1600		3063	236	362	CFLCLSGDFMVMTIFFNVSRRFGYVAFQNYV
339	1689	A	2003	250		PSSVTTMLSWV
				<del></del>	1249	DI WOFTPLHEAASKNRVEVCSLLLSYGADP
340	1690	Α	3065	3	1247	LI NCHNK SAIDLAPTPOLKERLAYEFKGHSL
1				j		QAAREADVTRIKKHLSLEMVNFKHPQTHETA
1	1					LHCAAASPYPKRKQICELLLRKGANINEKTK
		1				FLTPLHVASEKAHNDVVEVVVKHEAKVNAL
	1	1	1		1	I LI IDI HVANEKAMNIJYYEYYYILMAN YIM
	i	1	ĺ	1	1	DNLGQTSLHRAAYCGHLQTCRLLLSYGCDP

					To discount and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ł	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	}	1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		1		amino acid	of peptide	I=Inconinc, v=vainc, w=Tryptophan,
	}	l	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ	}	peptide	1	/=possible nucleotide deletion, \=possible
	1	1	ì	sequence		nucleotide insertion
	<del> </del>	<del>                                     </del>	<del> </del>			IISLQGFTALQMGNENVQQLLQEGISLGNSEA
		1			ļ	DRQLLEAAKAGDVETVKKLCTVQSVNCRDIE
	}	1	1		[	GRQSTPLHFAAGYNRVSVVEYLLQHGADVH
	1	1	1			AKDKGGLVPLHNACSYGHYEVAELLVKHGA
	1	1	1			VVNVADLWKFTPLHEAAAKGKYEICKLLLQ
			1			HGADPTKKNRDGNTPLDLVKDGDTDIQDLLR
	1	1	1	1		GDAALLDAAKKGCLARVKKLSSPDNVNCRD
			1			TOGRHSTPLHLAGK
		<b>_</b>	2070	<u> </u>	547	GVLIPSFQNQLFADILAGIESVTSEHNYQTLIA
341	1691	A	3070	1	)41	NYNYDRDSEEESVINLLSYNIDGIILSEKYHTI
	[			1	1	RTVKFLRSATIPVVELMDVQGERLDMEVGFD
ļ	1	i	1			NRQAAFDMVCTMLEKRVRHKILYLGSKDDT
	1	1	ł		}	RDEQRYQGYCDAMMLHNLSPLRMNPRAISSI
	1	}	ļ		}	HLRMQLMRDALSANPDLDGVFCTN
						RINRCRKPSDADILVPGDTISLIGTTSLRIDYNE
342	1692	A	3073	463	3	IDDNRVTAEEVDILLREGEKLAPVMAKTRILR
		ł	İ		1	IDDNKV I AEEV DILLREGERLAF VIJAK I IDHAE
ł		Į.	1			AYSGVRPLVASDDDPSGRNVSRGIVLLDHAE
ì	)	)	1	}		RDGLDGFITITGGKLMTYRLMAEWATDAVC
						RKLGNTRPCTTADLALPGSQEPAKVP
343	1693	A	3075	250	1	LLIYLAIFAPVAMSALAGVKSVQQVRIRAAQS
1 343	1 10,55	1		1		LGASRAQVLWFVILPGALPEILTGLRIGLGVG
	j	}				WSTLVAAELIAATRGLGFM
344	1694	A	3076	2	138	LYFDAYLQSLQVAAISTFCCLLIGYPLAWAV
344	1074	1 '	33.7			AHSKPSTRNILLLL
345	1695	A	3078	469	3	LKIRGQRIELGEIDRVMQALPDVEQAVTHAC
343	1095	1	1 3070	( ,0)		VINOAAATGGDAROLVGYLVSQSGLPLDTSA
		1	-			LOAOLRETLPPHMVPVVLLQLPQLPLIANGKL
			l l		ì	DRKALPLPELKAQAPGRAPKAGSETIIAAAFS
			1	ł	1	SLLGCDVODADADFFALGGHSLLAMKLAT
-	1.00		3082	404	2	ONITSKOLDVRLDPOTVPIELEQLVLSFNHMI
346	1696	Α	3082	404	1 ~	ERIEDVFTROSNFSADIAHEIRTPITNLITQTEI
	1			ì		ALSOSRSOKELEDVLYSNLEELTRMAKMVSD
}	1	1	i		1	MLFLAQADNNQLIPEKKMLNLAHEVGKVFD
	ì			ł		OFEALPE
				<del></del>	340	NELTFKEAEISKLYTKVHPAYRTLLEKRQALE
347	1697	A	3084	3	340	DEKAKLNGRVTAMPKTQQEIVRLTRDVESGQ
1		1		1		QVYMQLLNKEQELKITEASTVGDVRIVDPAIT
	1			1	1	QPGVLKPKKGLIILGAI
				1	+,,,	TQAMVWQQKACAEDDPQLSGRHWLHAATL
348	1698	A	3086	723	10	YNIAAYPHLKGDDLAEQAQALSNRAYEEAA
				1		QRLPGTMRQMEFTVPGGAPITGFLHMPKGDG
	1	1		1	1	PFPTVLMCGGLDAMQTDYYSLYERYFAPRGI
				1	1	TEL ADDITION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
		1		1		AMLTIDMPSVGFSSKWKLTQDSSLLHQHVLK
	1	-		}	J	ALPNVPWVDHTRVAAFGFRFGANVAVRLAY
1		Í		1		LESPRLKAVACLGPVVHTLLSGLKCQQQVPE
		-				MYLDVLASRLGMHDASTKSSTRENH
349	1699	A	3087	2	249	RIRSSDPEITLAGTPLHAAYLIGMTLICAGFSV
343	1077	^	1 500.	] -		GFGVAMSQALGPFSLRAGVASSTLGIAQVCG
1						SSLWIWLAAVVGIGAWNM
250	1700	<del></del>	3099	3	424	FAPEATPOPSOPGPSSPISLSAEEENAEGEVSR
350	1700	A	3033	١		ANTPDSDITEKTEDSSVPETPDNERKASISYFK
1		- {		1	1	NORGIOYIDLSSDSEDVVSPNCSNTVQEKTFN
1		1			1	KDTVIIVSEPSEDEESQGLPTMARRNDDISELE
1					1	DLSGMEDLK
				<u> </u>	104	IKKNHIIGYQLLHRRALFEKRTRLSDYALIFG
351	1701	A	3108	2	404	MFGIVVMVIETELSWGAYYKAPLYSLALKCL
				1		ISLFTIILLGLTIVYHAREIQLFMANYGADDWR
	1	1	1	1	1	19PL LITTPOPITA TITUTORIÓN INTELLOCUPO LIV
				İ	l l	CALTYEDIEI II I EAI DOWNATECRVSI SI WD
					ļ	SALTYEPIFLILLEALRGVIHATPCRVSLSLWD GLDLP

					- 1:	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	Ì		914	amino acid	of peptide	T=Threonine V=Valine, W=Tryptophan,
			ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		j	ļ	peptide	Sequence	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
2.50	1702	A	3110	341	2	AQLAEVCPPQTLLTTNTSSISITAIAAEIKNPER
352	1702	\ A	3110	1		VAGLHFFNPAPVMKLVEVVSGLATAAEVVE
		1				QLCELTLSWGKQPVRCHSTPGFIVNRVARPY
	1	1		į.	ĺ	YSEAWRALEEQVAAPEVI
353	1703	A	3111	3	188	HFSLFRIAFAVFLTYMTVGLPLPVIPLFVHHEL
333	1703	^	3222			GYGNTMVGIAVGIQFLATVLTRGYAGRLA
354	1704	A	3116	367	225	WQLFHLNGTFLNIGETDTESCVNGWVYDRSS
334	1704	) ^	}	1		FPFSNMTEVRGLVFLS
355	1705	A	3117	101	53	VINLVYLISSPRPELKPVDKESEVVMKFPDGF
333	1703	1.	1			EKFSPPILQLDEVDFYYDPKHVIFSRLSVSADL
		}		ì		ESRICVVGENGAGKSTMLKLLLGDL\APVRGI
1						RHAHRNLKIGYFSQHHVGAAGT*TFSACGNL
		1		ļ		LGTQVFLGRPEEEYRHQLGFGMGISGELGHA
			1	j	i	SSLPACLGGQKEAEVAFCSDGLLPCPNFL\IL\
		(				DEPTNHLGHGRAIEALGPCLQTISGVGVILVS
						HE*SALSRLVCRE\LWVC*GRSTSPF
356	1706	A	3121	137	466	RGGRDWGEHNQRLEEHQARAWQGAMDAG
330	1700	1		1		AASREHARWQGTGLAPGTRVAVAPTCVQGL
İ	}	}	1	1	1	POERSVCRPFFSSRWREGPVWALGAGAHGKP
,	1		1			RWSGGVRCVVRGGRWFTPAPH
357	1707	A	3124	1249	229	MLEAPGPSDGCELSNPSASRVSCAGQMLEVQ
337	1,0,	1				PGLYFGGAAAVAEPDHLREAGITAVLTVDSE
1	- {	-	1			EPSFKAGPGVEDLWRLFVPALDKPETDLLSH
	1		i			LDRCVAFIGQARAEGRAVLVHCHAGVSRSV
	ł		1	)	1	AIITAFLMKTDQLPFEKAYEKLQILKPEAKMN
1	Í	1	1			EGFEWQLKLYQAMGYEVDTSSAIYKQYRLQ
<b> </b>	1	1				KVTEKYPELQNLPQELFAVDPTTVSQGLKDE VLYKCRKCRRSLFRSSSILDHREGSGPIAFAH
	1			1		KRMTPSSMLTTGRQAQCTSYFIEPVQWMESA
1	1	1	[			LLGVMDGQLLCPKCSAKLGSFNWYGEQCSC
	J ·		1		{	GRWITPAFQIHKNRVDEMKILPVLGSQTGKI
		1				EVETLGPRTPGP/EAQSPTPGSCPGWQEPSPGP
358	1708	A	3127	816	139	TPPP*LSGPGPQGAPVLGKLLPDPEETPAGKTP
			1			LGKHFWWGL\PVTSANFSPGAAA*FGGALSPP
						GGDL/GHMLLQGPPSPFRLQQQ*QTPPGSHSP
			1			PTANREINPGPAAAADTRSCWGHKRSWRGW
					}	RGLAPWRLGFGSPGIP*PAPAGIP/GRPTWEGG
					1	KGAGGKPSETLTRSPPVWRGKRGSANGFLSW
		1		1		VQILQ
					101	HEHILLLLCVFLVKSOGVNDNEEGFFSARG
359	1709	A	3132	3	191	HRPLDKKREDAPNLRPALADUTVCDYRAQIA
				1	1	*AASTPKRAASIAHNAVSCR*AQIA
					1200	REPPRPALLFF*DRVSLCCPGWNAVVQSQLT
360	1710	A	3134	1	286	AAPTSQVQ/SDSPTFPSSWDYRHVPEYPANFL
1	1	1		}	1	*ROGFPMLPRLVSNSWAQTVHPPRPPKVLDL
	1	1				OA
1					1440	PVPAPRVSPSARGAPGRPRLPGVRGPRHS/WA
361	1711	A	3135	56	1449	AD*RGSRM/PPRAPAPSPTGP/APGGKKVRGR
	1	1				VPEDPDAYEPRCSAL*V*PTHVTSPQFCDP*N
		- 1		1	į	GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA
						I AR AIR AIR I I I DELIVERING TO A CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE C
				}	l	GPGROSTPAVTRDHROHEDPRGAGROWDAD
						GPGROSTPAVTRDHRQHEDPRGAGRQWDAD
						GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ
						GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGI PHRTSIRPGWRRLTEPEAWARRHRRPW
						GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GORGAVRPPPOGAAPPPSHOGRRTNTDPSAT
						GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRI.TVMSRCLAPDLKAPASGPRGWRRGMPQ
						GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA
						GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT
						GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ APGLPHRTSIRPGWRRLTEPEAWARRHRRPW GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT PRLTVMSRCLAPDLKAPASGPRGWRRGMPQ SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA

						- Alapine C=Cysteine
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ĺ	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	Ì	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
			1		Sequence	/=possible nucleotide deletion, \=possible
		1		peptide sequence		nucleotide insertion
			<del> </del>	sequence	<del> </del>	RNQSPLGNDTLSSGLPMGPRRQVWPLARVG
			1			GHSSPREPQVLKKPLWGQTDIAGVGSASLYP
			}	Ì	ł	DNL
0.0	1212	A	3136	1270	274	RVGMVLGTREVGDSTPPPSPPLYPFTGNEFVQ
362	1712	^	3130	12.0		HNTWQLSRVYPSDLRTDSSNYNPQELWNAG
		1		1		CQM/V*GGSRDWEEGVEEQQVGNKFSSDGR
	1		1	1		VGECSRKLLG*EMLSVDITSRYRAPSTYLLNS
		1				LKEGLEGLHGESCSSFLLGPSVAMNMQTAGL
	1		1	1		EMDICDGHFRQNGGCGYVLKPDFLRDIQSSF
		1			İ	HPEKPISPFKAQTLLNQVISVQQLPKVDKTKE
		İ	Ì	ì	(	GSIVDPLVKVQIFGVRLDTARQETNYVENNG
	1	1	1		Į.	FNPYWGOTLCFRVLGPDFPMLRFGKMDYDW FNPYWGOTLCFRVLGPDFPMLRFGKMDYDW
	1			j	ļ	KSRNDLLGKTPCPGTCMQQGYRHIHLLSKDG
		1				ISLRPASIFVYICIQEGLEGDES MFAGSYGKSMFSFSKKVLNCLPKWRYHFVIA
363	1713	C	3139	60	248	PAMNESPLAPHLHQHLVFSVFQVLTILIGV**
		1				SAFKTLQLPAFSLYFDLGSLKLLILRIHTSIVK
364	1714	A	3140	57	418	NHKVESPRTMSPG*DPQSFLQIPQPRPPQLRV
		1				GLTSGLIQHFHSPSSCQFPLLRGPPFPRQPPLGI
		1				SGASLCPVLSPPR*PLOPSSL
					413	1 I PVPSI EVELROCHEVT\RLECNGVVSAHCN
365	1715	Α	3145	122	413	I HI PGSSDSPASAS*VAGTTGVCHHTRLIF\VF
		1		1.	İ	LV*TGFHYVAQAGLELLTA*S\PPQLPKVVGL
1		-				OA
			3150	247	12	VGEKI HDIREGNDEDMTPKAQATKEKIDKLN
366	1716	Α	3130	247	1	FIKIKKLCIEGYY/NREPQNGRKIFANYVS/DK
				}	1	GLMATIYEELLKLSNKLIQ
365	1717	-	3152	3	2367	QKLKQNQPKRAHVEDGGSRSKQGNEQSKKT
367	1/1/	1	3132	1		PIEKSDFAAATHPRAFYLSKPDETPNAWMSD
		l l				SGTGLTYWKLEEKDMHHSLPETLEKTFISLSS
ŀ		-			0.	TDVSPNQVLTLDPTLHMKPKQQISGIQPHGLP
ŀ	}					NALDDRISFSPDSVLEPSMSSPSDIDSFSQASN NALDDRISFSPDSVLEPSMSSPSDIDSFSQASN
	į	1	Ì	1		VTSQLPGFPKYPSHTKASPVDSWKNQTFQNE SRTSSTFPSVYTITSNDISVNTVDEENTVMVAS
	1	1	ì	ì		ASVSQSQLPGTANSVPECISLTSLEDPVILSKIR
1		- 1		ì		QNLKEKHARHIADLRAYYESEINSLKQKLEA
	1	1		1		KEISGVEDWKITNQILVDRCGQLDSALHEATS
		}			1	RVRTLENKNNLLEIEVNDLRERFSAASSASKI
		ł			!	LQERIEEMRTSSKEKDNTIIRLKSRLQDLEEAF
		- }			İ	ENAYKLSDDKEAQLKQENKMFQDLLGEYES
	4	1				LGKEHRRVKDALNTTENKLLDAYTQISDLKR
	1	ļ				MISKLEAQVKQVEHENMLSLRHNSRIHVRPS
	1		[	Ţ		RANTLATSDVSRRKWLIPGAEYSIFTGQPLDT
	1	1	İ	Į		QDSNVDNQLEETCSLGHRSPLEKDSSP/GSSS
}			1	1		SLLIKKQRETSDTPIMRALKELDEGKIFKNWG
		1				TQTEKEDTSNSLL*/INPRQTETSVNASRSPEK
1		}				CAQQRQKRLNSASQRSSSLPPSNRKSSTPTKR
1		[				EIMLTPVTVAYSPKRSPKENLSPGFSHLLSKN
1		ĺ				ESSPIREKTYSEKATDNHVNHSSCPEPVPNGV
	İ	1		1		KKVSVRTAWEKNKSVSYEQCKPVSVTPQGN
	1	ì				DFEYTAKIRTLAETERFFDELTKEKDQIEAAL
İ	1	{				SRMPSPGGRITLQTRLNQVKCLSLNLL
						EFKSGGCGAGLVAAGAVLVLYPASRAGERT
368	1718	A	3163	2	2350	RVPGSPAPSSLPLHSPGACGTEVDMDPQRSPL
300	1	1				LEVKGNIELKRPLIKAPSQLPLSGSRLKRRPDO
		Ì		İ		MEDGLEPEKKRTRGLGATTKITTSHPRVPSLT
		- [				TVPQTQGQTTAQKVSKKTGPRCSTAIATGLK
1	j				(	NOKPVPAVPVQKSGTSGVPPMAGGKKPSKR
		j	1			AWDLKGQLCDLNAELKRCRERTQTLDQENC

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nucleotide seq- uence  1914  1914  1914  1914  1916  1914  1916  1914  1916  1914  1916  1914  1916  1914  1916  1914  1916  1916  1914  1916  1914  1916  1914  1916  1914  1916  1916  1916  1916  1916  1916  1916  1916  1917  1916  1917  1917  1917  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1	NO of	NO: of	hod	ID NO:	beginning		D=Aspartic Acid, E=Glutaniic Acid,
sequence    Sequence	_		]	in	nucleotide	*	F=Phenylalanine, G=Glycine, H=ristidile,
uence    0,496		F - 4	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
penice with a print of the mino scid residue of peptide of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of period of period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with the period of peptide sequence with t			ł		correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
amino acid residue of sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per seq		defice	ì			acid residue	O=Glutamine, R=Arginine, S=Serine,
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			İ	1	sequence		nucleotide insertion
VQELOKKQVELQEEREGIMSQLEEKERING    SEAALSSSQAEVASLRQETVQAALITEREER     LHGLEMERRI.HMQLQELKGNIRVFCRVPG    SEARGILSGAPAPPITHDFSPDR.VFPRSGQDED    LHGEFFPPFGLLLFSPGGGSPSPTRLSLSRSD     ERRGILSGAPAPPITHDFSPDR.VFPRSGQDED    VFEEIAML VQSALDGFYVCIFAYGGGSEKT     TJMEGGPGGDPQLEGLEPRALRHLFSVAQELS    QGWTYSFVASVELYTHTEVTRULATGTRIGQ     QGWTYSFVASVELYTHARYVPVSCSEK    DALLHLARQINAVARTAQNERSSRSISVEVQL     QISGEHSSRGLQCGAPLSLVATAGSERLJPGL     ALGPGERERLEFOLANSLSTLGJVMALSN     KESHYPYRNSKLTYLLQNSLGSSAKMLMFV     NISPLEENNSSLINTLGJVMALSN     KESHYPYRNSKLTYLLQNSLGSSAKMLMFV     NISPLEENNSSLINTLGJVMALSN     KESHYPYRNSKLTYLLQNSLGSSAKMLMFV     NISPLEENNSSLINTLGJVMALSN     KESHYPYRNSKLTYLLQNSLGSAKMLMFV     NISPLEENNSSLINTLGJVMALSN     NISPLEENNSSLINTLGJVMALSN     STYRDAJPYKLITFFINLDKLILKFYLKTKIAK     NRIKTFYMRRKLGDSS     NRKWKTPFINLDKLILKFYLKTKIAK     NRIKTFYMRRKLGDSS     A 3170 393 42 GASSSFSAVIDGVSLKFMGQGEAGGFCLD     HIMAPEQWVAPRIKLIFRILFSVIHALILANG     STYRDAJPYKLITFFINLDKLILKFYLKTKIAK     NRKTFYMRRKLGDSS     NRKWKTPFINLDKLILKFYLKTKIAK     NRKTFYMRRKLGDSS     A 3180 381 76 GNGGCGLSQIPFSHLGAFSRGSLISRGUPRGP     PPHYVFFVVVEQGFTVLARMVSIS*PCDPP     ALASOSAGITGVSHLARPQNLY     STYRULHSONAGY*TSDRINGWYHCLQKCL     QHYAYVEK     AND STRANGE     SALVAADDARKTCSPKGARCDYTLDELTSV     NRKWKTYSTULHISTONAGY*TSDRINGWYHCLQKCL     QHYAYVEK     NRKWKTYSTULHISTONAGY*TSLUCHON     SALVAADDARKTCSPKGARCDYTLDELTSV     NRKWKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULHISTONAG     NRKKTYSTULH							QLQDQLRDAQQQVKALGTERT TLEGGLARV
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VFEEIAML/QSALDG/PVC/IFAYQG/TGSKTF	1	1			1	1	EDBCTI SCAPARDTRHDESEDR VEPPGSGODE
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peptide sequence    Peptide		1		Ì	amino acid		I=Inreonine, v-value, w-rtyptophan,
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NDCGDYSDETHANCTNOATRIPEGGCHTDEN QCRLDGLCIPLR WRCDGDTDENDSSDENSE GYTHVCDPSVKFGCKDSARCISKAWCDGE NDCEDNSDENGELACREPSHPCANNTSV LPPDKLCDGNDDCGGGSDEGELCOCLOSLN GGCSHNCSVAPGEGIVCSCPLGMELGPDNH CQIQSYCAKHLKCSQKCDQNKFSVKCSCYE WYLEPDGESCRSLDPFKPFIFFSNRHEIRIDL KGDYSVLYGLRNTALDHLBLSQSALYWTD VEDKIYRGKLLDNGALTSFEVVIQYGLATPE LAVDWIAGNIYWVESNLDQIEVAKLDGTLR TLLAGDIEHPRAIALDPRDGILFWTDWDASL RIEAASMSGAGRRTVHRETGSGGWPGIATPE LAVDWIAGNIYWVESNLDQIEVAKLDGTLR TLLAGDIEHPRAIALDPRDGILFWTDWDASL RIEAASMSGAGRRTVHRETGSGGWPGIATPE LAVDWIAGNIYWVESNLDQIEVAKLDGTLR TLLAGDIEHPRAIALDPRDGILFWTDWDASL RIEAASMSGAGRRTVHRETGSGGWPGIATPE LAVDWIAGNIYWVESNLDQIEVAKLDGTLR TLLAGDIEHPRAIALDPRDGILFWTDWDASL RIEAASMSGAGRRTVHRETGSGGWPWGIATPE ROPHAFFAVTLYGGGTVWTDWRTNILL KANKWTGHNYTVVQRTNTQPFDLQVYHPS QPMAPNPCEANGQGPCSHLCLINYNRTVS ACPHLMKLHKDNTTCYERKELLYARQME GYDLDAPYNYISISTYPDDNNYTVLDYDAR QRYWWSDWTQAKKRAWGGPCSHLCLINYNRTVS ACPHLMKLHKDNTTCYERKELLYARQME GYDLDAPYNYISISTYPDDNNYTVLDYDAR QRYWWSDWTQAKKRAWGGPCSHLCLINYNRTVS ACPHLMKLHKDNTTCYERKELLYARQME GYDLDAPYNYNISTYPTDNNYTVLDYDAR QRYWWSDWTQAKKRAWGGPCSHLCHNYNTSY ACPHLMKANAWGGPCSHLVHYLERGKL WTDGBNISMANMDGSNRTLLFSGGGWPG AIDFPSEKLYWISSGNHTINLFSGGGFUC AMRSQLGKATALAMGDKLWWADQVSEK GTCSKADGSGSVVLNNSTLLAGGGGPVG AIDFPSEKLYWISSGNHTINLFSGQGKPVG AMRSQLGKATALAMGDKLWWADQVSEK GTCSKADGSGSVVLNNSTVLAMMKVVDG QLDHKGTNYCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GIPLDPNNSKDALPVSGTSLAVGIDFHAEN TYWVDMGLSTISRAKRDQTWREDVVTNG RVEGLAVDWIAGNTYWTDQGFDVIEVARLN SFRYVVISOGLDKFRAITVHPEKGYLFWTE GQYPRIERSRLDGTERVLVNSISWPNGIS DYQDGKLYWCDARTDKERIDLETGENRE LSSNMMMFSSVSFEDTYWSDRTHANGSI DYQDGKLYWCDARTDKERIDLETGENRE LSSNMMMFSSVSFEDTYWSDRTHANGSI RGSKDNATDSVPLRTGIGVQLKDRKYNRD QKGTNVCAVANGCQQLCLYRGRORAC CAHGMLABGASCREYAGVLLYSETILKS HLSDERNLNAPVQPFEDFEHMKNVLALAGNN TLERDIRFNIFSDIHFGRIQQNIDDGSRR VENVGSVEGGLAYHRGWDTLYWTSTTST. RHTTDQTREGAGERTLYTMSGDDHFAEN THETDDTREGAGERTETTMSGDDHFAEN THETDDTREGAGERTETTMSGDDHFAEN THETDDTREGAGERTETTMSGDDHFAEN THENDETGRAGERTELTGGRAVELYSDATLUR RCEYDGSRRYVANKLLRVDIP QPMGILAVANTNGCGGRILODDLTCRAVNSS AQDEFCCANGCNSTALGGVGERCLDG LTHQGHVACSCRGGRIL			1	1	1	1	DEAGCSHSCSSTOFKCNSGRCIPEHWTCDGD
QCKLDGLCPLRWRCDGDTDCMDSSDENSC GVTHVCDPSVKGCCDSARCISKAWCDGC NDCEDNSDENCESLACRPPSHPCANNTSVC LPPDKLCDGNDDCGGDSGELDCOSCLNN GGCSHCSVAPGEGIVCSCPLGMELIGPDNH CQIQSYCAKHLKCSQKCDNKFSVKCSCVE WYLEPDGESCRSLDPFKPHTFSNRHEIRRIDL KGDYSVLVFGLRNTTALDHLLSSTWCDTATP LAVDWIAGNIYWVESNLDQLEVAKLDGTLR TLLAGDEHPRAALDPRBGLLWYTDWDASL RIEAASMSGAGRITYHETGSGGWPNGLTV DYLEKRILWDARSDATSARVDGSGHMEV RGHEFLSHFFAVTLYGGEVYWTDWTNTLL KANK WTGIRNTYVQRTNTQFFDLQVYHFS QPMAPNPCEANGGGGCSHLCLINYRITYS ACPHLMKLHKDNTTCYFFKKFLLVARQME GYDLDAPYYNYISFTVPDDNVTVLDYDAR GYVYWSDVRTQAKKAFTSYDTNKKQNV RLDGSFKNAVQQLEQPHGLVVHPLRCKL WTDGSNISMANMOGSNITLLFSGQKGPVQ AIDFPESKLYWISSGHTINRCNLDGSGLEV AMRSQLGKATALAIMGBKLWADQVSEK GTCSKADGSGSVLLRSTTLWHBKKYYDE QLDHKGTINFCSVNNGDCSLLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLXYSHEG GIPLPNNKSDALVPNSGTLAVGDFHAEN TYWVDMGLSTISRAKRDOTWREDVYNG RVGGLAVBWAGNITHNSWLGDFHAEN TYWVDMGLSTISRAKRDOTWREDVYNG RVGGLAVBWAGNITHNSWLGDFHAEN SFRYVVISGGLDKFRATTVHPEKGYLFWTE GQYPRERSRLDGTERVALVSISWPGGIS DYQGKLYWCDARTDKERDLFTGENRE LSSNNMMFSVSYFEDFTYWSDRTHANGSI RGSCDNATDGFPCANGGQACC CAHGMLAGAGYTLAYSERIL HLSDERNLAPVQFFEDFEHMKNVALAFL HLSDERNLAPVQFFEDFEHMKNVALAFL HLSDERNLAPVQFFEDFEHMKNVALAFL HLSDERNLAPVQFFEDFEHMKNVALAFL HLSDERNLAPVGFFEDFEHMKNVALAFL RGTSFCTTRNIFFSDLIFGQNQDNDGSRR RGSCDNATDSVPLRTGIGVQLNDBCRYRG RGSCDNATDSVPLRTGIGVQLNDBCRYRG RGSCDNATDSVPLRTGIGVQNDGDSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQLNDBCRYRG RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDDGSRR RGSCDNATDSVPLRTGIGVQNDGCODL RGTTPGGAFFECTUTMSGDDHPAFK RTTDQTTFRGAFFETTVTMSGDDHPAFK RTTDQTTFRGAFFETTVTMSGDDHPAFK RTTDQTTFRGAFFETTVTMSGDDHPAFK RCTYGSBRTVVLRSGFRINNGCQDL LTHQGHVYCSCRGGRILQDDLTCRANNSC RGDDGGGGSBETCNINGCQCDL LTHQGHVYCSCRGGRILQDDLTCRANNSC RGDDGGGGSBETCNINGCCQDL LTHQGTVYCSCRGGRILQDDLTCRANNSC		1	1	ŀ			NDCGDYSDETHANCTNQATRPPGGCHTDEF
GYTHVCDPSYKFGCKDSARCISKA WCDGL NDCEDNSDEENCESLA CREPSHPCANNTSYC LPPDKLCDGNDDCGGGSDEGELCOGENN GGCSHCSVAPGEGIVCSCPLGMELGPDNH CQIGSYCAKHLKCSQKCDQNKFSYKCSCYE WYLEPDGESCRSLDPFKPHTESNHEIRRIDL KGDYSYLVFGLRITHALDHLSQSALYWTD VEDKIYRGKLLDNGALTSFEVYIQYGLATPE LAVDWIAGNIYWYESNLDQEVAKLDGTLR TLLAGDEHPRAIALDPRDGILFWTDWDASL RIEAASMSGAGRRYNHETTGSGGWPNGLTY DYLEKRILWIDARSDAYSARYDGSGIMEV RGHEFLSHFFAVTLYGGGYWTDWRTNIL KANK WTGHNYTVVQRTNTQFFDLQVYHFS QPMAPNCEANGGQGCSLLLNYNRTYS ACPHLMKLHKDNTTCYSFKKFLLYARGME GVDLDAFYTYNTISFTYDDDWYTLDYDAS QRYYWSDWTQAKKAFNGTGVETVVSAL PNAHGLAVDWYSRNLFWTSYDTNKQNV RLDGSFKNAVQGLEGPFGLVHFLRCKL WTDGDSTRAMAWQGLEGPFGLVHFLRCKL WTDGDSTRAMAWQGLEGPFGLVHFLRCKL WTDGDSTRAMAWQGLEGPFGLVHFLRCKL WTDGDSTRAMAYQGLEGPFGLVHFLRCKL WTDGDSTRAMAWQGLEGPFGLVHFLRCKL WTDGDSTRAMAWQGLEGPFSLTYVHEGG GIPLPPNKSSALYPVSGTSLAVGIDFHAEN TYWVDMGLSTISRAKRDQTWREDVYNG QLDHKGTNPCSVNNGDCSQLCLFTSETTRS MCTAGYSLRSGQACGGVGSTLLYSVEGGI GIPLPPNKSSALYPVSGTSLAVGIDFHAEN TYWVDMGLSTISRAKRDQTWREDVYNG RYGGLAVDWIAGNIYWTDGGFDVEVARLN SFRYVVISGGLDKFRATTVHPEKGYLFWTE GYYFRIERSRLDGTERVLVNSISWPHGIS DYQDGKLYWCDARTDKERDLETGENRE LSSNNMDMFSVSYEDFJTWSDRTHANGSI DYQDGKLYWCDARTDKERDLETGENRE LSSNNMDMFSVSYEDFJTWSDRTHANGSI RGSKDNATDSYPLRTGIGVQLKDKYFND QKGTTVCAVANGGCQQLCLYRGRGQRAC CAHGML AEDGASCRETAGYLLYSERTILKS HLSDERNLNAPVQFEEDFEHMKNYNTALAFD RAGTSGTTRIFFSDIHEFGIQQVDLKDKYFND QKGTTVCAVANGGCQQLCLYRGRGQRAC CAHGML AEDGASCRETAGYLLYSERTILKS HLSDERNLNAPVGFEEDFEHMKNYNTALAFD RAGTSGTTRIFFSDIHEFGIQQVDLKDRKYFND QKGTTVCAVANGGCQCLCLYRGRGQRAC CAHGML AEDGASCRETAGYLLYSERTILKS HLSDERNLNAPVGFEEDFEHMKNYNTALAFD RAGTSGTTRIFFSDIHEFGIQQVDLKDRKYFND QKGTTVCAVANGGCQCLCLYRGRGGRAC CHGML AEDGASCRETAGYLLYSERTILKS HLSDERNLNAPVGFEEDFEHMKNYNTALAFD RAGTSGTTRIFFSDIHEFGIQQVDLKDRKYTTS RHTTDOTTGFGAFERTYTTMSGDDHFAARV DECQNLMF WTWNFQCHSIMRALLRNDIP QFMGILAVANDTNSCEGGRGRLQDDLTCRANNSS AQDEFCCANGCNNSTICTCGVPHCKDKS ADDCGGGSDEJEPCNIKTAGGVGEFCCDG		1	1				OCRUDGLCIPLRWRCDGDTDCMDSSDEKSCE
NDCEDNSDEENCESLACRPFSHPAANTISV LPPBKLCDGNDDGGBGBGELCDQCSLNN GGCSHNCSVAPGGIVCSCPLGMELGPDNH CQIQSYCAKHLKCSQKCDQMKFSVKCSCVE WVLEPDGESCRSLDPFKPHIFSNRHEIRRIDL KGDYSVLVPGLRNTALDHLSGSALYWID VEDKIVRGKLLDNGALTSFEVVIQYGLATPE LAVDWIAGNIYWVESNLDQEVAKLDGTLR TLIAGDIEBPRAALDPROGLPWTDWDASL RIEAASMSGAGRRTVHRETGSGGWPNGLTV DYLEKRIL WIDARSDAYSARYDGSGIMEV RGHEFLSHPFAVTLYGGEVYWTDWTNTL KANKWTGHNVTVQRTNTQPFDQVYUHP QPMARNPCEANGGGGPGSHLCLINYNRTVS ACPHLMKLHKDNTTCYEFKKFLYARQME GVDLDAPYYNYIBSTTVPDIDNVTVLDYDAR GRVYWSDVRTQAIKRAFINGTGVTVVSAL HOALDDWYSRNLFWFSYDTNKXQINV RLDGSFKNAVVGGLEQPIGLVVHPLRGKL WTDGDNISMANMGSTLLFSGGKGEV AMRSQLGKATALAIMGDKLWADQVSEK GTGSKADAVGGLEQPIGLVHPLRGKL WTDGDNISMANMGSTLLFSGGKGEV AMRSQLGKATALAIMGDKLWADQVSEK GTGSKADGSGSVLRNSTILVMHMKVYDE GLDHGTNPCSVNNGDCSQLCLFTSETTRS MCTAGYSRSQQAGCGGGSFLLYSVHEG GIPLDPIDKSDALVPVSGTSLAVGDFHAER TITYVVDMGLSTISRAKRDQTWREDVVTNG RVEGIAVDWIAGNIYWTDQGFDVEVARIN SFRYVISQGLDKPRAITVHPEKGYLFWTE GGYPRIERSRLDGTBRVTUNNVSISWPNGIS DYQGGKLYWCDARTDKIERDILGTGENER LSSNNMDMFSSVSPEDFTYWSDRTHANGSI RGSKDNATDSYPLRTGIGVQLKDKYFNRD QKGTNYCAVANGGCQUCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILK HLSDRNLDAMPGVSPTEDFTYWSDRTHANGSI RGSKDNATDSYPLRTGIGVQLKDKYFNRD QKGTNYCAVANGGCQUCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILK HLSDRNLDAMPGVSPTEDFTYWSDRTHANGSI RGSKDNATDSYPLRTGIGVQLKDKYFNRD QKGTNYCAVANGGCQUCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILK HLSDRNLDAMPGVSPTEDFTYWSDRTHANGSI RGSKDNATDSYPLRTGIGVQLKDKYFNRD QKGTNYCAVANGGCQUCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILK HLSDRNLDAMPGVSPTEDFTYWSDRTHANGSI RGSKDNATDSYPLRTGIGVQLKDKYFNRD QKGTNYCAVANGGCQUCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILK HLSDRNLDAMPGVSPTEDFTYWSDRTHANGSI RGSKDNATDSYPLRTGIGVQLKYFNRD QKGTNYCAVANGROQUCLTYRGRGRAC CAHGMLAEDGASCREYAGYLLYSERTILK HLSDRNLDAMPGVSPTEDFTYWSDRTHANGS RGSKDNATDSYPLRTGIGVGCDCLCTRANTSCRIP QCPGGLAYRGRACACREYAGYLLTSERTILK HLSDRNLDAACCREGGRACACREYAGYLLTSERTILK GCTGGGRACCCRANGCCNGTAC GGADDCGGGGDEDFCKTACGGCOSNMLWC GGDDCGGGGDEFCKTACGGGGRAC	1	}		1	1		GVTHVCDPSVKFGCKDSARCISKAWVCDGD
LPPKLCDGNDDGGBSBGELDCQSLNN GGCSHNCSVAPGGIOVSCPLQMELGPONH CQIQSYCAKHLKCSQKCDQNKFSVKCSCVE WVLEPDGESCRSLDPFKPHIFSNHEIRRID KGDYSVLVPGLRNTALDFHLSQSALYWTD VEDKIYRGKLLDNGALTSFEVVIQYGLATPE LAVDWIAGNIYWESNLDQUEVAKLDGTLR TLLAGDEHPRAIALDPROGLPWTDWDASL RIEAASNAGAGRRTVHEGTGSGWPNOLTV DYLEKRILWIDARSDAIYSARYDGSGHNEVY RGHEFLSHPFAVTLYGGEVYWTDWRTNTL KANKWTGHNVTVVQRTNTQFDLQVYHPS QPMAPNPCEANGGQFOSHLCLINYNRTVS ACPHLMKLHKDNTTCYFKKFLLYARQME GVDLDAPYYNYIISFTVPDIDNYLDYDAR QRYYWSDVRTQAIKAFNNGTGVETVVSAL PNAHGLAVDWVSRNLFWTSYDTINKQONV RLDGSFKNAVVQGLQPHGLVVFHLGKL' WTDGDNISMANNDGSNRTLLFSGQKGPVG AIDFPESKLYWISSGNHTINKCINLDGSGLEVY ANRSQLGKATALAIMGDKLWWADQVSEK GTCSKADGSGSVVLRNSTTLYHMKVYDE QLDHSGTFPCSVNNGDCSQLCLFTSSTTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEG GIPLDPNDKSDALVPVSTSTLAVGDFHAE TITYVVDMGLSTISRAKRDQTWREDVYNG RVEGIAVDWIAGNTYWTDQGFDVEVARLN SFRYVVISQGLDKPRATTVHFEKGYLFWTE GQYPRIERSRLDGTERVVLNVSISWPNGIS DYOGGKLYWCDARTAITVHFEKGYLFWTE GQYPRIERSRLDGTERVVLNVSISWPNGIS DYOGGKLYWCDARTAITVHFEKGYLFWTE GQYPRIERSRLDGTERVVLNVSISWPNGIS DYOGGKLYWCDARTAITVHFEKGYLFWTE GQYPRIERSRLDGTERVVLNVSISWPNGIS DYOGGKLYWCDARTICREDILETGENRE LSSNNMDMFSVSVFEDFTWSDRTHANGST RGSKDNATDSYPLRTIGIGVQLKDIKVFNDD QKGTNVCAVANGGCQOLCLYRGRGQRAC CAHGMLAEDGASCREYAGTLLYSERTILKS HLSDERNILNAPVOPFEDPFHMKNVALAFE RAGTSPGTPRIEFSDHFGNIQONDDGSRR IVENVGSVEGLAYHRWINDLYSTTST RHTVDQTRRGAFERETVTIMSGDDHPRAFV DECQNLMFWTNWNEQHFBIMRAALSGANN TLIEKBURTPNGADHRAEKLYFSDATLAR RGTSPGTPRIEFSDHFGNIQONDDGSRR IVENVGSVEGLAYHRWSDMLLYTSTSTT RHTVDQTRRGAFERETVTIMSGDDHPRAFV DECQNLMFWTNWNEQHFBIMRAALSGANN TLIEKBURTPNGADHRAEKLYFSDATLAR RCEYDGSHRYVLRSEFVHFGALVGCHIM WTDWVRRAVQRANKHVGSNMKLIRVDIP QPMGILAVANDTINSCELSPCRNNGGCODL LTHQGHVNCSCRGRRQDDLTCRAVNSS AQDEFECANGECNISTLCDGVPHCKDKSD KYSYCNSRCKKTFRQCSNGCXSNMLWC GADDCGGGGGGGGGGGGGGGDLQDDLTCRAVNSS CADDEFGCANGECONSHLWC		1	1	1	1		NDCEDNSDEENCESLACRPPSHPCANNTSVC
GGCSHNCSVARGEGIVCSCPLGRLGPIDNH CQIQSVCAKHLKCSQCDQNKFSVKCSCYE WVLEPDGESCRSLDPFKPHIFSNHEIRINDL KGDYSVLVPGLRNTALDPHLSQSALYWTD VEDKIYRGKLLDNGALTSFEVVIQYGLATPE LAVDWIAGNIYWESNLDQIEVAKLDGTLR TLLAGDIEHPRAIALDPHDGILFWTDWDASL RIEAASMSGAGRRTVHRETGSGWPNGLTV DYLEKRILWDARSDAJYSARYDGSGIMMEV RGHEFLSHPFAVTLYGGEVYWTDWRTNTL KANKWTGHNYTVVQRTNTQPPDLQVYHPS QPMAPNPCEANGQQPCSHLCLINYNRTVS ACPHLMKLHKUNTCYEFKKFLLVARQME GVDLDAPYNYNISTTVPDIDNVTVLDYDAF QRVYWSDVRTQAKRAFINGTGVTVVSAL PNAHGLAVDWYSRNLFWTSYDTNKKQINV RLDGSFKNAVVQGLEQPHGLVHPLRGKLV WTGDNISMANMDGSNRTLLFSGQKGPV AIDFPESKLYWISSGNHTINRCNLDGSGLEV AMRSQLGKATALAIMGKLWADQVSEK GTGSKADGSGSVVLRNSTTLVMHMKVYDE QLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSRLSQQACCGYGSFLLVSTHETH GIPLPPIDKSDALVPYSGTSLAVGIDHHAEN TTYVVDMGLSTISRAKRDQTWREDVYNG RVEGIAVDWIAGNIYWTDOGFDUEVARIN SFRYVVISQGLDKPRATTYHPEKGYLFWTE GQYPRIERSRLDGTERVVLNVSISWPNGIS DYQDGKLYWCDARTDKERDLETGENRE LSSNNMDMFSVSYEDETYWSDRTHANGSI RGSKDNATDSVPLRTGIGYQLKDKYFNED QKGTNVCAVNGGCQQLCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTLIK HLSDERNLNAPVQPEDPPHMKNNALAFP RAGTSPGTPNRIFFSDIHFGNIQNIDDGSRR IVENNGSVEGLAYFREGWTLYSERTLIK HLSDERNLNAPVQFEDPPHMKNNALAFP RAGTSPGTPNRIFFSDIHFGNIQNIDDGSRR IVENNGSVEGLAYFREGWTLYSERTLIK HLSDERNLNAPVQFEDPPHMKNNALAFP RAGTSPGTPNRIFFSDIHFGNIQNIDDGSRR IVENNGSVEGLAYFREGWTLYSERTLIK HLSDERNLNAPVQFEDPPHMKNNALAFP RAGTSPGTPNRIFFSDIHFGNIQNIDDGSRR IVENNGSVEGLAYFREGWTLYSERTLIK HLSDERNLNAPVQFEDPPHMKNNALAFP RAGTSPGTPNRIFFSDIHFGNIQNIDDGSRR IVENNGSVEGLAYFREGWTLYSERTLIK HLSDERNLNAPVQFEDPPHMKNNALAFP RAGTSPGTPNRIFFSDIHFGNIQNIDDGSRR IVENNGSVEGLAYFREGWTLYSTSTTL RITVDQTRRGAFERETVTIMSGDDHPRAFV DECQNLMFWTNWNEQHPSIMRALSGANN TLIEKBURTPNGALDBHAALSGANN TLIEKBURTPNGALDBHAALSGANN TLIEKBURTPNGALDBHAALSGANN TLIEKBURTPNGALDBHAALSGANN TLIEKBURTPNGALDBHAALSGANN TLIEKBURTPNGALDBHAALSGCANNALWCH GADDCGGGSDEPLEVNTAGCGODLA LTHQGHVNCSCRGRRQCDOLALTHQGGGDELCTRAVNSSK		1					1_PPDKLCDGNDDCGDGSDEGELCDQCSLNN
CQIQSYCAKHLKCSQKCPONKFSVKCSCYLE WYLEPDGESCRSLDPFKPFIIFSNRHEIRIDI KGDYSVL.YPGLRNTIALDFHLSQSALYWTD VEDKIYRGKLLDNGALTSFEVVIQYGLATPF LAVDWIAGNIYWYESNLDQIEVAKLDGTLR TILLAGDIEHPRAIALDPROGILFWTDWDASI REAASMSGAGRTVHETGSGGGWPMGLTV DYLEKRILWIDARSDAIYSARYDGSGHMEVY RCHEFL.SHPFAVILWETGSGGWPMGLTV CHEFL.SHPFAVILWETGSGGWPMGLTV QMAPPHPCEANGGGGPCSHLCLINYNRTVS ACPHLMKLHKDNTICYSFKKFLLYARQME GVDLDAPYYNYIISTVPDIDNTVLLDYDAF GRYWSDWTRQAIKRAFINGTOVETUVSAL PAHGLAVDWSRNLFWTSYDTNKKQINV RLDGSFKNAVVQGLOPHGLVVHPLRGKL WTDGDNISMANMDGSNRTLLPSGQGEPVG AIDFPESKLYWISSGNHTINRCNLDGSGLEV AMRSQLGKATALAIMGDKLWWADQVSEK GTCSKADGSGSVVLRNSTILWHMKVYDE QLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GPLDPDKSDALVSGTSLAVUSGTSLAVUSDHAEN TIYWVDMGLSTISRAKRDQTWREDVVTNG RVEGIAVDWIAGNIYWTDGOFDVIEVARLN SRYYVISGGLDKPATIVHPEKGYLFWTE GQYPRIERSRLDGTERVVL.NVSISWPNGIS DYQDGKLYWCDARTDKERDLETGENRE LSSNNMDMFSVSVFEDFJWSDRTHANGSI RGSKDNATDSVPLRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRQRAC. CAHGMLAEDGASCREYAGYLLYSERTILS RGSKDNATDSVPLRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRQRAC. CAHGMLAEDGASCREYAGYLLYSERTLLS HSDERNLANPYOFFEDPFHMKNNALAFD RAGTSFGTPRRIFFSDHHEGNIQNDDGSRR IVENVGSVEGLAYHGWDIT.YWTSYTSTT. RHTVDQTRFGAFERETVITMSGDDHPAEN DECQNLMFWTNWNEQHESIMRAALSAGNI TLIEKDIRTPNGLADHRAEKLYFSDATLGM WTDWVRRAVQRAKHVPFGLAVYGEHI WTDWVRRAVQRAKHVPFGLAVYGEHI WTDWVRRAVQRAKHVPFGLAVYGEHI WTDWVRRAVQRAKHVPFGLAVYGEHI WTDWVRRAVQRAKHVPFGLAVYGEHI WTDWVRRAVQRAKHVPFGLAVYGEHI WTDWVRRAVGRAKHVOSNMKLLRVDIP QPMGIIAVANDTNSCELSPCRINGGCQDL LTHQGHYNCSCRGGRILLQDDLTCRAVNSS GAPDEFCANGECRINSLTCDGYPHCKDKSD KFSYCNSRRCKKTFRQCSNGRCVSNMI.WC				1			GGCSHNCSVAPGEGIVCSCPLGMELGPDNHT
WVLEPDGESCRSLDFFKFFIIFSNRHEIRIND KGDYSVL.VPGLRITLADFHLSQSAL/WTD VEDKIYRGKILDNGALTSFEVVIQYGLATFE LAVDWIAGNIYWVESNLDQIEVAKLDGTLR TILLAGDIEHRAALDPROGILFWTDWDASL RIEAASMSGAGRITVHETGSGGWPNGLITV DYLEKRILWIDARSDAIYSARYDGSGMEV RGHEILSHPFAVTLYGGEVYWTDWRTNITL KANKWTGHNVTVVQRTNTQPFDLQVYHES QPMAPPPCEANGGQGPCSHLCLINYNRTVS ACPHLMKLHKDNTTCYEFKFLLYARQME GVDLDAPYYNYISISTYPDDNVTVLDYDAR QRYYWSDVRTQALKRAFINGTGVETVYSAL PNAHGLAVDWYSRIFWTSYDTNKKQINV RLDGSFKNAVVQGLEQPHGLVVHELRGKL WTDGDNISMANMDGSNRTLLFSGQKGPVG ADFPESKLYWISSGNHTINRCNLDGSGLEV AMRSQLGKATALAIMGGKLWWADQVSEK GTCSKADGSGSVVLRNSTLLVMHMKVYDE QLDHKGTNPCSVNNGDCSQLCLFTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GPLDPJNKSDALVPVSGTSLAVGIDFHAEN TIYWVDMGLSTISRAKRDQTWREDVYNTO RVEGIAVDWIAGNIYDQGFDVIEVARIN SFRYVVISQGLDKPRATTVHPEKGYLFWTE GQYPRIERSRLDGTERVVLVNVSISWPMGIS DYQDGKLYWCDARTOKIERDLETGERREN LSSNNMDMFSVSVFEDFTYWSDRTHANGSI RGSKDATDSVPLRTGIGGYQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILKS HSDBERNLNAPYQFFEDPEHMKNVALAFD RAGTSPGTFNRIFTSDLHFGRIQQINDGGSRR VENNGSVEGLAYHGWDTLYTSYTSTT RHTVDQTRPGAFERETYTIMSGDDHFRAFY DECQNLMFWTNWNEQHPSIMRAALSGAN TLIEKDIRTPRGLABHRAEKLYFSDATLDK RCEYDGSHRTYVILKSEPVHPFGLAYYGEHII WTDWVRRAVQRANKHVGSNMKLLRVDIP QPMGILAVANDTNSCELSPCRNNGGCQDLL LTHQGHYNCSCRGGRILQDDLTCRAVNSSS AQDEFFCANGECINFSLTCDGYPHCKNSD KFSYCNSRRCKKTFRQCSNGCVSNMI.WC		1			1		COLOSYCAKHLKCSOKCDQNKFSVKCSCYEG
KGDYSVLVPGLRNTIALDFHLSQSALYPGILTP VEDKIPGKLLINDGLYSEVUQYGLATP LAVDWIAGNIYWVESNLOQUEVAKLDGTLR TILAGDIEHPRAIALDPROGILFWTDWDASI RIEAASMSGAGRTYHRETGSGGWPNGLTV DYLEKRILWIDARSDAIYSARYDGSGIMEV RHEFI.SHPFAVILYGGEVYWTDWRINTL KANKWTGHNVTVVQRTNTQPFDLQVYHPS QPMAPPCEANGGGPCSHLCLINYNRTVS ACPHLMKLHKDNTTCYFFKKFLLYARQME GVDLDAPYTYYISFTVPDDNVTVLDYDAR GRYVWSDNTRQAIKRAFINGTOVETVVSAL PNAHGLAVDWYSRNLFWTSYDTNKKQINV RLDGSFKNAVVQGLQPHGLVVHPLRGKL WTDGDNISMAMMDGSNRTLLFSGQKGPVG AIDFPESKLYWISSGNHTINRCRLDGSGLEV AMRSQLGKATALAIMGDKLWWADQVSEK GTCSKADGSGSVVLRNSITLMHIMKVYDE QLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVSFLLYSVHEG GPLDPDNKSDALVPVSGTSLAVGIDPHAE TIYWVDMGLSTISRAKRDOTWREDVYTNG RVEGIAVDWIAGNIYWTDQGFDVIEVARLN SFRYVVISQGLDKFRAITVHPEKGYLFWTE GQYPRIERSRLDGTERVVLVNVSISWPNGIS DYQDGKLYWCDARTDKIERDLETGENRE LSSNNMDMFSVSVFEDFJYWSDRTHANGSI RGSKDNATDSVPLRTGIGGQLKDKVFND QKGTNVCAVANGGCQQLCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILKS H.SDERNLNAPVGPFEDPEHMKNVIALAFD RAGTSFGTFNRIFFSDHHEGIQQLDDDGSRR IVENVGSVEGLAYHGWDIT, WTSYTTST RHTVDQTRPGAFERETVITMSGDDHPRAEV DECQNLMFWTNWNEQHFSDHERGNQNDDGSRR IVENVGSVEGLAYHGWDIT, WTSYTTST RHTVDQTRPGAFERETVITMSGDDHPRAEV DECQNLMFWTNWNEQHFSDHERGNQCOLC LTHQGHYNCSCRGGRILLQDLTCRAVNSS UNDWGRAVANKHVGSNMKLLKVDIP QPMGIIAVANDTNSCELSPCRNNGGCQDL LTHQGHYNCSCRGGRILLQDLTCRAVNSS AQDEFFCANGECRINSLTCDGYPHCKDKSD KFSYCNSRRCKKTFRQCSNGRCVSNML WC	!	1			1		WVLEPDGESCRSLDPFKPFIIFSNRHEIRRIDLH
VEDKIYRGKILDNOALTSFEVVIQGGIATPE LAVDWIAGNIYVESNILDQIEVAKLIGGTIR TILLAGDIEHPRAIALDPROGIL FWTDWDASL RIEAASMSGAGRRTVHRETGSGGWPNOLTY DYLEKRIL WIDASDAIYSAR YDGSGHMEV. RGHEFLSHPFAVTLYGGEVYWTDWRITIL KANK WTGHNIVYOGRTNIQPDFLQVYHFS QPMAPNPCEANGGGPCSHLCLINYNRTVS ACPHLMKLHKDNTTCYEFKKFLLYARQME GVOLDAPYYNYJUSFTVPDIDNVTVLDYDAF QRYYWSDVRTQAIRAFINGTGVETVVSAL PNAHGLAVDWSRNLFWTSYDTINKKQINV RLDGSFKNAVVQGLEQPHGLVVHPLRGKL' WTDGDNISMANINDGSNETLLFSGGKGPVG AIDFPESKLYWISSGNHTINRCNLDGSGLEV. AMRSQLGKATALAIMGDKLWWADQVSEK GTCSKADGSGSVLRNSTILWHMKVYDE GLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GIPLDPNDKSDALVPVSGTSLAVGIDFHAEN TIYWVDMGLSTISRAKRDQTWREDVVTNG RVEGIAVDWIAGNIYWTDQGFDVIEVARLN SFRYVISQGLDKPRAITVHPEKGYLFWTE GQYPRIERSRLDGTERVVLINVSISWPNGIS DYQDGKLYWCDARTDKIERIDLETGENREN LSSNNMDMFSVSVFEDFTYWSDRTHANGSI RGSKDNATDSVIRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQLCLYRGRGGRAC CAHGMLAEDGASCREYAGYLLYSETLIKS HLSDERNLNAPVQPFEDPEHMKNVIALAFD RAGTSPGTPNRIFFSDIHEFGIQQUNDDGSRR VENNGSVEGLAYHRGWDTLYWSTYTTST NETTVDQTRRGAFERETVTINMSQDDHFRAFV DECQNLMFWTNWCQHPSIMRALSGANN TLIEKDIRTPNGLADHRAEKLYFSDATLDK RCEYDGSHRYVLRSEPVHPFGLAVYGEHI WTDDWVRRAVQRANKHYGSNNKLLRVDIPI QPMGILAVANDTNSCELSPCRINNGGCQDLL LTHQGHVNCSCRGGRILQDDLTCRAVYSSS AQDEFCANGECOPISCLTCRAVSIS.		j		1			KGDYSVLVPGLRNTIALDFHLSQSALYWIDV
LAYDWIAGNIYWYESNILDQIEVAKLDGTLR TILAGDIEIPRAIALDPROGILFWTIDWDASI RIEAASMSGAGRRTVHRETGSGGWPNGLTY DYLEKRILWIDARSDAITYSARYDGSGHMEV RGHEFLSHPFAVTLYGGEVYWTDWRTNITL KANKWTGHNYTVVQRTNIQFPDLQVYHPS QPMAPNPCEANGQGPCSHLCLINYNRTVS ACPHLMKLHKDNTTCYEFKKFLLYARQME GVDLDAPYYNYIBSFTVPDIDNYTVLDYDAF QRVYWSDVRTDQAKRAFINGTGVETVVSAL PNAHGLAVDWSRNLFWTSYDTNKKQINV RLDGSFKNAVVQGLEOPHGLVVHPLRGKL' WTDGDNISMANMDGSNRTLLFSGQKGPVG AIDFFESKLYWISSGNHTINRCNLDGSGLEV AMRSQLGKATALMOBKL WWADQVSEK GTCSKADGSGSVVLRNSTILWHIMKVYDE QLDHKGTNPCSVNINGDCSQLCLPTSETTRS MCTAGYSLRSQQACEGVGSYLLYSVHEGI GIPLDPNDKSDALVPVSGTSLAVGIDFHAEN TIYWVDMGLSTISRAKRDQTWREDVYTNG RVEGIAVDWIAGNIYWTDQGFDVIEVARLN SFRYVISGGLDKPRAITVHPEKGYLFWTEN GVYPIERSRLDGTERVVLNVSISWPNGIS DYQDGKLYWCDARTDKIERDLETGENREV LSSNINDMFSVSYFEDFIYWSDRTHANGSI GRSCDNATDSVPLRTGIGVQLKDIKVFNED QKGTNVCAVANGGCQQLCLYRGRQRAC CAHGMLAEDGASCREYAGYTLYSFRTLIKK HLSDERNLNAPVQPFEDPEHMKNVIALAFD RAGTSPGTPNRIFFSIOQUNDDGSSR IVENVGSVEGLAYHRGWDTLYWSTYTST RHTVDQTRGAFGRETYTTMSGDDHPRAFV DECQNLMFWTNWFGQFSINKALSGAN TLIEKDIRTPNGLADHRAEKLYFSDATLDK RCEYDGSHRYVLKSEVHFGLAVYGEHI WTDWVRRAVQRANKHYGSNMKLLRVDIP QPMGIIAVANDTNSCELSPCRINNGGCQDLL LTHQGHVNCSCRGGRILQDDLTCRAVNSS AQDEFECANGECNFSLTCDGVPHCKDKSD KYSYCNSRCKKTFRQCSNGCVSNMLWC GADDVGGNEGGEFFCRLOG		ļ	ĺ			1	VEDKIYRGKLLDNGALTSFEVVIQYGLATPEG
TILLAGDEHPRAIALDPROBLEWTUNDASL RIEAASMSGAGRYNGLTV DYLEKRILWIDARSDAIYSARYDGSGHMEV RGHEFLSHPFAVTLYGGGVYNTDWRTNTL KANK WTGHNYTVVQRTNTQPFDLQVYHPS QPMAPNPCEANGGQGPGSHLCLINYNRTVS ACPHLMKLHKDNTTCYEFKKFLLYARQME GVDLDAPYYNYDSTVPDIDNVTVLDYDAF QRVYWSDVRTQAIRKAFNGTGVETVVSAL PNAHGLAVDWYSRNLFWTSVDTNKKQNVV RLDGSFKNAVVQGLGPHGLVVHPLRGKL' WTDGDNISMANMGSNRTLLFSQKGPVG AIDFPESKLYWISSGNHTINRCNLDGSGLEV AMRSQLGKATALAIMGBKLWWADQVSEK GTCSKADGSGSVVLKNSTILVMHMKVYDE QLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GIPLDPNDKSDAUVYSGTSLAVGDFHAEK TIYWVDMGLSTISRAKRDQTWREDVVTNG RVEGIAVDWIAGNIYWTDQGFDVIEVARLN SFRYVVISQGLDRFRAITVHPEKGYLFWTE GQYPRIERSRLDGTERVVLVNVSISWPNGIS DYQDGKLYWCDARTDKERDLETGENREV LSSNNMDMFSVSVFEDFTYWSDRTHANGSI RGSKDNATDSVPLRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILKS HLSDERNLNAPVQPEEDPEHMKNVIALAFD RAGTSGTPNAPVFFSDIFFSDIHFGNIQQNDDGSRR IVENVGSVEGLAYHRGWDTL YWTSYTTST. RHTVDQTRRGAFRETVITMSGDDHPRAFV DECCNLMFWTNNFCQHPSIMRAALSGANN TLIEKDBRTPNGLADHRAEKLYFSDATLDK RCEYDGSHRYVILKSEPVHPFGLAVYGEHI WTDWVRRAVQRANKHYGSNMKLLRVDIP QPMGIIAVANDTNSCELSPCRINNGGCQDLC LTHQGHVNCSCCGGRILQDLTCRAVNSSS AQDEFECANGECNFSLTCDGVPHCKDKSD KPSYCNSRRCKKTFRQCSNRCCVSNMLWC GADDGGGGSBEPCNKTACGVGSFRCCVSNMLWC	İ	ì	1				LAVDWIAGNIYWVESNLDQIEVAKLDGTLRT
RIEAASMGAGRRTVHRETGSGGWPNGLTV DYLEKRIL WIARSDAIYSARYDGSGIMEV RGHEFLSHPFAVTLYGGEVYWTDWRTNTL KANKWTGHNVTVVQRTNTQPFDLQVYHPS QPMAPNPCEANGGGGPGSHLCLINYNRTVS ACPHLMKLHKDNTTCYEFKKFLLYARQME GVDLDAPYNYIISFTVPDDDNVTVLDYDAR QRVYWSDVRTQAIKRAFINGTGVETVVSAL PNAHGLAVDWVSRNLFWTSYDTNKKQINV RLDGSFKNAVVQGLQPHGLVVHPLRGKL WTDGDNISMANMDGSNRTLLFSGQKGPVG AIDFPESKLYWISSGNHTINRCNLDGSGLEV AMRSQLGKATALAIMGDKL WWADQVSEK GTCSKADGSGSVVLRNSTTLVMHMKVYDE QLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GIPLDPNDKSDALVPVSGTSLAVGIDFHAEN TITVWDMGLSTISRAKRDQTWREDVVTNG RVEGIAVDWIAGNIYWTDQGFDVIEVARLN SFRYVVISQGLDKPRAITVHPEKGYLFWTE GQYPRIERSRLDGTERVVLVNVSISWPNGIS DYQDGKLYWCDARTDKERDLETGENREV LSSNNMDMFSVSVEDDFTYWSDRTHANGSI RGSKDNATDSVPLRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILKS HLSDERNLNAPVQFFEDPEHMKNVIALAFD RAGTSPGTPNRIFFSDHFGRNQONDDGSRR IVENVGSVELAYHRGWDTLYWTSYTTST: RHTVDQTRFGAFERETVITMSGDDHFRAEV DECQNLMFWNWEQHFSIMRAALSGAN TLIEKDIRTPNGLADHRAEKLYFSDATLDK RCEYDGSHRTVYLKSEPVHPFGLAVYGEHI WTDWVRRAVQRANKHVGSNMKLLRVDIP QPMGIIAVANDTNSCELSPCRINNGGCQDL LTHQGHVNCSCRGGRILQDDLTCRAVNSS AQDEFECANRCKITTCQSVRCKSDM. KPSYCNSRRCKKITRQCSNGRCVSNML.	j	1	1	1		1	TLLAGDIEHPRAIALDPROGILFWTDWDASLP
DYLEKRILWIDARSDAYSARYDGSGHMEN' RGHEFLSHPFANTLYGGEVYWTDWRINTLL KANKWTGHNYTVVQRTNTQPFDLQVYHPS QPMAPNPCEANGGQDCSHLCLINYNRTVS ACPHLMKLHKDNTTCYEFKKFLLYARQME GVDLDAPYYNYISFTVPDDNVTVLDYDAR QRVYWSDVRTQAIKRAFINGTGVETVVSAL PNAHGLAVDWYSRNLFWTSYDTNKKQINV RLDGSFKNAVVQGLEQPHGLVVHPLRGKL' WTDGDNISMANMDGSNRTLLFSGQKGPVG AIDPESKL YWISSGNHTINRCNLDGSGLEV AMRSQLGKATALAIMGDKLWWADQVSEK GTCSKALDGSGVVLRNSTTLYMHMKYYDE QLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GIPLDPHDKSDALVPVSGTSLAVGIDFHAEN TITYWVDMGLSTISRAKRDQTWREDVYTNG RVEGIAVDWIAGNIYWTDQGFDVIEVARLN SFRYVVISQGLDKPRAITVHPEKGYLFWTEI GQYPRIERSRLDGTERVVLVNVSISWPNGIS DYQDGKLYDARTDKLERDLETGEFNEE LSSNNADMFSVSVFEDFIYWSDRTHANGSI RGSKDNATDSVPLRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRGGRAC. CAHGMLAEDGASCREYAGYLLYSERTLKS HLSDERNLMAPVQPFEDPEHMKNVIALAFD RAGTSPGTFNRIFFSDHIFGNIQQINDDGSRR IVENVGSVEGLAYHRGWDILYWTSYTTST. RHTVDQTRPGAFERETVITMSGDDHPRAFV DECQNLMFWTNWNEQHFSIMRAALSGAN TLIEKDIRTPNGLADHRAEKLYFSDATLDK RCEYDGSHRYVILKSEPVHPFGLAVYGEHI WTDWVRRAVQRANKHVGSNMKLLRVDIP QPMGIIAVANDTNSCELSPCRINNGGCQDLL LTHQGHVNAVGSNGCLSCRGREILQDDLTCRANNSS AQDEFECANGECNFSLTCDGVPHCKDKSD KPSYCNSRRCKKTFRQCSNGRCCNSNML	1	1		1			RIEAASMSGAGRRTVHRETGSGGWPNGLTV
RGHEFLSHPFAVILYGGENYWTDWRINIL KANKWTGHNVTVVQRINTOPPDLQVYHPS QPMAPNPCEANGGQGPCSHLCLINYNRTVS ACPHLMKLHKDNITTCYEFKKFLLYARQME GVDLDAPYYNYIISTTVPDDNVTVLDYDAR QRVYWSDVRTQAIKRAFINGTGVETVVSAL PNAHGLAVDWVSRNILWTSYDTNKKQINV RLDGSFKNAVVQGLEQPHGLVVHPLRGKL WTDGDNISMANMDGSNRTLLFSGQKGPVG AIDFPESKLYWISSGNHTINRCNLDGSGLEV AMRSOLGKATALAMGDKLWWADQVSEK GTCSKADGSGSVVLRNSITLVMHMKVYDE QLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GIPLDPNDKSDALVPVSGTSLAVGIDFHAER TIYWVDMGLSTISRAKRDQTWREDVVTNG RVEGIAVDWIAGNIYWTDQGFDVIEVARLN SFRYVVISQGLDKPRAITVHPEKGYLFWTE GQYPRIERSRLDGTERVVLWVSISWPNGIS DYQGKLYWCDARTDKIERIDLETGENREN LSSNNMDMFSVSVEEDFIYWSDRTHANGSI RGSKDNATDSVPLRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRGQRAC CAHGMLAEDGASCREYAGYLLYSERTILKS HLSDERILNAPVQPFEDPEHMKNVALAFD RAGTSPGTPNRIFFSDIHFGNIQQINDDGSRR IVENVGSVEGLAYTHGWDTLYYSTYTST. RHTVDQVTRGAFERETVTIMSGDDHPRAFV DECQNLMFWTNWNEQHPSIMRAALSGAN TLIEKDIRTPNGLADHRAEKLYFSDATLDK RCEYDGSRTYULKSEPVHPFGIAVVGGEHI WTDWVRRAVQRANKHVGSNMKLLRVDIP QPMGIIAVANDTINSCELSPCRINGGCQDL LTHQGHVNCSCRGGRILQDDLTCRAVNSS AQDEFECANGECINFSLTCDGVPHCKDKSD KPSYCNSRRCKKTFRQCSNGRCVSNMLUG GADDCGDGSDEIPCNKTACGVGEFRCRDG	İ						DYLEKRILWIDARSDAIYSARYDGSGHMEVL
KANK WTGHNYTVQRTNTQFFDLQYHRIVS QPMAPNELANGQQGCSHLCLINYNRITVS ACPHLMKLHKDNITCYEFKKFLLYARQME GVDLDAPYYNYIBSTYVPDIDNYTVLLYDAD RVYWSDVRTQAIKRAFINGTGVETVVSAL PNAHGLAVDWVSRNLFWTSYDTNKKQINV RLDGSFKNAVVQGLEQPHGLVVHPLRGKLY WTDGDNISMANMDGSNRTLLFSGQKGPVG AIDFPESKLYWISSGNHTINRCNLDGSGLEV AMRSQLGKATALAIMGDKLWWADQVSEK GTCSKADGSGSVVLRNSTILVMHMKVYDE QLDHKGTNPCSVNIGDCSQLCLPTSETTRS MCTAGYSLRSQQACEGYGSFLLYSVHEGI GIPLDPNDKSDALVPVSGTSLAVGIDFHAEN TIYWVDMGLSTISRAKRDQTWREDVVTNG RVEGIAVDWIAGNIYWTDQGFDVLEVARLN SFRYVVISQGLDKPRAITVHPEKGYLFWTE GQYPRIERSRLDGTERVVLVNVSISWPNGIS DYQDGKLYWCDARTDKLERIDLETGENREV LSSNNMDMFSVSVFEDFTYWSDRTHANGSI RGSKDNATDSVPLRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRGQRAC CAHGMLAEDCASCREYAGYLLYSERTILKS HLSDERNLNAPVQPFEDPEHMKNVIALAFD RAGTSPGTPNRIFFSDIHGNIQONDDGSRR IVENVGSVEGLAYHRGWDTLYWTSYTTST RHTVDQTRPGAFFRETVITMSGDDHPRAFV DECQNLMWTNWNEQHPSIMRAALSGANY TLIERDIRTPNGLADHRAEKLYFSDATLDK RCEYDGSHRYVILKSEPVHPFGLAVGGEHI WTDWVRRAVQRANKHVGSNMKLLRVDIP QPMGIIAVANDTNSCELSPCRINNGGCQDLC LTHQGHVNCSCRGGRILQDDLTCRAVNSSI AQDEFECANGECINFSLTCDGVPHCKDKSD KPSYCNSRRCKKTRQCSNGRCVSNMLWG	)	j			1		RGHEFLSHPFAVTLYGGEVYWTDWRTNILA
QPMAPNPCEANGGGPCSHLCLINYNRIVS ACPHLMKHKDNTTCYSPKKFLLYARQME GVOLDAPYNYIISFTVPDIDNVTVLDYDAF QRVYWSDVRTQAKKAFINGTGVETVVSAL PNAHGLAVDWVSRNLFWTSYDTNKKQINV RLDGSFKNAVVQGLEQPHGLVVHPLRGKLY WTDGDNISMANMDGSNRTLLFSGQKGPVG AIDFPESKLYWISSGNETINRCNLDGSGLEV AMRSQLGKATALAIMGDKLWWADQVSEK GTCSKADGSGSVVLRNSTTLVMHMKVYDE QLDHKGTNPCSVNNGDCSQLCLPTSETTRS MCTAGYSLRSGQQACEGVGSFLLYSVHEGI GIPLDPNDKSDALDVPSGTSLAVGIDFHAEN TYYWVDMGLSTISRAKRDOTWREDVVTNG RVEGIAVDWIAGNIYWTDQGFDVIEVARLN SFRYVVISQGLDKRAITVHPEKGYLFWTEY GQYPRIERSRLDGTERVVLVNVSISWPNGIS DYQDGKLYWCDARTDKIERDLETGENREY LSSNNMMFSVSTEDFTYWSDRTHANGSI RGSKDNATDSVPLRTGIGVQLKDIKVFNRD QKGTNVCAVANGGCQQLCLYRGRGGRAC CAHGMLAEDGASCREYAGYLLYSERTILKS HLSDERNLNAPVQPFEDPEHMKNVIALAFD RAGTSPGTPNRIFFSDHFGNQONDDGSRR IVENVGSVEGLAYHRGWDTLYWTSYTTST RITTVQTRPGAFERETVITMSGDDHPRAFV DECQNLMFWTNWNEQHPSIMRAALSGAN TLIEKDIRTPNGLAIDHRAEKLYFSDATLDK RCEYTDGSHRYVLKSEPVHFFGLAVYGEHI WTDWVRRAVQRANKHVGSNMKLLRVDP QPMGIIAVANDTNSCELSPCRINNGCQDLL LTHQGHVNCSCRGGRILQDDLTCRAVNSSI AQDEFECANGECINFSLTCDGVPHCKDKSD KPSYCNSRRCKKTRQCSNGRCVSNMLWC GADDXGDGSDEIPCNKTRACGYGEFRCRDG		· I					KANKWTGHNVTVVORTNTQPFDLQVYHPSR
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						- Contries
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutarnic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1	İ	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	}			residue of	sequence	/=possible nucleotide deletion, \=possible
	1	1		peptide		nucleotide insertion
				sequence	ļ	RLGVKGVLFQPCERTSLCYAPSWVCDGAND
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ļ			Ì	1		MSWTCDKEDDCEHGEDETHCNKFCSEAQFE
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	ļ	1	1	1		DGADESIAAGCLYNSTCDDREFMCQNRQCIP
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Í		{				GQDDCGDSSDERGCHINECLSRKLSGCSQDC
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			-			TLLKQGLNNAVALDFDYREQMIYWTDVTTQ
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		1				DWVGGNLYWCDKGRDTIEVSKLNGAYRTVL
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					1	VTCAPNQFQCSITKRCIPRVWVCDRDNDCVD
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						I RETT VODNIOWPTGLAVDYHNERLY WADA
		Ì				KI SVIGSIRI NGTDPIVAADSKRGLSHPFSIDV
	1	Ì	ĺ	į		FEDYTYGVTYINNRVFKIHKFGHSPLVNLTGG
	1	- 1				I SHASDVVI YHOHKOPEVTNPCDRKKCEWL
						CLISPSGPVCTCPNGKRLDNGTCVPVPSP1PP
						DIDADD DGTCNI OCENGGSCELNARROPKCRC
				]		OPRYTGDKCELDOCWEHCRNGGTCAASPSU
						MPTCRCPTGFTGPKCTOOVCAGYCANNSICI
		1		1		VNOGNOPOCRCLPGFLGDRCOYRQCSGYCE
		1		1		NFGTCQMAADGSRQCRCTAYFEGSRCEVNK
		- 1				CSRCLEGACVVNKQSGDVTCNCTDGRVAPS
		j				CLTCVGHCSNGGSCTMNSKMMPECQCPPHM TGPRCEEHVFSQQQPGHIASILIPLLLLLLVL
1						VAGVVFWYKRRVQGAKGFQHQRMTNGAM
						NVEIGNPTYKMYEGGEPDDVGGLLDADFAL
			_l_			NVEIUNT I TAM I EOOLI DE TOOLEENTE

SEQ ID SEQ ID NO: of NO: of nucl- ootide sequence   Sequence	ic Acid, c, H=Histidine, Leucine, ine, P=Proline, S=Serine, =Tryptophan, *=Stop codon, on, \=possible  MGGHGSRHSLASTD A LLAPAPTMTSLMPG LSSLGAIPAAALDPNI SKIDEIRRTVYVGNL GEVKFVRMAGDET RALAFNGVMFGDRP PQAAAKELEEVMKR HSTSLCNDFLGCF*RR CLIINWDL*LF*AYTA VRSRSHTRSKSRSSK NRSRSRQKDRRSK RSHSRDKRKDTREKI REKEREKEKERGKN KDREREREKEHEKD
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uence    914   ng to first amino acid residue of peptide sequence   T=Threonine, V=Valine, W y=Tyrosine, X=Unknown, /-possible nucleotide delet nucleotide insertion   DPDKPTINFINPVYATLY   EKRELLGRGPEDEIGDP   CLELASAGKIPEESKAL   AGLPIPTINFINPVLITLGVS   ATLGEIPQPPLMGNVDI NSQITTADQLLEFFKQV QPTRFAFVEFADQNSVI LKINHSNNAIVKPPEMT VREAQSFISAAIEPGWL RMYRE*APCTICGTFHL K*FFPRVVKEQ*KKRI SHSRKRSQSKHRSRSS SPHKKRSKSRERKSRS KEKERVKEKDREKERE KDRDKEREKDEK GDREKERE KORDKEREKDEK GREKERE KORDKEREKDEK GREKERE KSRTPPRSYNASRSRS. PRTSKTIKRKSSRSPSPF HISERRERESTSMKS SWFFTYP*SPDLQIPSSF-PDLDGAYVKK   STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT STORT	=Tryptophan, *=Stop codon, on, \=possible  MGGHGSRHSLASTD .A  LLAPAPTMTSLMPG LSSLGAIPAAALDPNI SKIDEIRRTVYVGNL GEVKFVRMAGDET RALAFNGVMFGDRP PQAAAKELEEVMKR HSTSLCNDFLGCF*RR CLIINWDL*LF*AYTA \RSRSHTRSKSRSSK NRSRSRQKDRRSK RSHSRDKRKDTREKI REKEREKEKERGKN KDREREREKEHEKD
residue of peptide sequence /=Tyrosine, X=Unknown, /=possible nucleotide delet. nucleotide insertion DPDKPTNFTNPVYATLY EKRELLGRGPEDEIGDP EKRELLGRGPEDEIGDP CLELASAGKIPEESKAL AGLLPIPTPNPLTTLGVS ATLGEIPQPPLMGNVDF NSQTTTADQLLEFFKQV QPTRFAFVEFADQNSVI LKINHSNNAIVKPPEMT VREAQSFISAAIEPGWL RMYRE*APCTICGTFHL K*FFPPRVWKEQ*KKRI SHSRKKRSQSKHRSRSI SPHKKRSKSRERKSRSI KEKERVKEKDREKERE KDRDKEREKDREKDKI RDKEKEKEQDKEKERE KSRTPPRSVNASRRSRS PRTSKTIKRKSSRSPSP HISERRERERSTSMRKS SPHKKSSKSPSPF HISERRERERSTSMRKS SWIFFYP*SPDLQIPSSFI PDLDGAYVKK  375 1725 A 3192 415 101 AHSSHQTRAILQEFQW PFPNLKKSLRGTHFSSI WF/FFYP*SPDLQIPSSFI PDLDGAYVKK  376 1726 A 3199 931 418 GV*WCDLGSPQPPPPG ASQSAGITGVSHTWPK K  377 1727 A 3201 274 1285 KTGYTSRGSPLSPQSSL GYKLQDLTDVQIMARI VSRHSSSVSLSSGKGG FEDHLPPPQRLPRCSP RRSPSSOYFFSNNYOOG	*=Stop codon, on, \=possible  MGGHGSRHSLASTD .A  LLAPAPTMTSLMPG LSSLGAIPAAALDPNI SKIDEIRRTVYVGNL GEVKFVRMAGDET RALAFNGVMFGDRP PQAAAKELEEVMKR HSTSLCNDFLGCF*RR CLIINWDL*LF*AYTA \RSRSHTRSKSRSSK NRSRSRQKDRRSK RSHSRQKDRRSK RSHSRDKRKDTREKI REKEREKEKERGKN KDREREREKEHEKD
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ATLGEIPQPPLMGNVDF NSQTTTADQLLEFFKQV QPTRFAFVEFADQNSVI LKINHSNNAIVKPPEMT VREAQSFISAAIEPGWL RMYRE*APCTICGTFHI K*FFPPRVWKEQ*KKRI SHSRRKRSQSKHRSRSI SPHKKRSKSRERKSRS SPHKKRSKSRERKSRS KEKERVKEKDREKERE KDRDKEREKDDKEKERE KSRTPPRSYNASRRSRS PRTSKTIKRKSSRSPSPF HISERRERERSTSMRKS S  375 1725 A 3192 415 101 AHSSHQTRAILQEFQW PIFPNLKKSLRGTHFSSY WF/FFYP*SPDLQIPSSF PDLDGAYVKK  376 1726 A 3199 931 418 GV*WCDLGSPQPPPPG HVPPHPANFVFLLETGI ASQSAGITGVSHTWPK K  377 1727 A 3201 274 1285 KTGYTSRGSPLSPQSSI GYKLQDLTDVQIMARI VSRHSSSVSLSSGKKG EFDHLPPPQRLPRCSP RRSPSSOYFPSNNYOO	SKIDEIRRTVYVGNL GEVKFVRMAGDET RALAFNGVMFGDRP PQAAAKELEEVMKR HSTSLCNDFLGCF*RR CLIINWDL*LF*AYTA NRSRSHTRSKSRSSSK NRSRSRQKDRRRSK RSHSRDKRKDTREKI REKEREKERGKN KDREREREKEHEKD
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VREAQSFISAAIEPGWL RMYRE*APCTICGTFHI K*FFPPRVWKEQ*KKRI SHSRRKRSQSKHRSRSI SPHKKRSKSRERKSRS; SPHKKRSKSRERKSRS; KEKERVKEKDREKERE KDRDKEREKDEKI RDKEKEKEQDKEKERE KSRTPPRSYNASRRSRS PRTSKTIKRKSSRSPSPE HISERRERERSTSMRKS S  375 1725 A 3192 415 101 AHSSHQTRAILQEFQW FYFPNLKKSLRGTHFSSY WF/FFYP*SPDLQIPSSF PDLDGAYVKK GV*WCDLGSPQPPPG HVPPHPANFVFLLETGI ASQSAGITGVSHTWPK K  377 1727 A 3201 274 1285 KTGYTSRGSPLSPQSSL GYKLQDLTDVQIMARI VSRHSSSVSLSSGKKG EFDHLPPPQPRLPRCSP RRSPSSOYFPSNNYQOG	HSTSLCNDFLGCF*RR CLIINWDL*LF*AYTA \RSRSHTRSKSRSSSK NRSRSRQKDRRRSK RSHSRDKRKDTREKI REKEREKEKERGKN KDREREREKEHEKD
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EQLQAMRHIVTGTTRE	APYIIFGPPGTGKTVT
LVEAIKQVVKHLPKAF	ILACAPSNSGADLLC
QRLRVHLPSSIYRLLAF	SRDIRMVPEDIKPCCN
WDAKKGEYVFPAKKK	OEYRVLITTLITAGR
LVSAQFPIDHFTHIFIDI	- CUC CONTROL MAIAC
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LMEVKETGDPGQQLV	AGHCMEPEST VAIAG
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120 PKAAPSVXI WEPPEL*	AGDPRQLGPVLRSPL YNSLYKKGPDGYDPQ PNQLYYEGELQACA RQGFPIIFHGVMGKD VTSYLKLLLAPSSKK KQVEKIRYCITKLDR STVTPCLPCAPTCPLP LLNRARALPEPLTPGD NTSCHS
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AXLLFGFGGFGFVASLEARAQASSOVITNOG	380	1730	^	320.	1	1	PEQRDHPAPHKQIEAGQGLPGPQAWGG*KGP
381   1731   A   3225   1   840   GGRTYPYFTFSGE	j	Į		ļ	1	1	AXLLPGPGGGPGPVASLEARAQASSGVTPNG
1731   A   3225   1   840   GTRFGHLPAPSDGFCVHL*SIPSWGSF*GESL*	{	1	1	1	ļ		GGRTYPYPTFSSGE
EMQLITSLGI,QEPDIARNVLELLYAQITLYWIGI   FCPCHLPFIQNIME,FMPYSKINSLMMRTQPPS   KAWRASQMMIFFIFILLIVALIATI   WRILKPSADCQFFGGLPLIFIERSISWIDILSTRP   GYLWYWIYRNLIGSVHFFELTLIVLIATI   WRILKPSADCQFFGGLPLIFIERSISWIDILSTRP   GYLWYWIYRNLIGSVHFFELTLIVLIATI   WRILKPSADCQFFGGLPLIFIERSISWIDILSTRP   GYLWYWIYRNLIGSVHFFELTLIVLIATI   WRILKPSADCQFFGGLPLIFIERSCMSMFLIERLI   KLQDMEKKANPSLVLERREVEQQQFLHLGE   HDGSLDLRSRRSVQEGNPRA		<del> </del>	<del> </del>	2226	<b>-</b>	840	GTRPGHT.PAPSDGFCV/HL*SIPSWGSF*GESL/
FFCPLLPFIQMIMEFIMFYSKNISLMINRQPPS	381	1731	A	3223	1	040	FMOLITSLGLOEFDIARNVLELIYAQTLVWIGI
KAWRASQMMTFFILLFRSFTGVCLTAINI   WRILRPSADGOFFRGLPIFISITSWIDTISTRP GYLWVWYYRNLIGSVHFFILLTIVLIITYLY WQMTEGRKIMFILEKLI   KLQDMEKKANPSSLVLERREVQQOFLHLGE   HDGSLDLRSRRSVQEGNFRA   LUMIKVSSTCFSCHLHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Ì	1	1	1	<b>\</b>		FECRI I PEIOMIMI FIMFYSKNISLMMNFQPPS
WRILFSADCGPFRGLPLFHSITYSWIDLTSTIPY GYLWVVWYRNLIGSWIFFELTLIVLIITYLY WQITEGRKIMIRLIHEQIINEGKDKMFLIEKLI KLQDMEKKANPSSLVLEREVEQQGFLH.GE HDGSLDLRSRRSVQEGNPRA LIMIKVSSTCFSCHLHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	1	1		1			VAMPASOMMTEFIFILI FFPSFTGVLCTLAITI
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SSTEFCAYGFMPAKATIFNI.KCDPVFDFGTG PRNAAYYSPHGHI.VI.AGFGNILLQI'ADJMK VWNVKNYKLISKPVASDSTYFAWCPDGEHII. TATCAPRI.RVNNGYKIHYTTGSILHKYDVPS NAELWQVSWQPFLDGIFPAKTITYQAVPSEVP NEEPKVATAYRPPALRIKPITNSKLHEEPPQ NMKPQSGNDKPLSKTALKNQRHEAKKAAK QEARSDKSPDLAPTPAPQSTPRNTVSQSISGDP EIDKKIKNI.KKLIKALRIQLKEQAATGKQLEK NQLEKIQKETALLQELEDLELGI IRSPAARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS ASLVRATVRAVSKRKLQTRAALTLTPSAVN KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTI. EYYKTKGDSDEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES FNI VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEELIPEPGSETPTVASEALAELHGALLRR GPEMGYLPGPPLGPEGGEEETTTTIITTTTVTT TVTSPVL.CNNNISEGEGYVESPDLGSPVSRTL GLLDCTYSHVYPGYGIEQVQTLNLSQEFELL VLAGGGSPGLAPRLLANSSMLGEQQVLRSPT NRLLHFGSPRVPRGGFRHYQAYLLSCGFP PRPAHGDVSVTDLHPGGTATTHCDSGYQLQG EETLICLNGTRPSWNGETPSCMASCGGTIHNA TLGRIVSPEPGGAVGPNLTCRWIEAAEGRRL HLHFENVSLDENDRILMVRSGGSPLSPVIYDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLRFEAFEEDRCFAFFLAHGNVTTTDPEYRPG ALATTSCLLPGYALEPPGPPNAIECVDPTEPHW NDTEPACKAMCGGGLSEPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKERILQVELINVREG DMLTLFDGOGPSARVLAQLRGPQPRRRLLSS GPDLTLQFQAPPGPPRNGLGQGFVLHFKEVPR NDTCPELPPFWGWRTASHGDLIRGTVLTQ	ł	1		1			FOTLHYIATNGESAVVOLPKNGPIYDVVWNS
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VWNVKNYKLISKPVASDSTYFAWCPDGEHIL TATCAPRIRVNNGYKIWHYTGSLHKYDVPS NAELWQVSWQPFLDGIFPAKTITYQAVPSEVP NEEPKVATAYRPPALRIKNETITNSKLHEEEPPQ NMKPOSGNDKPLSKTALKNQRKHEAKKAAK QEARSDKSPDLAPTPAPQSTPRNTVSQSISGDP EIDKKIKNLKKLKALRIGLKEQAATGKQLEK NQLEKIQKETALLQELEDLELGI IRSPARSPGLETPTCLLFVIAALAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRRPTGFPRHGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLLKDKPEHVGVVGVRTRGCNLSYTI EYYTKKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES FNI VAMGTPRAQHPPPQLLFLILLSCPWIQČLPL KEEEILPEPGSETPTVASEALAELLHGALLRR GPEMGYLPGPPLGPEGGEETITTIIITTTVTT TVTSPVLCNNISEGGGYVESPDLGSPVSKTL GLDCTYSIHVYPGYGIEIQVQTLALSQEEELL VLAGGGSPGLAPRLLANSSMLGEGQVLRSPT NRLLHFGSPRVPRGGGFRIHYQAYLLSCGFP PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG EETLICLNGTRPSWNGETTSCMASCGGTIHNA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRRL HLHFERVSLDEDNDRLMVRSGGSPLSPVTYDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLRFEAFEEDRCFAFFLAHGNVTTTDPEYRFG ALATFSCLPGYALEPPGPPNAIECVDPTEPHW NDTEPACKAMCGGELSPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILLQVELLNVREG DMLTLFDQDGPSARVLAQLRGPOPRRRLLSS GPDLTLCPQAPPGPPRNGLGQGFVLHFKEVPR NDTCPELPPFWGWRTASHGDLIRGTVLTYQ	1	1	ļ		1		PRNA AVYSPHGHILVLAGFGNLILQI*AD/IMK
TATCAPRIRVNNGYKIWHYTGSILHKYDVPS NAELWQVSWOPPLDGIFPAKTITYQAVPSEVP NEEPKVATAYRPPALRNKPITNSKLHEEEPPQ NMKPQSGNDKPLSKTALKNQRKHEAKKAAK QEARSDKSPLAFTPARQSTFRNTVSQSISGDP EIDKKIKNLKKKLKAIEQLKEQAATGKQLEK NQLEKIQKETALLQELEDLELGI  384 1734 A 3242 3 678 IRSPAARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTL EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVDEKLSSEFVFNNPNIKGTCGCGES FNI  385 1735 A 3243 3190 664 VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEELPPGSETFIVASEALAELLHGALLRR GPEMGYLPGPPGEGEEETTTTIITTTTVTT TVTSPVLCNNNISEGEGYVESPDLGSPVSRTL GLUDCTYSHVYPGYGIEQVQTLNLSQEEELL VLAGGGSPGLAPRILANSSMLGEQQVLRSPT NRLLHFQSRVPRGGFRIHYQAYLLSCFP PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG EETLICLNGTRPSWNGETPSCMASCGGTHNAA TLGRIVSPEPGGAVGPNLTCRWIEAAEGRRI, HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS DMDDVPERGLISDAQSLYVELLSETFANPLLL SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRRG ALATFSCLPGYALEPPGPPNAIECVDPTEPHW NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILLQVEUILNVEEG DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS GPDLTLQFQAPPGPPNFGLGQGFVLHFKEVPR NDTCPELPPPEWGWRTASHGDLIRGTVLTYQ	ŀ	i		Į.	1		VUNIVENIVE ISKPVASDSTYFAWCPDGEHIL
NAELWQVSWQPFLDGIFPAKTITYQAVPSEVP NEPKVATAYRPPALRNKPITNSKLHEEEPPQ NMKPQSGNDKPLSKTALKNQRKHEAKKAAK QEARSDKSPDLAPTPAPQSTPRNTVSQSISGPP EIDKKIKINKKKLKAIEQLKEQAATGKQLEK NQLEKIQKETALLQELEDLELGI  384 1734 A 3242 3 678 IRSPARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRPTTGPRHRGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLITSAVN KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTL EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES FNI  385 1735 A 3243 3190 664 VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEEILPEPGSETPTVASEALAELHGALLRR GPEMGYLPGPPLGPEGGEETTTTITTTTTT TVTSSPYLCNNNISEGEGYVESPDLGSPVSRTL GLLDCTYSIHVYPGYGIEIQVQTLNLSQEEELL VLAGGGSPGLAPRLLANSSMLGEGQVLRSPT NRILLHFGSPRVPRGGGFRHYQAYLLSCGFP PRPAHGDVSVTDLHFGGTATFHCDSGYQLOG EETLICLNGTRPSWNGETPSCMASCGGTHNA TLGRIVSSPEGGAVGPNLTCRWVIEAAEGRRL HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRPG ALATFSCLPGYALEPPGPPNAIGCVDPTEPHW NDTEFACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILQVEILINVREG DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS GPDLTLQFQAPPGPPPRGEGGEVLHFKEVPR NDTCPELIPPFWWGWRTASHGDLIRGTVLTYQ	1	l			1		TATCAPPI RYNNGYKIWHYTGSILHKYDVPS
NEEPKVATAYRPPALRNKPITNSKLHEEEPPQ NMKPQSGNDKPLSKTALKNORKHEAKKAAK QEARSDKSPDLAPITPAPQSTPRNTVSQSISGDP EIDKKIKNLKKKLKAIEQLKEQAATGKQLEK NQLEKIQKETALLQELEDLELGI IRSPAARSPGLETITCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRPHTGAGTAKMS ASLVRATVRAVSKRKLQPITRAALTLITSAVN KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTL EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES FNI VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEEILPEPGSETPTVASEALAELHGALLRR GPEMGYLPGPPLGPEGGEEETTTIITTTTVTT TVTSPVLCNNNISEGGGYVESPDLGSPVSRTL GLLDCTYSHVYPGYGIEIQVQTLNLSQEEELL VLAGGGSPGLAPRILANSSMLGEQVLRSPT NRLLLHFQSPRVPRGGGFRHYQAYLLSCGPP PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG EETLICLNGTRPSWNGETPSCMASCGGTHNA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRIL HLHFERVSLDEDNDRLMVRSGGSPLSPVTDS DMDVPERGLISDAQSLVVELLSETPANPLLL SLRFEAFEEDRCFAFFLAHGNVTTTDPEYRPG ALATFSCLPGYALEPPGPPNAIECVDPTTEPHW NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCVWGYHVQEEKRILLQVELINVREG DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS GPDLTLQFQAPPGPPNPGLGQGFVLHFKEVPR NDTCPPETPPPEWGWRTASHGDLIRGTVLTYQ		ļ		1	1		NATI WOVSWOPEL DGIEPAKTITYOAVPSEVP
NMKPQSGNDKPLSKTALKNQRKHEAKKAAK QEARSDKSPDLAPTPAPQSTPRNTVSQSISGDP EIDKKIKNLKKKLKAIEQLKEQAATGKQLEK NQLEKIQKETALLQELEDGI  384 1734 A 3242 3 IRSPARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLLKDKPEHVGVKVGVRTRGCNGLSYTL EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGGES FNI  VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEEILPEPGSETTTVASEALAELLHGALLRR GPEMGYLPGPPLGPEGGEETTTTIIITTTTVTT TVTSPVLCNNNISEGEGYVESPDLGSPVSRTL GLLDCTYSIHVYPGYGEIQVQTLNLSQEEELL VLAGGGPGAPRLLANSSMLGEGQVLRSPT NRLLHFQSPRVPRGGGFRIHYQAYLLSCGFP PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG ETTLICLNGTRPSWNGETPSCMASCGGTHNA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRRL HLHFERVSLDEDNDRLMVRSGGSFLSPVIYDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLFFEAFEEDRCFAFFLAHGNVTTTDPEYRPG ALATFSCLPGYALEPPGPPNAIECVDPTEPHW NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCWGVHVQEEKRILLQVELINVREG DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS GPDLTLQFQAPPPRPGLGQGFVLHFKEVPR NDTCPPEPPEWGWRTASHGDLIRGTVLTYQ	1	1					NAELWQVSWQITEDGITTISKI.HEEEPPO
QEARSDKSPDLAPTPAPQSTRNTVSQSISGDP EIDKKIKNLKKKLKAIEQLKEQAATGKQLEK NOLEKIQKETALLQELEDLELGI  384 1734 A 3242 3 IRSPAARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILLDPLYLPGQCAPPQP LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLLKDKPEHVOVKVGVRTRGCNGLSYTI EYTKTKGDSDEEVIQDGVVVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES FNI  385 1735 A 3243 3190 664 VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEGILPEPGSETFTVASEALAELLHGALLRR GPEMGYLPGPPLGGEGEETTTTIITTTTVT TVTSPVLCNNNISEGEGVVESPDLGSPVSRTL GLLDCTYSHVYPGYGIEIQVQTLNLSQEEELL VLAGGGSPGLAPRLLANSSMLGEGQVLRSPT NRLLHFGSPRVPRGGFRHYQAYLLSCGFP PRPAHGDVSVTDLHPGGTATFHCDSGYQLOG EETLICLNGTRPSWNGETPSCMASCGGTHNA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRRL HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRPG ALATTSCLPGYALEPPGPPNAIECVDPTTEPPW NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSFGQDCVWGVHVQEEKRILLQVEILNVREG DMLTLFDGDGPSARVLAQLRGPOPRRRLLSS GPDLTLQFQAPPGPPNPGLGQGFVLHFKEVPP NDTCPFLPPPPWGWRTASHGDLIRGTVLTYQ	1		1	1			AN EXPOSED OF SKTALKNORKHEAKKAAK
BIDKKIKNLKKKLKAIEQLKEQAATGRQLEK NQLEKIQKEGATGRQLEK NQLEKIQKETALLQELEDLELGI  384 1734 A 3242 3 IRSPARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLKDKPEHVGVKVGVRTRGCNGLSYTL EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGGES FNI  385 1735 A 3243 3190 664 VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEGILPEPGSETPTVASEALAELLHGALLRR GPEMGYLPGPPLGPEGGEEETTTTIITTTVTT TVTSPVLCNNNISEGGGYVESPDLGSPVSRTL GLLDCTYSHVYPGYGIEIQVQTLNLSQEEELL VLAGGGSPGLAPRLLANSSMLGEGQVLRSPT NRLLLHFQSPRVPRGGFRIHYQAYLLSCGFP PRPAHGDVSVTDLHPGGTATTHCDSGYQLQG EETLICLNGTRPSWNGETPSCMASCGGTIHNA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRAL HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLRFEAFEEDRCFAPFLAHGNVTTTDPETRPG ALATTSCLPGYALEPPGPPNAIECVDPTEPHW NDTEPACKAMCGGELSEPAGVVLSPDWPQS YSFGQDCVWGVHVQEEKRILLQVEILNVREG DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS GPDLTLQFQAPPGPPNPGLGQGFVLHFKEVPR NDTCPGLPPPEWGWRTASHGDLIRGTVVLTYQ	ĺ	1	1				OF A DODY CDDI ADTRA POSTPRNTVSOSISGDP
NQLEKIQKETALLQELEDLELGI  IRSPAARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTOHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRRPTFGPRHRGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLLKDKPEHVGVKVGVVGVRTRGCNGLSYTL EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES FNI  VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEEILPEGSETPTVASEALAELLHGALLRR GPEMGYLPGPEGGEETTTTIITTTTVTT TVTSPVLCNNNISEGEGVVESPDLGSFVSRTL GLLDCTYSHVYPGYGIEIQVQTLNLSQEEELL VLAGGGSPGLAPRLLANSSMLGEGQVLRSPT NRLLHFQSRVPRGGGFRHYQAYLLSCGFP PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG EETLICLNGTRPSWNGETPSCMASCGGTHNA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRRL HLHFERVSLDEDNDRLMVRSGGSPLSPVIVDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRPG ALATFSCLPGYALEPPGPPNAIECVDPTEPHW NDTEPPACKAMCGGELSEPAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILLQVEILNVREG DMLTLFDGGGPSARVLAQLRGFQPRRRLLSS GPDLTLGPAPPGPPNPGLGQGFVLHFKEVPR NDTCPPLPPEWGWRTASHGDLIRGTVLTYQ	<b> </b> .	1	)	]	1	1	QEARSDRSPDLAFIFAFQSITIATIVEQUEDE
384 1734 A 3242 3 IRSPAARSPGLETPTCLLFVIAAIAAVFVDSAIP RLTQHRPQDGSFPYTILDPPLYLPGQCAPPQP LSQCARRVHGEKLRRPTFGPRIRGAGTAKMS ASLVRATVRAVSKRKLQPTRAALTLTPSAVN KIKQLLKDKPEHVGVKVGVRITRGCNGLSYTL EYTKTKGDSDEEVIQDGVRVFIEKKAQLTLL GTEMDYVEDKLSSEFVFNNPNIKGTCGCGES FNI VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPL KEEEILPEPGSETPTVASEALAELLHGALLRR GPEMGYLPGPPLGPEGGEEETTTIIITTTVTT TVTSPVLCNNNISEGEGYVESPDLGSPVSRTL GLLDCTYSIHVYPGYGIEIQVQTLNLSQEEEL VLAGGGSPGLAPRLLANSSMLGEGQVLSSPT NRILLHFQSPRVPRGGGFRIHYQAYLLSCGFP PRPAHGDVSVTDLHPGGTATFHCDSGYQLQG EETLICLNGTRPSWNGETPSCMASCGGTIHNA TLGRIVSPEPGGAVGPNLTCRWVIEAAEGRIL HLHFERVSLDEDNDRLMVRSGGSPLSPVIYDS DMDDVPERGLISDAQSLYVELLSETPANPLLL SLRFEAFEEDRCFAPFLAHGNVTTTDPEYRPG ALATFSCLPGYALEPPGPPNAIECVDPTEPHW NDTEPACKAMCGGELSEFAGVVLSPDWPQS YSPGQDCVWGVHVQEEKRILLQVEILNVREG DMLTLFDGDGPSARVLAQLRGPQPRRRLLSS GPDLTLQFQAPPGPPPPDGGQGFVLHFKEVPR NDTCPELPPPEWGWRTASHGDLIRGTVLTYQ			ì				EIDKKIKNLKKLKAIEQLKEQAATORQEDK
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						Amino acid sequence (A=Alanine C=Cysteine,
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1	1	ļ	1	peptide		/=possible nucleotide deletion, \=possible
	1	ļ	ļ	sequence		nucleotide insertion
<b> </b>	<del> </del>	<del> </del>	<del> </del>	Sequence	<del> </del>	MTCADPGEIANGHRTASDAGFPVGSHVQYRC
(	ĺ		(		1	LPGYSLEGAAMLTCYSRDTGTPKWSDRVPKC
1		1	ì		1	ALKYEPCLNPGVPENGYQTLYKHHYQAGESL
	1	1				RFFCYEGFELIGEVTITCVPGHPSQWTSQPPLC
i	1	ì	1			KVTQTTDPSRQLEGGNLALAILLPLGLVIVLG
1		]	1			SGVYIYYTKLQGKSLFGFSGSHSYSPITVESDF
	ļ	1	ì		ļ.	
ļ	1		l			SNPLYEAGDTREYEVSI
386	1736	A	3250	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDT
1				1		RKLLMTWALEVAVVMKKSETYAPLFCLPSF
ļ	1		1			HKFCKGLLADTLVEDVNICLQACSSLHALSSS
ļ	1	ł			ļ	LPDDLLQRCVDVCRVQLVHRGTCIRQAFGKL
[	1	1	1		1	LKSIPLGVFLSNNNHTEIQEISLALRSHMSKAP
1	1	1				SNTFHPQDFSD/VISFILYGNSHRTGKDNWLE
	1		1	1		RLFYSCORLDKRDOSTIPRNLLKTDAVLWQW
1		1	1	1		AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIR
1	1	1	İ			SLAGHTLNPDQDVSQWTTADNDEGHGNNQL
Į.		1	j			RLVLLLQYLENLEKLMYNAYEGCANALTSPP
	ì		]		}	KVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLA
1		1	ł	i		GOPAVTVRHGFDLLTEMKTTSLSQGNELEVSI
	l		ĺ			MMVVEALCELHCPEAIQGIAVWSSSIVGKHL
İ	1			ļ	j	LWINSVAQQAEGRFEKASVEYQEHLCAMTG
1	ĺ		1			VDCCISSFDKSVLTLASAGCKSASLKHCLNGE
	ł	ì	1	i		SRKSVLSKPTDSSPEVINYLGNKACECYISTA
		1	i			DWAAVQEWQNAIHDLKKSTSSTSLNLKADF
1	ł	1	1	1	1	DWAAVQEWQNAIHDLAKSISSISLINLADI
			1			NYIKSLSSFESGKFVECTEQLELLPGENINLLA
1	1		1			GGSKEKIDMKKLLRNM
387	1737	A	3255	380	76	MDIFLYNCKYQVQTEI*NSIQHIMA\SKKLSRF
1 .						LKYVHNL*AENYKTLMK*INEDLNKQRDVPY
İ		1	}			S*TARLNKMSIPTKTIFRFKAIYIKIPATYFIET
ļ	1	1	-	}	l	NMQ
388	1738	A	3260	685	428	PQWLGLQVYALPPANFVFFVEMRSTILAQTG
500	1,20	"				FELLDSSDLPASASKSAGITCMSHHARTLSLK
1				)		*WPFCLSATQEKFC*PASEGVAW
389	1739	A	3269	1	332	LDGYHTPIYMLNRIIRLPAAL*IISDQTGHALTI
389	1739	1 ^	3207	1 *	1	LTRLETQMINADYQNKLTLDYLLTTDREVYE
1		1	1	1	1	PFNLTNYCLHIHNQRLGAYDLG*V*Q/KLAHV
		1			1 '	PVQV*HGFDPEAMFR
	4	<del></del>	10000	<del> </del> -	1277	GRCHDQNKGKS\DGPDAQAEACGGESTYQEL
390	1740	A	3270	2	372	LVNQNPIGQPLACRRLTRKIYEGIKKAVKPNH
		1				SPRGVKKVHKFVNKGEKGIMVLAGDTLGIGV
1	}	1		ļ	}	YCLLPCMC*DRKLTYAHIPSTTDLGAGAGY
L_	1			1	1.00	FFQEMLDIMKAISDMMGKCTYPVLKEDAPRQ
391	1741	A	3273	1	187	TOURNELLING AND CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
	1			1	1	HVETFFQ\EELTRSQEGMKLGENFLMFAMPP
1		1		[		DDSKESKGK*FFQEMLDIMKAISDMMGKCTY
1				1		PVLKEDAPRQHVETFFQVGINQKSRGHEVRR
				1		KFPDVCHAPR
392	1742	A	3281	901	521	FFFGDGVSPCRQAGV*WHDLDSLQNLPPGFK
372	1,72	' `	120.	1		RFSYLSLPSSW\DYRHVLPRQANFCIF/M*RRG
	1			1	1	FTMLARMVSIS*PRDLPALASQSAGITGVSHH
		1		1	1	APPQMDFTFALLCFALKGCLPRQKEGGTLNLI
-005	1.513	4	1202	1205	3	RNRSVVPEFVLLGLSAGPQTQTLLFVLFVVIC
393	1743	A	3283	385	] 3	LLTVMGNLLLLVVINADSCLHTPMYFFLGQL
		1		1	}	SFLDLCHSSYTAPKLLENLLSEKKTISVEGCM
		1				A*VFFVFATGGTESSLLAVMAYDRYVAIRTR
1					L	G
394	1744	A	3284	575	1054	CTKCKADCDTCFNKNFCTKCKSGFYLHLGKC
1 394						TO THE PROPERTY OF A PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
394	1					LDNCPEGLEANNHTMECVSIVHCEVSEWNP
394	',''					WSPCTKKGKTCGFKRGTETRVREIIQHPSAKG
394	1,44					WSPCTKKGKTCGFKRGTETRVREUQHPSAKG NLCPPTNETRKCTVQRKKCQKGERGKKGRE

		- T	1000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	noa	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł		peptide	-	/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
			<del> </del> -			RKRKKPNKGESKEAIPDSKSLESSKEIPEQREN
						KQQQ
395	1745	A	3286	1	340	RVLYVPSMGFCILVAHGWQKISTKSVFKKLS
373	1743	1.	3200	-		WICLSMVILTHSLKTFHRNWDWESEYTLFMS
	1	1	1			ALKVNKNNAKLWNNVGHALENEKNFERAL
	1	ł		)		KYFLQATHVQPDDIGAHMNVGR
396	1746	A	3293	1	172	GFRAVVMTVKTEAAKGTLTYSRMRGMVAIL
370	1740	\	1 32/3	15		IAFMKQRRMGLNDFIQKIANNSYACKQ
397	1747	A	3295	12	401	AEPACGASSCTPPSLRSSSSQSVGPLRPGRPL
371	1/4/	1	3270	1	1	WSEACAFL*AAAPQGPASPCCGLPSGFPRVW
	ì		1			AQCCPPGGALRFPEGLGSVLSPRRCPQVSRGS
	1	1	-			GLSAVPQEVPSGFLGPGLRACPQEAPSRFLRA
		}	j			GLT
398	1748	A	3300	1912	2768	KQRRWQNIQRKGPKRYIVIAGNSQSHQPMIFS
J70	1770	1	1			MIRKLPKVTCRDVLPEIRAICIEEIGCWMQSY
		1	1			STSFLTDSYLKYIGWTLHDKHREVRVKCVKA
		1		ì	Ì	LKGLYGNRDLTARLELFTGRFKDWMVSMIV
	j	]	ł	}		DREYSVAVEAVRLLILILKNMEGVLMDVDCE
		1		1		SVYPIV*ASN*GLASAVGEFLYWKLFYPECEI
	1	1				RTMGGREQRQSPGAQRTFFQLLLSFFVESKSH
	1	1	1			SVTQAGVQWQFSAHRDLCLPGSSNSHVSASR
		}	1 .	1	l	VAGIAGAHRHTWLIYVFFSWRQGFAVLAGL
		1				VSNS
399	1749	A	3301	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSE
3//	1	]	}			SPPPITDSWAPFISLTHHVLSQSQSPLSSNCWI
	į	1	1			CLSTHTQ*FTALPADLLTWTQSNVSLHISYLA
	ì		- 1			PFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
	į					GRAVALLHLIASGLTSIQTNTASSKPPIWGY\L
	- 1	-	}			STQTSFISPPPLCLSRTYPNPAHATMVGQVPQ
	İ	1	1			SLCGLIFTL/RTPCRPSILHPNYKIISTSAWQKV
		1	l l			LCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAAN
	1	-	1	1		SALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGS
	1					N/RLTVDKDNFFLSPKPNSLHQLPSQ\TPYQAL TGAALAGSYPIWENENTLSWLPTFTYNFCLST
			1			PSLFFLCDTN*YLCLPANWSGTCTLVFQAPTI
		1	1	İ		NILPPNQTILISVEASISSSPIRNK WALHLITLLT
	}	ļ.				GLGITAALGTGIAGITTSITSYQTLFTTLSNTVE
		1				DMHTSITSLQRQLDFLVGVILQNWRVLDLLT
	1		- 1	1	Ì	TEKGGTCIYLQEECCFCVNESGIVHLAVRRLH
]			l			DRAAEL*HQVADSWWQGSSLLRWIPWVAPF
	1		1			LGPLIFLFLLLMIGPCIFNLVSRFISQRLNCFIQ
}	}	-	ì	}	1	ASMQKHIDNIFHLCHV*YQSLRGNHSEAPEPR
	1		1		Ì	
	}					P THWRHSSGVPGSTTARRRRELEIATSDNQE
400	1750	A	3303	2	453	YYNRLCQEVINRERNDQKMLADLDDLNRTK
1					1	KYLEERLIELLRDKDALWQKSDALEFQQKLS
			1	1		AEERWLGDTEANHCLDCKREFSWMVRRHHO
	1		1	1		RICGRIFCYYCCNNYVLSKHGGKKERCC
			1_			MAPQHSSLDDKVPQQASTVCFEFQDILQHSQ
401	1751	A	3304	1	626	CTEHKDSLWGPGARSQPFGAHNTRLSPDSCP
			}	1		EKIVLRALKDSRAGMPEQDKDPGVQENPDD
		1	l	İ		QRRVPQGTGDAPSAFRPLWDNGGLSPFVSRP
1	1	1		1		ON EDDY IT OBSERVED TO SUCCEDIVISEDED OF THE OBSERVED TO SUCCEDE A SUCCEDIVISEDED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSERVED OF THE OBSER
1				1		GPLERDLHAQRSEVTYNQRSQSSWMSSFPKR
1	1					NAFVSPYSSMGQAQP/GLPKTNPIGESCCWEC
	1	1		- }		LSLSTQILG*QKPSKYIPSLCKR
		!	,	1		
402	1752	A	3305	1678	172	MELPSGPGPERLFDSHRLPGDCFLLLVLLLYA
402	1752	A	3305	1678	172	PVGFCLLVLRLFLGIHVFLVSCALPDSVLRRF
402	1752	A	3305	1678	172	MELPSGPGPERLFDSHRLPGDCFLLLVLLLYA PVGFCLLVLRLFLGIHVFLVSCALPDSVLRRF VVRTMCAVLGLVARQEDSGLRDHSVRVLISN HVTPFDHNIVNLLTTCSTVSESEAESATGRFP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence	1		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	]	}		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	Į	l		residue of	sequence	/=possible nucleotide deletion, \=possible
	1	1	1	peptide		/=possible nucleonde detenon, (=possible
	Į.	1	Ī	sequence	[	nucleotide insertion
	<del> </del>	<del> </del> -				GAQLKAPLSPLAFRMEDTEALPLTPILYPTCQ
	Į.	1	1	1	1	FFFFIFLNIFLLAFSSPGSQPLLNSPPSFVCWSR
		ł				GFMEMNGRGELVESLKRFCASTRLPPTPLLLF
	ì	1	1	}	<b>\</b>	PEEEATNGREGLLRFSSWPFSIQDVVQPLTLQ
	1	}		}	Į.	VQRTLVSVTVSDASWVSELL\WSLFVPFTVY
	1	1	1	Į.		QVRWLRPVHRQLGEANEEFALRVQQ\LVAKE
	1		1	1		LG\QTGTRLTPA\DKAEHMKRQRHPR\LRPQS
	)	}	-	ł		AOSSEPPSPWVLSS/SDVOTGOTLGFREFKESF
			Į.			CPHVAIGVFIPERPWPKTGCCKTLTIHLILL*G
	1		1			GPVSESCPE\DIHPRGT*VPTOOASGLPSFPSYG
	ł	1	1	1		PARGGVL*HPSAQQPLTFA\KSS\WARAGRAL
1	1		]	}		QERKQ\ALYEYARRFTERRAPGGLD
			1			DPSPSLLAVALGLRAGERTRSGPGSSSPSGGIS
403	1753	Α	3307	44	447	GGASAGLASSPECACGRSHFTCAVSALGECT
	1	1			ļ	CIPAQWQCDGDNDCGDHSDEDGCILPTCSPL
1			}			DFHCDNGKCIRRSWVCDSDNDCEDDSDEQD
ľ		1				
	l l		1			CPPRECEED PRHGWGRRVLGRDRPRLQKVKKSVKAIYIPG
404	1754	TA	3311	409	1	PRHGWGRRVLGKDRPKLQKVKRSVKAITITO
404	1,754	1				QDHVQNEEIYARVLDKFGSNFLSRDNADLGT
1	1	ì				AFVKFSTLTK*LSALLKNLLQGLSRNVIFTLDS
	1	1	Į.	1	•	LLKGDLKGVKGDLKKPFDKAWKDYETKFAK
	1	1	- {			IEKEKREREWR
406	1755	A	3322	12	458	AAVPVENPWDDPRVRPRVRIFTWEDCIAGQA
405	1/33	A	3322	1-		KVLCNDSYGVTIDWSPKGAFIRLTSQSVGNG
l	1	1	1			HPASKENDQMVDTIKNTTKVPIIWTYGDMVE
1	į	1			i	PRPOMIRPAVGAKHKELWKILMALKKIKWE
	1	1	1			GKYTKPSOYNPNYMLELAHNDSVW
		<del></del>	3324	1	426	I SMI STISTEHRLSVLWPIWYCCHCPTHLSAV
406	1756	A	3324	\ <b>1</b>	120	MCVLLWALSLLOSILEWMFCSFLFSDVDSDN
	- 1	1	i	l		WCOILDELTAVWLIFLI\LVLCGFTLVLLVRIIC
	1	i	ł	į		GSQKMPLTRLYVTILLTGLVFLFCSLPLSIQ*F
1	l l		}	)		LI VWIEKDI DDI.
					1841	SGDI SPAFLMMLTIGDVIKQLIEAHEQGKDID
407	1757	A	3328	213	1041	INKVKTKTAAKYGLSAOPRLVDUAAVPPQY
1	l	j	1	1		RKVLMPKLKAKPIRTASGIAVVAVMCKPHRC
	1	1	1	ì	1	PHISFTGNICVYCPGGPDSDFEYSTQSYTGYEP
1		1	1	1	ì	TSMRAIRARYDPFLQTRHRIEQLKQLGHSVD
1	- 1			i		KVEFIVMGGTFMALPEEYRDYFIRNLHDALS
		- 1	- 1			GHTSNNIYEAVKYSERSLTKCIGITIETRPDYC
		i		}	}	MKRHLSDMLTYGCTRLEIGVQSVYEDVARD
						TNRGHTVKAVCESFHLAKDSGFKVVAHMMP
	ļ				ļ.	DLPNVGLERDIEQFTEFFENPAFRPDGLKLYP
1	1				1	TLVIRGTGLYELWKSGRYKSYSPSDLVELVA
		1		}		ILVIKUTULI ELWASUKI ASI SI SIDLI IDI A
.	1		1			RILALVPPWTRVYRVQRDIPMPLVSSGVEHG
1				1		NLRELALARMKDLGIQCRDVRTREVGIQEIH
			ì	}		HKVRPYQVELVRRDYVANGGWETFLSYEDP
	1	1	- }			DQDILIGLERLRKCSEETFRFELGGGVSIVREL
		Ì	ļ			HVYGSVVPVSSRDPTKFQHQGFGMLLMEEA
			1	- [		ERIAREEHGSGKIAVISGVGTRNYYRKIGYRL
	1	j	1	1		OCPYMVKMLK
		<del></del>	2225	$\frac{1}{3}$	467	ALASPRAAGIRHELTSTMAAGKNKRLTKGGK
	1758	A	3335	٠	10.	KGAKKKAV/DNIINIGKTLVTRTQRTKIASDG
408		1				LKGRVFEESLADLOND\TDGYLLRVI*VAFTT
408		l l		ł .	l	ERTNQI/REVFNKLIPDSIGKDIEKACQSIYPLH
408		ļ	}	1	1	FRANCINE ALVERTING TO STORE THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE CASE AND THE
408						DDEARKVKMI.KKPKFELRKLMELHGEGSS
408					10.53	DDFARKVKMLKKPKFELRKLMELHGEGSS
408	1759	A	3338	7	1252	DDFARKVKMLKKPKFELRKLMELHGEGSS  PB WRNSARDEILLSFPONYYIQWLNGSLIHGL
	1759	A	3338	7	1252	DDFARKVKMLKKPKFELRKLMELHGEGSS PRWRNSARDEILLSFPQNYYIQWLNGSLIHGL WAII ASLESNI.CLEVLMPFAFFFLESEGFAGLK
	1759	A	3338	7	1252	DDFARKVKMLKKPKFELRKLMELHGEGSS  PB WRNSARDEILLSFPONYYIQWLNGSLIHGL

PCT/US01/03800

NO: of NO: of hod ID NO: beginning nucleotide location corresponding sequence USSN location corresponding to last amino coid residue.	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LLLCTPVGL\SRMFTVMGQLLVKPTILEDLDE
nucl- ectide seq- uence uence    NO. 01	F=Phenylalanine, G=Glycine, H=Histidine, l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
eotide seq- uence USSN location corresponding to last amino acid residue of peptide sequence peptide corresponding to last amino acid residue of peptide sequence	l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
seq- uence 09/496 correspondi ong to first amino acid residue of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide corresponditor of peptide correspondi of peptide correspondi of peptide correspondi of peptide correspondi of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor of peptide corresponditor o	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
uence 914 ng to first amino acid residue of peptide sequence peptide	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
amino acid of peptide residue of peptide peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
residue of sequence peptide	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion 111 CTPVGL\SRMFTVMGOLLVKPTILEDLDE
peptide	/=possible nucleotide deletion, \=possible nucleotide insertion 111 CTPVGL\SRMFTVMGOLLVKPTILEDLDE
	nucleotide insertion
sequence	LLI CTPVGL\SRMFTVMGOLLVKPTILEDLDE
	I I I I PAGE/SIGNI I AMOGEDATE TITLE I
	QIYIITLEEEALQRPTKWAVFIRW/KYNIMELE
	QELENVKTLKTKLERRKKASAWERNLVYPA
	VMVLLLIETSISVLLVACNILCLLVDETAMPK
	GTRGPGIGNASLSTFGFVGAALEIILIFYLMVS
	GTRGPGIGNASLSTFOFVOAALEILLIT TENTYS
	SVVGFYSLRFFGNFTPKKDDTTMTKIIGNCVS
	ILVLSSALPVMSRTLGITRFDLLGDFGRFNWL
	GNFYIVLSYNLLFAIVTTLCLVRKFTSAVREE
	LFKALGLHKLHLPNTSRDSETAKPSVNGHQK
	AL AL
410 1760 A 3339 127 1433	GSHRFSLASPLDPEVGPYCDTPTMRTLFNLL
410 1700 12 2001	WLALACSPVHTTLSKSDAKKAASKTLLEKSQ
	FSDKPVQDRGLVVTDLKAESVVLEHRSYCSA
	KARDRHFAGDVLGYVTPWNSHGYDVTKVFG
	SKFTQISPVWLQLKRRGREMFEVTGLHDVDQ
	GWMRAVRKHAKGL\P*CLGSCLRTGLTMISG/
	YVLDSEDEIEELSKTVVQVAKNQHFDGFVVE
	VWNQLLSQKRVGLIHMLTHLAEALHQARLL
	ALLVIPPAITPGTDQLGMFTHKEFEQLAPVLD
	GFSLMTYDYSTAHQPGPNAPLSWVRACVQV
	LDPKSKWRSKILLGLNFYGMDYATSKDAREP
	VVGARYIQTLKDHRPRMVWDSQVSEHFFEY
	KKSRSGRHVVFYPTLKSLQVRLELARELGVG
	VSIWELGQGLDYFYDLL*VGIAASAVDVFFSK
	PWSE
411 1761 A 3342 74 2701	VATRKLAKGFTQFAKMTEGTKKTSKKFKFFK
411   1761   A   3342   74   2761	FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF
	EATQDDMVTVPKSPPAYARSSDMYSHMGTM
	PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV
	PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS
	AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA
	GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE
	ELKLSSTDLRSHAWYHGRIPREVSETLVQRN
	GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN
	KVVVKAGESYTHIQYLFEQESFDHVPALVRY
	HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS
	YGLGOGSSKPASPVSPSGPKGSHMKKKSVIM
	TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA
	LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA
	APAAPSATALPASPVARRSSEPOLCPGSAPKI
	HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS
	GHYCOLOPPVRGSREWAATETSSQQARSYGE
	PI KEI SENGAPEGDWGKTFTVPIVEVTSSFNP
	ATFOSILIPRONRPLEVGLLRKVKELLAEVDA
	PTI ARHVTKVDCLVARILGVTKEMQTLMGV
	P.WGMELLTLPHG\RKLRLDLLERFHTMSIML
	AVDIL GCTGSAEERAALLHKTIOLAAELRGT
	MGNMESEAAVMGALDMAOISRLEQTWVILK
	ORUTEGATI VEKKLKPFLKSLNEGKEGPPLSN
	TTEPHVLPLITLLECDSAPPEGPEPWGSTEHGV
	EVVLAHLEAARTVAHHGGLYHTNAEVKLQG
	FQARPELLEVFSTEFQMRLLWGSQGASSSQA
	RRYEKFDKVLTALSHKLEPAVRSSEL
	IDRAAECRTKPLPMAVSIRGNADSIVACLVLM
412 1762 A 3347 1 898	VLYLIKKRLVACAAVFYGFAVHMKIYPETYI
	LPITLHLLPDRDNDKSLRQFRYTFQACL*ELL
	KRLCNRTALMFVAVAGLTFFALSFGFYYEYG
	WEFLEHTYFYHLTRRDIRHNFSPYFYMLYLT
	AESKWSFSLGIAAFLPQLILLSAVSFAYYRDL
	VFCWFLHTSIFVTFNKVCTSQYFLWYLCLLPL
	ALCALDIONALLINGACISALICA LECEBIE

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		Ì	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uonoc	)	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	İ	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		peptide		/=possible nucleotide deletion, \=possible
	ŀ			sequence	1	nucleotide insertion
	ļ		<del> </del>	Sequence		VMPLVRMPWKRAVVLLMLWFIGQAMWLAP
	1	1	1	ļ		AYVLEFQGKNTFLFIWLAGLFFLLINCSILIQII
	1	1	1	ĺ		SHYKEEPLTERIKYD
				<u> </u>	474	PIPVRWNSLEGRLLRGYEQHANDGKDYISRN
413	1763	A	3361	3	474	*DLRSWTAADMAAQITKRKWEAEEFAEQIKA
						YLEGTCVER/LRTHLENGKETLQLTEQSSQPTI
			İ	1		PIVGIVAGLVLLGAVVTGAVVSAVMCRKKNS
	1		ļ	ļ		PIVGIVAGEVEEN A SCHULOGSDVSI TACK
	<b>[</b> *	1				GHFLPTDRVSYSEAASSDHAQGSDVSLTACK
	ļ					V V V V V V V V V V V V V V V V V V V
414	1764	A	3363	1488	453	HQILELKKKILKTYNPDYDEDLVQEASSEDVL
7,7	1	1				GVHMVDKDTERDIEMKRQLRRLRELHLYST
			1		1	WKKYQEAMKTSLGVPQRERDEGSLGKPLCP
	1	1	1	1		PEILSETLPGSVKKRVCFPSEDHLEEFIAEHLP
	1		1	İ		EASNQSLLTVAHADAGTQTNGDLEDLEEHGP
	Ì	İ	1	İ		GOTVSEEATEVHMMEGDPDTLAELLIRDVLQ
		1				ELSSYNGEEE\DPEEVKTSLGVPQRGDLEDLE
Ì				1		EHVPGOTVSEEATGVHMMQVDPATLAKSDL
		ì				EDLEEHVPEQTVSEEATGVHMMQVDPATLA
ł	ļ	ł	1	1		KQLEDSTITGSHQQMSASPSSAPAEEATEKTK
		ĺ	1			VEEEVKTRKPKKKTRKPSKKSRWNVLKCWD
Į		1	1			IFNIF
					216	IPWSWVGRLSVRKMSILF*LTYNYNAILNKTP
415	1765	Α	3369	431	315	
	1	1	ļ			PSFSPSL RQEKMGLGEIGASGVLRSMLKERKKQNMKG
416	1766	A	3373	42	651	NGNVTLTPLLPAVQCGCHLQPAGRSPLPSSHS
	1					NGNVILIPLEPAVQCGCHLQPAGRSI EI SSIIS
			1			APGLCSPLHPLQPQQEASTCPSGTLQGREKAA
1	i	-	1		1	PGQGRPLCSLWAGGAGA\PGERGAEGRGPSD
[	[					QAPDPKSGPWLFPPGLGAPAEVRLHNVPHNL
	İ	1				RRPPLP*ARGK*PPNSGCPWSEGRAKQPLSCG
				ļ		PKPQCSLPSQVPGDTH
417	1767	A	3382	2	2061	EAQDPRACGPDAGGRFAARDAPGNSLRPPPS
**/	1,,,,	1		ł		SPP/GWPGQLRLLPRVPGSELRCGKPERGRLP
1	ł		1	1		ASPPGKIRGWPPGISKRPGLGGRSFPPGFAPRT
[			į	1		WRPEARGPSVQSLPPIFSPQSAQTTAR*RPGAP
			ì			KNAGRCGGA\RGPRLSLGPPPGPPPAPALPAR
1			l l	1		ASAGAGAAAAALAVGGVRGAGGARGTGGY
1		1	1			GHCSGR/PTGRTGPGPQGPGPPMPARPR*AS\S
1	}			ļ.		TRGSRRGPGSRPARAAAAPRAGDHGRRPVRV
	1	1		1		HLRQHTAV*EPRLGDATAPPGGAAGPGAPAP
			1			R\GPGWDCALLPSPGPRSPRAVGCAEPEIWDP
		1				SPRRGTSPVPSVRSLRSEPANPRLGLPALLNSY
1	İ					PLKGPGLPPPWGPRTQTGHVIITVQPSGSCIEH
				1		SKSLD/RGPWGAPPWGPSSSGLCSPKLATAGP
1	}		}	1	1	PQSWGLCQIGRRRGLGGPGLKRGET/GLL*GC
**	1					FUSWULCUIORARULUUFULARULFIULE UC
						SMDHANRTKGPGVPTSNRCFSHIPG\GDGCSD
1		1		1		HSSCEGHPDLHAGREMPAAPGLSELERVRFT
		J		1	}	VGCGGLASGISSASVSGLSPNRAGGPGQGDW
						EMYPVSWQTQESGGQG/SPKTGR*VGMLQA
1		1	1			GAGSLQGGTGDGVWGLWEDGP/RG*DSPLPS
		1				GTGTEP*TPTTSIPFFPQPSGVYPSRATLLPMPS
1		i				Y*ALGPSANKSEKPLLSFLYRGLCCRISLQLA
		-				KGIGQLSEIPLLNVETAFWSMWVTYFRK
1	1,200		3398	304	2121	EEEEEEDEDDDDNNEEEEFECYPPGMKVQV
418	1768	A	3398	704	2121	RYGRGKNQKMYEASIKDSDVEGGEVLYLVH
1		-				YCGWNVRYDEWIKADKIVRPADKNVPKIKH
1				i		RKKIKNKLDKEKDKDEKYSPKNCKPPALGPN
L .				1	1	10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10dd days and 10
					i	PPEOTNPISWK WYPKI DI TDAKNSDTAHIKSI
					j	PPFQTNPISWKWYPKLDLTDAKNSDTAHIKSI FITSII NGLOASESSAEDSEOEDERGAODMDN
						PPFQTNPISWKWYPKLDLTDAKNSDTAHIKSI EITSILNGLQASESSAEDSEQEDERGAQDMDN NGKEESKIDHLTNNRNDLISKEEQNSSSLLEE

No. of							Amino acid sequence (A=Alanine C=Cysteine,
No. of contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribution   No. of the contribut	SEQ ID	SEQ ID	Met				Amino acid sequence (A-Aminino C Cystalia)
USSN   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion   Olosetion	NO: of	NO: of	hod	ID NO:			D=Aspartic Acid, E=Glucine H=Histidine
uence uence uence opides correspondi sequence per per per per per per per per per pe		peptide					r=pnenylalanine, 0=Olycine, 1=Triscione,
### Bender   1914   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Bender   1915   ### Be	eotide	seq-		USSN		corresponding	1=Isoleucine, K=Lyslic, L=Loucine,
1914   mg to first   minion acid residue of peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide	seq-	uence	Ì	09/496	correspondi		M=Memionine, N-Asparagine, 1-110me,
				914			Q=Glummine, K=Arginile, S-Serine,
## ## ## ## ## ## ## ## ## ## ## ## ##	1	1	ľ	1	amino acid		T=Threonine, V=Valine, w=Tryptopilati,
	ļ	Į.		ì		sequence	Y=Tyrosine, X=Unknown,Stop codon,
				}	peptide	į .	
YEEDEVTKIKKDVKDTTDKSSKPQIKRGEN   RYCNTECLKICSGSKKEEKAKKESLCMEN   SSNSSSDEDEETIKAKMITTKKYNGLEEKKE   RYCNTECLKICSGSKKEEKAKKESLCMEN   SSNSSSDEDEETIKAKMITTKKYNGLEEKKE   SSNSSSDEDEETIKAKMITTKKYNGLEEKKE   SSNSSSDEDEETIKAKMITTKKYNGLEEKKE   SLRITGFYSGFSEVAKERILLINSDERLONS   RAKDRKDWSSIQGWPKKTLKELFSDEDTIT   AAASPPIPAPEEQAFESLQTVAKESCSTSV   ELEKPPYNVDSKPIEKTYEVNDRKAEPSS   GSNRSA*IPLPYLHLINRLHQSL*QKESCSSS   SNRSA*IPLYLHLINRLHQSL*QKESCSS   SNRSA*IPLYLHLINRLHQSL*QKESCSS   SNRSA*IPLYLHLINRLHQSL*QKESCSS   SNRSA*IPLYLHINRLHQSL*QKESCS   SNRSA*IPLYLHINRLHQSL*QKESCS   SNRSA*IPLYLHINRLHQSL*QKESCS   SNRSA*IPLYLHINRLHQSL*QKESCS   SNRSA*IPLYLHINRLHQSL*QKESCS   SNRSA*IPLYLHINRLHQSL*QKESCS   SNRSA*IPLYLHINRLHQSL*QKESCS   SNRSA*IPCCELKQ* SARTIFYCE   SKLYNESKSERCSGRKFIKKAEKKPSNSOK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK   QQKCSCK		1	Ì	1		]	nucleotide insertion
RYCNTEECLKTGSPOKKEEKAKNNESLCMEN   SSNSSSDEDEEFRAKMTPTKYNGLEEKRK   SLRTTGFYSGFSEVAEKRIKLLINNSDELONS   RAKDRADWSSJQOWPKKTKKYNGLEEKRK   SLRTTGFYSGFSEVAEKRIKLLINNSDELONS   RAKDRADWSSJQOWPKKTKELFSDSDTT   AAASPPHAPEGGVAEESLQTVAEESCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTVATERSCSPSV   ELEKPPEVNDSKPIEKTSV   SKJVSEKSERCSGRKFIKKAEKKP*SNSGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QKEGK   QK	<u> </u>	<del> </del>	<del> </del> -				NKVHADLVISKPVSKSPERLRKDIEVLSEDID
SSNSSSDEDEETKAKMTPTKKYNGLEERR	Į.	1		ŀ			YEEDEVTKKRKDVKKDTTDKSSKPQIKRGKR
SSNSSSDEDEETKAKMTPTKKYNGLEERR	1	1	1	1	1		RYCNTEECLKTGSPGKKEEKAKNKESLCMEN
SIRTIGFYSGFSEVAERRIKLLINNSDELQNS	1	1	1	1	l	ł	SSNSSSDEDEEETKAKMTPTKKYNGLEEKRK
RAKDRKDWSIGGQWPKKTLKELESDDTE	1		1	1			SLRTTGFYSGFSEVAEKRIKLLNNSDERLQNS
AAASPHPAPEGVAEESLQTVAEESCSPSV	Į	1	<u> </u>	Į.			RAKDRKDVWSSIQGQWPKKTLKELFSDSDTE
			1		1		AAASPPHPAPEEGVAEESLOTVAEEESCSPSV
GSNFSA*IPLPYLHLINRLHQSL*QKGSRQQSS	1	ì	1	1		}	FLEKPPPVNVDSKPIEEKTVEVNDRKAEFPSS
1769	ļ	)	1	1	}	ł	GSNESA*IPI PYLHI NRLHOSL*OKGSROQSS
LQDLQSERP*LASRF*CQCELKQ**SARTRIS*   KSLYASEKSERCSGRKFKKAEKKP*SNSGK     CQKECK  KSLYASEKSERCSGRKFKKAEKKP*SNSGK     CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQKECK  CQ		ļ	ĺ	1			VTVSEPI APNOEEVRSIKSETDSTIEVDSVAGE
	1	1	1	[		1	LODI OSERE*L ASRE*COCELKO**SARTRTS*
1769	1	1	ļ .	1		1	VELVEEP CECEPPK FIKK A FKKP SNSGK
1769   A   3399   206   463	1				1		
1770   A   3408   1010   685   RRLSFFF1WSSVLVTQARVQWRDLGSPQFLP   PGFKRFSCLSLPSSWDVRHPSPRPVNFHVFLV   VMGFHHVQQAOLELITSGDLPALASQSARIT   GVNHCAQPRGHFH   GANGLELITSGDLPALASQSARIT   GVNHCAQPRGHFH   ADSNLIESCWGELGGWGGDWRVEQVGAS   ADSNLIESCWGELGGGWGGDWRVEQVGAS   ASLRFPREVCSIRFLFTAVSLLSLFLSAFWLGL   LYLVSPLENEPKEMLTLSFYHERVRSQGQL   QQLQAEIDKIHKEVSTVRAANSERVAKLVF   QRLNEDFYKRPDYALSSVGASIDLQKTSHDY   ADRNTA YFWNRFSYWNYARPFYVLEPHVPF   GNCWAFEGDQGOVVIQLFGRYQLSDHTLQHP   PFSVEHTGGANSAPRDFAVFFLLSFFTHQGLO   VYDETEVSLGKTFTDVEKSEQITFHLQNDPPA   APRNTA YFWNRFSYWNYARPFYVLEPHVPF   GNCWAFEGDQGOVVIQLFGRYQLSDHTLQHP   PFSVEHTGGANSAPRDFAVFFLLSFFTHQGLO   VYDETEVSLGKTFTDVEKSEQITFHLQNDPPA   APRNTA YFWNRFSYWNYARPFYVLEPHVPF   GNCWAFEGDQGOVVIQLFGRYQLSDHTLQHP   PFSVEHTGGANSAPRDFAVFFLLSFFTHQGLO   VYDETEVSLGKTFTDVEKSEQITFHLQNDPPA   APPKVKIQLISNWGHPRFTCLYRVRAHGYRT   SEGABGSAQGPH   PFSVEHTGGANSAPROFGAVFRYTDMGRPPP   PYPSVSPCPLFGSLAIAPHSPEPHPWEQQPPRG   QARSPPGGWLGSATRVRRPHNHIP/RGHIHSP   VYDTAGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPDVCE   GANGAPASSPOVALDANDAPAVEY   GANGAPASSPOVALDANDAPAVEY   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDAPAVETTO   GANGAPASSPOVALDANDA	1		1			1.62	ODECL SINIGOACIOIGDACWEI VCI FHGIOP
1770   A   3408   1010   685   RRLSFFF;WSSVL/QRVQWRDLGSFQFLP   PGFKRFSCLSLPSSWDYRHPSPRPVNF/AIVFLV   VMGFHHVGQAGLELLTSGDLPALASQSARIT   GVNHCAQPRGHFH     421	419	1769	Α	3399	206	463	VICEUSINIOQAGIQIODAC WEET CERTIFICE
1770   A   3408   1010   685   RRLSFF*IWSVLVTQARVQWRDLGSPQPLP   PGFKRFSCLSLPSSWDYRHPSPRPVNF/HVFLV   VMGFHHVQQAGLELLTSGDLPALASQSARIT   GVNHCAQPRGHFH     421   1771   A   3409   355   1326   ADSNLESCWGELGGPWGGDWRVEQVGAS   ASLRSPREVCSIRFLETAVSLLSLFLSAFWLGL   LYLVSPLENFEKEM.TLSEYLERVRSQGQQL   QQLQAELDKLHKEVSTVRAAMSERVAKLVF   QRLNEDFYRKPDYALSSVGASDLQKTSHDY   ADRNTAYFWNRFSFWNYARPTVLLEPHVPP   GNCWAFEGDQGQVVIQLPGHVQLSDITLQHP   PPSVEHTGGANSAPRDFAVFILLSFFHQGLQ   VYDETEVSLGKFTFDVEKSEIQTFHLQNDPPA   AFPKVKQQLSNWGHPRTCLYRVRAHGVRT   SEGAEGSAQOPH   PSSCAFSGAGGPGTARDYTPMGRPPP   PVPSVSPGPLPGSLALAPHSPEPHPWEQQPPRG   QARSPPGGWLGSATRVRRPHNHP/RGH/HSP   VDTAGAPASSRGDVC   VTVSVSMRSPESGKGEPGTARDYTPMGRPPP   VDTAGAPASSRGDVC   VTVSVSMRSPESGKGPGTARDYTPMGRPPP   VDTAGAPASSRGDVC   VTVSVSMRSPESGKGPGTARDYTPMGRPPP   VDTAGAPASSRGPDVCE   GROWARSPCGWLGSATRVRRPHNHP/RGH/HSP   VDTAGAPASSRGAPASKCGPVGAVSLCSKD   VTVSVSMRSPESGKAPARVKVGDDRAVEVEG   FFONKVNLAELFKGKKGVLFGVPGAFTPGCS   KTHLPGFVEQAEALKAKGVQVACLSVNDA   FVTGEWGRAHKAGKGVRLLADPTGAFGKET   DLLLDDSLVSIFGRRRLKFSSMVVQDGIVKA   LNVEPDGTGLTCSLPRISQL   VTVQVLDNDNAPTGAFGKET   DLLLDDSLVSIFGRRRLKRFSSMVVQDGIVKA   LNVEPDGTGLTCSLPRISQL   VTVQVLDNDNAPTGAFGKET   DLLLDDSLVSIFGRRRLKRFSMVVQDGIVKA   LNVERDFGTGLTCSLSVPLGY   LVLHVQAIDADAGDNARLEYRLAGVGHDFP   FTINNGTGWISVAAELDRECVFYSGVEAR   DHGTFALTASASVSVTALDVNDNNPTTTQPE   YTVRLNEDAAVGTSVVTVSAVDDAHSVITY   QITSGNTRNFFSITSQSGGGLVSLAPLDVKLE   RQYVLAVTASDGTRQDTAQIVVNVTDANTH   RPVFQSSHVTVNVNEDRPAGTTVVLISATDEATTCATTER   LTVRANTAGDTRAGTTVVLISATDEATTCATTCATTCATTCATTCATTCATTCATTCATTCATT					1		TD A CYTHADD VI EALDI EDLAIDUUGID
421 1771 A 3409 355 1326 ADSNLESCWQELGLGPWGGDWRVEQVGAS ASLRFPREVCSIRFLFTAVSLLSLFLSAFWLGL LYLVSPLENEPKEMLTLSCHERVRSQGQL QQLQAELDKLHKEVSTVRAANSERVAKLVF QRLNEDFVRRYDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPFVNLEPHYFP GNCWAFEGDQGQVVIQLPGRVQLSDITLQHP PPSVBHTGGANSAPRDFAVFFLLSFTHQGLQ VYDETEVSLGKFTFDVEKSEIQTFHLQNDPN AFPKVKIQLLSNWGHPRFTCLYRVRAHGVRT SEGAEGSAQGPH FEDAPPSIGALVYFKRP*ATTGSDPGPKRGMN YLVSCSMRSPESGKGEPGTARDYTPMGRPPP PYPSVSPGPLPGSLAIAPHSPEPHPWEQQPPRG QARSPFGGWLGSATRVRRPHNHP/RGHHISP VDTAGAPASPOPDVCE ADAQAIYSSVGPAVSLRQRQQDGAVKESGR/ RGGVRSFRAAAAMAPIKVGDAIPAVEVFGG EPONKVNLAELFKGKKQVLFGVPGAFTPGCS KTHLPGFVCQAEALKAKGVQVVACLSVNDA FVTGEWGRAHKAEGKVLLADPTGAFGKET DLLLDDSLVSIFGRRRLKRFSMVVQDIVKA LNVEPDGTGLTCSLAPNIISQL  424 1774 A 3421 4 7688 RQVTRVGTRVLGSTTAAVFLSVEDDNDNAPQ FSEKRYVVQVREDVTPGAPVLRVTASDRDKG SNAVVHYSINSGNARGGFYLDAQTGALDVV SPLDYETTKEYTLRVRAQDGRPPLSNVSGL VTVQVLDNDNAPIFVSTFPGAVTVLSSYPLGY LVLHVQAIDADAGDNARLEVRLAGGGHDFP FTINNGTGWISVAAELDREVDFYSFGVEAR DHGTPALTASASVSVTALDVNNNPITTQPE YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNFSITSQSGGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVVEDRAGTITVLIATDE			1		l		TRAUKHYPRALFYDLEFTYIDOIR
421 1771 A 3409 355 1326 ADSNIESCWOELGLGPWGGDWRVEQVGAS ASLREPREVCSIRELITAVSLLSLFLSAFWLGL LYLVSPLENEPKEMLTLSEYHERVRSQGQL QQLQAELDKLHKEVSTVRANSERVAKLVF QRLNEDFVRKPDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPPTVILEPHYPP GNCWAFEGDQGQVIQLPGRVQLSDITLQHP PFSVEHTGGANSAPRDFAVFFLLSFTHQGLQ VYDETEVSLGKFTDVEKSEIQTFHLQNDPPA AFPKVKIQILSNWGHPRFTCLYRVRAHGVRT SEGAEGSAQGPH  422 1772 A 3412 2 421 EFDAQFSIGALVVFKRP*ATTGSDFGPKRGMN YLVSCSMRSPESGKGEPGTARDYTPMGRPPP PVPSVSPGPLPGSLAIAPHSPEPHPWEQQPPRG QARSPPGGWLGSATRVRRPHNHP/RGH/HSP VDTAGAPASPOPDVCE DAQRAIYSSVGAVELRQRQQDGAVKESGR RGGVRSFRAAAAMAPIKVGDAPAVEVEG EPONKVNLAELFKGKKQVLFGVPGAFTPGCS KTHLPGFVQAEALKAKGVQVVACLSVNDA FVTGEWGRAHKAEGKVRLLADPTGAFGKET DLLLDDSLVSIFGNRRLKRFSMVVQDGIVKA LNVEPDCTIGLTSLAPHISIQL  424 1774 A 3421 4 7688 RQVTRVGTRVLGSTTAAVFLSVEDDNDNAPQ FSEKRYVVQVEQDGAPAVELEDDNDNAPQ FSEKRYVVQVEQDGRPLSNVSGL VTVQVLDNDNAPIFVSTPPQATVLESVPLGY LVLHVQAIDADAGDNARLEVRLAGGGPPF FTINNGTGWISVAAELDREVDFYSFGVEAR DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDRAHSVITY QITSGNTRNFSITSQSGGLVSLAPLDFYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDERAGTITVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA	420	1770	A	3408	1010	685	RRLSFFF*IWSSVLVIQARVQWRDEGSFQIEI
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ASLRFPREVCSIRFLETAVSLLSLFLSAFWLGL LYLVSPLENEPKEMLTLSEYHERVRSQOQL QQLQAELDKLHKEVSTVRAANSERVAKLVF QRLNEDFVRKPDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPPTVILEPHPP GNCWAFEGDQGQVVIQLPGRVQLSDITLQHP PPSVEHTGGANSAPRDFAVFFLLSFTHQGLQ VYDETEVSLGFTDVEKSEIQTFHLQNDPA AFPKVKIQILSNWGHPRFTCLYRVRAHGVRT SEGAEGSAQGPH 422 1772 A 3412 2 421 EFDAQPSIGALVVFKRP*ATTGSDFGPKRGMN YLVSCSMRSPESGKGEPGTARDYTPMGRPPP PVFSVSSPGPLPGSLALAHPSPEPHPWEQQPPRG QARSPPGGWLGSAT/RVRRPINHP/RGH/HSP VDTAGAPASPQDVCE  DAQRAIYSSVGPAVSLRQRQQDGAVKESGRV RGGVRSFSRAAAAMAPIKVGDAJPAAVEVFEG EPGNKVNLAELFKGKKGVLFGVPGAFTPGCS KTHLPGFVEQAEALKAGVQVVACLSVNDA FVTGEWGRAHKAGGKVRLLADPTGAFGKET DLLLDDSLVSIFGNRRLKRFSMVVQDGIVKA LNVEPDGTGLTCSLAAFNISQL RQVTRVGTKVLGSTTAAVFLSVEDDNDNAPQ FSEKRYVVQVREDVTPGAPVLRVTASDRDKG SNAVVHYSIMSGNARGGFYLDAGTGALDV SPLDYETTKEYTLRVRAQDGGRPPLSNVSGL VTVQVLDNDNAPIFVSTPFQATVLESVPLGY LVHVQAIDADAGDNARLEYRLAGVGHDFP FTINNGTGWISVAAELDREEVDFYSFGVEAR DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDDRAHSVTTQA RQVYLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRAGTTVVLISATDE DTGFNARTITYFMEDSPOFRIDADTGAVVTQA	ı	l l		1	1		GVNHCAQPRGHFH
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VTVQVLDINDNAPIFVSTPFQATVLESVPLGY LVLHVQAIDADAGDNARLEYRLAGVGHDFP FTINNGTGWISVAAELDREEVDFYSFGVEAR DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNRFSITSQSGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA	}		1		1		SNAVVHYSIMSGNAKGQFYLDAQIGALDVV
LVLHVQAIDADAGDNARLEYRLAGVGHDFP FTINNGTGWISVAAELDREEVDFYSFGVEAR DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNRFSITSQSGGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA	1	Ì					SPLDYETTKEYTLRVRAQDGGRPPLSNVSGL
FTINNGTGWISVAAELDREEVDFYSFGVEAR DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNRFSITSQSGGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA	1				ľ		VTVQVLDINDNAPIFVSTPFQATVLESVPLGT
DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNRFSITSQSGGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA				1			LVLHVQAIDADAGDNARLEYRLAGVGHDFP
DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNRFSITSQSGGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA	[	1					FTINNGTGWISVAAELDREEVDFYSFGVEAR
YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNRFSITSQSGGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA	1		Ì			1	DHGTPALTASASVSVTALDVNDNNPTFTQPE
QITSGNTRNRFSITSQSGGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA			l l	1			YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY
RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA			1				OITSGNTRNRFSITSOSGGGLVSLALPLDYKLE
RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPOFRIDADTGAVTTQA	1		i				ROYVLAVTASDGTRODTAQIVVNVTDANTH
DTGENARITYFMEDSIPOFRIDADTGAVTTQA			- 1		1		RPVFOSSHYTVNVNEDRPAGTTVVLISATDE
EL DYPDOVSYTI.ATTARDNGIPOKSDTTYLEI	1	1	i				DTGENARITYFMEDSIPOFRIDADTGAVTTOA
	1				1	1	ELDYEDQVSYTLAITARDNGIPQKSDTTYLEI
LVNDVNDNAPQFLRDSYQGSVYEDVPPFTSV							LANDANDA POET R DSVOGSVYEDVPPETSV
LQISATDRDSGLNGRVFYTFQGGDDGDGDFI				1	1		I OIS A TOPOS GI MOR VEYTE OGGODGOGDEI
LQISATDRDSGLINGKVF11FQGGDDGDST1							LAISVIDVOSOFIACKAL I ILAGOODOOPIT

						(A Al-in-O-Ordaina
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
l .		1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		Ì		1		Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	]	residue of	sequence	/=possible nucleotide deletion, \=possible
l l	1	1	}	peptide	1	/-possible flucteonide deterion, / possible
1	1	1	Ì	sequence		nucleotide insertion
						VESTSGIVRTLRRLDRENVAQYVLRAYAVDK
1	ľ			1		GMPPARTPMEVTVTVLDVNDNPPVFEQDEFD
	Į.	}	1	1	{	VFVEENSPIGLAVARVTATDPDEGTNAQIMY
	į					QIVEGNIPEVFQLDIFSGELTALVDLDYEDRPE
	ì	l		1		YVLVIQATSAPLVSRATVHVRLLDRNDNPPV
ı			1			LGNFEILFNNYVTNRSSSFPGGAIGRVPAHDP
	1	}		1		DISDSLTYSFERGNELSLVLLNASTGELKLSR
1		1				ALDNNRPLEAIMSVLVSDGVHSVTAQCALRV
	1	1	1			TITTDEMLTHSITLRLEDMSPERFLSPLLGLFIQ
1		1	1	ł		AVAATLATPPDHVVVFNVQRDTDAPGGHILN
ļ	1		1	1		AVAAILAIPPDHVVVPNVQRDIDAI GGIIEN
						VSLSVGQPPGPGGGPPFLPSEDLQERLYLNRS
	1	1		ļ		LLTAISAQRVLPFDDNICLREPCENYMRCVSV
1				1		LRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGF
	1		1	1		TGDYCETEVDLCYSRPCGPHGRCRSREGGYT
1	1	1	1			CLCRDGYTGEHCEVSARSGRCTPGVCKNGGT
		1	1			CVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP
	1	1				AHSFITFRGLRQRFHFTLALSFATKERDGLLL
1			1	1		YNGRFNEKHDFVALEVIQEQVQLTFSAGEST
-	1	1	1			TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG
- 1		İ	ì			QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS
		1			-	VLGNYSCAA\QGTQGGSKKSLDLTGPLLLGG
l	-		ł	1		VPDLPESFPVRMRQFVGCMRNLQVDSRHIDM
ļ	)	1	1			ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC
İ			1	}		ADFIANNOI VPGCPARRIVCDSRICHNOOTE
İ	1	1	1			VNQWDAFSCECPLGFGGKSCAQEMANPQHF
			1	Į.	1	LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD
1	1	1	1	1		GVLLQAITRGRSTITLQLREGHVMLSVEGTGL
	l l	İ	1	1		QASSLRLEPGRANDGDWHHAQLALGAIGGP
1	1	l				GHAILSFDYGQQRAEGNLGPRLHGLHLSNITV
	ł	1		1		GGIPGPAGGVARGFRGCLQGVRVSDTPEGVN
- {	1	1		[	!	SLDPSHGESINVEQGCSLPDPCDSNPCPANSY
	1	1	ļ	1	į	CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC
	1					EHQSVCTRKPSAPHGYTCECPPNYLGPYCET
1	1	1	j	}		RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC
- 1	[		İ			NKTSGECHCKENHYRPPGSPTCLLCDCYPTG
ļ						SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF
ļ			1			SUSKYCDFEDOQCI CKI GYIGKQCDKODIWI
1						AEVITINGCEVNYDSCPRAIEAGIWWPRTRFG
		1				LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF
	1	1			1	NCTSITFSELKGFAERLQRNESGLDSGRSQQL
ł					1	ALLLRNATQHTAGYFGSDVKVAYQLATRLL
		1				AHESTQRGFGLSATQDVHFTENLLRVGSALL
	1		ļ	1		DTANKRHWELIQQTEGGTAWLLQHYEAYAS
		1	ĺ	1	1	ALAONMRHTYLSPFTIVTPNIVISVVRLDKGN
		- [				FAGAKLPRYEALRGEOPPDLETTVILPESVFR
1		1				FTPPVVRPAGPGEAOEPEELARRORRHPELSQ
		i				GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK
1		- (				RPIINTPVVSISVHDDEELLPRALDKPVTVQFR
1						LLETEERTKPICVFWNHSILVSGTGGWSARGC
	1			1		EVVFRNESHVSCQCNHMTSFAVLMDVSRRE
1						EVVEKNESHVSCQCHMMISEAVLIVIDVSKC
1	1	1	1			NGEILPLKTLTYVALGVTLAALLLTFFFLTLL
		1				RILRSNQHGIRRNLTAALGLAQLVFLLGINQA
	1	1				DLPFACTVIAILLHFLYLCTFSWALLEALHLY
		1				RALTEVRDVNTGPMRFYYMLGWGVPAFITG
	ļ	1				LAVGLDPEGYGNPDFCWLSIYDTLIWSFAGP
	1					VAFAVSMSVFLYILAARASCAAQRQGFEKKG
						PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL
	}	}		}		FHYLFATCNCIQGPFIFLSYVVLSKEVRKALK
ĺ		1				LACSRKPSPDPALTTKSTLTSSYNCPSPYADG
						LACSKAPSPURALITASILISSINCISITADO
				1		RLYQPYGDSAGSLHSTSRSGKSQPSYIPFLLR
						EESALNPG\QGPPGLGGIPGR/LCFLGRFKDQQ
						H\DS*TRDFDSDLSLEDDQSGSYASTHSSDSEE
L						

SEQ ID Men look of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No. of No.							Amino acid sequence (A=Alanine C=Cysteine,
NO: of uncertainty of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of the propriet sequence of	SEO ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Atalinic C-Cysteme,
in mucleotide location (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974) sequence (1974)			hod	ID NO:	beginning		D=Aspartic Acid, E=Olitianic Acid,
sequence    Sequence				in	nucleotide		F=Phenylalanine, G=Glycille, II=Institution,
Wence   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914				USSN	location		I=Isoleucine, K=Lysine, L=Leucine,
perice    14			\ \			to last amino	M=Methionine, N=Asparagine, P=Profine,
amino seid residue of peptide sequence peptide sequence peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide se	•	dence				acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of popular countries and proposed proposed popular countries and proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed proposed pr	uence			314			T=Threonine, V=Valine, W=Tryptophan,
pepilde meleotide deletion, "possible meleotide insertion encorotide insertion encorotide insertion encorotide insertion encorotide insertion encorotide insertion encorotide insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic insertion encorotic encorotic insertion encorotic insertion encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic encorotic en			1	1	******		Y=Tyrosine, X=Unknown, *=Stop codon,
nucleotide ilsertion    Sequence   HEEEEEEAAFPGGGWBSLLGFGAERLPLHS		Į.	1	1		sequence	/=possible nucleotide deletion, \=possible
### FEEEEEEAAPGGGWBSLLGFGAERLPH.H ### TRKDGGPGFGAPAPPGGGTTARESSGNGAP EERLRENGBALSEGSLGPLFGSSAQPHKGIL KKKCLPTISKKSSLLRIPLEQCTGSSRGSASS GSRGGPPSRPPRQSLGEQLRGMMPIAMSIKA GTVPEDSSGSFLFFNTHH #### GEPAVQSCDCGTGRSCPWLLVAPGLLSSSSS GASGGPSRPPRQSLGEQLRGMMPIAMSIKA GTVPEDSSGSFLFFNTHH #### GEPAVQSCDCGTGRSCPWLLVAPGLLSSSSS GASCLPGDPLGARRATRAHSPYPGPPSLPA AGTAVRELDPG-SATIPSQGNSGPGSL GASCLPGDPLGARRATRAHSPYPGPPSLPA AGTAVRELDPG-SATIPSQMSARP SLGCLPSWASPGTEHEPPGQGGPGPS-DLCSV- KREPGRPWAGMVILHUSAADPARAPGFDS NUQSALQPATICSEPAAVYSPFGLWGA**P PGYPOHSLPG-TAPADR-PAGIKDRVYSNS1 YELLBUGQRGTGVLF-TAPADR-PAGIKDRVYSNS1 YELLBUGQRGTGVLF-TAPADR-PAGIKDRVYSNS1 YELLBUGQRGTGVLF-TAPADR-PAGIKDRVYSNS1 YELLBUGQRGTGVLF-TAPADR-PAGIKDRVYSNS1 YELLBUGQRGTGVLF-TAPADR-PAGIKDRVYSNS1 YELLBUGQRGTGVLF-TAPADR-PAGIKDRVYSNS1 YELLBUGQRGTGVLF-TAPADR-PASSGDPR SQSLHCLSPRQPHYLQALRA-VAGGCOPYN- SVGRSGAGONR-GGGL-GRUP-GUGA-PASSGDPR-PAR-PAR-PAR-PAR-PAR-PAR-PAR-PAR-PAR-P			}	1			nucleotide insertion
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residur of peptide peptide per per per per per per per per per pe			l	914			T-Thronine V=Valine W=Tryptophan.
peptide sequence    Image: Committee   Image: Committee							V-Tyrosine Y=Unknown *=Stop codon.
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LETLAEIDER, VSP.LEAKAEN, HIKGAHT YU.  LILQERVLINNVYHLLGEDEPRYRHYAAASL.  IRLYPKLFYKCDQQADPVVAVARDQSSYY.  KLIMHETQPPSIFESVSTITRYRQTYNLLBSTID  VTMENNLSRVIAAVSHELITSTRALTFGCC.  ALCLLSTAFPCVISILGWHCGYPSLASDESR  KSCTVGMATMILTILISSAWFFLDLSAHDDAL  LIAGMILAASAPKSLIRSSWASEAPAATK  QEEVWPALGDRALVPMVEQLFSHLLKVING  AHVLDDVAPGRAIKAALPSLINPSLSPIRRK  GKEKEPGROASVILSPKKGSEASAASRQSTIN  GRYTTSKSSSLGSYYHPSYKLHDVIKATHA  NYXYTI.DLONSTEKFGGFLRSALDVISQUELL  ATIQDIGCCVEELGYLKSCFSREPMATVC  VQQLLKTLFGTNLASQFDGLSSNPSKSQRA  QRIGSSSVRPGLVHYCFMAPTHTQALADA  SLENMYQAEQENDTSGWFDVLQKVSTGKAKLK  ATITTTCVOLQKQVIDLLAQLVQLRVNYCLL  DSTYTTITTCVOLQKQVIDLLAQLVQLRVNYCLL  DSTYTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ł	(	1	i	Į.		ADCIPLLRKTLKDESSVICKLACIA VRICEVIII
LKLQERVLNNVVIILLGDEDPRVRITAVAASL RLVPKLFYKCOQQADPVAVARQOSSVYL KLLMHETOPPSHESVSTITRIYAGYNLLPSTID VTMENNLSRVIAAVSHELITSTTRALTFGCCE ALCLISTAFPVCIWSLGWHCGVPPLSASDESR KSCTVGMATMILTLISSAWFIDLISAHQDAL ILAGNILAASAPKSLRSSWASEEBANPAATK QEEVWPALGDRALVPMVEGSHLKVINIC QEEVWPALGDRALVPMVEGSHLKVINIC AHVLDDVAPOPARKALPSLTNPPSLSPIRK GKEKPDGGASVPLSPKKGSEASAASROSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDQNSTEKFGGFLSSAMASROSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDQNSTEKFGGFLSSMPSKSCGRA QRLGSSSVRPGLYHYCTMAPYTHFTOALADA SLRNMVQAEQENDTSGWFDVLQKVSTOLKT NLTSYTKNRADKNAHHWIRLFEPLVIKALKQ YTTTTCVQLQKQVLDLAQLVQLRVNVCLL DSDQVFIGFVLKQFEYEWGGFRESAHIPNEF FLVLLSYERYHSKQIIGPKIQLCDGIMASGR KAVTHAPALQHVHDLFYLLQTNRADAGKE LETOKEVVVSMLLRLIQYHQVLEMFILVQQ CHKENEDKWKRLSRQADILLEMLKQQMHI DSHBALGVLNTLFELLAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWSGLALRAVLISQSTED IVJSRIQBLSSSPYLISCTVINRLRXDGSTSTLE BHSGGQINLDEFTSFRILQLVGILLBINS GMFRITAAATRLFRSDGCGGSFYTLDSLNIK ARSMITTHPALVLLWCQLLLVHITDYRWW AEVQOTPKRIRSJSKLLSPGNGGEEDSITSTILE BHSGGQRATLTYVQELGTTLHVCLHFNS GMFRITAAATRLFRSDGCGGSFYTLDSLNIK ARSMITTHPALVLLWCQLLLVHITDYRWW AEVQOTPKRIRSLSSKLLSPGNGGEEDSITHDSNIK ARSMITTHPALVLLWCQLLLVHITDYRWW AEVQOTPKRIRSLSSKLLSPGNGGEEDSITHDSNIK ARSMITTHPALVLLWCQLLLLVHITDYRWW AEVQOTPKRIRSLSSKLLSPGNGGEEDSITHDSNIK ARSMITTHPALVLLWCQLLLLVHITDYRWW AEVQOTPKRIRSLSSKLLSPGNGGEEDSITHDSNIKS SPPVSSHPLDGDGHVSLETVSPDKDWYWLLWS SQCWTRSDSALLIFADLVYDRLLCTPFRVLARMYDIL ACRAVEMILAAMLQSSMAQLPMEELNIQEY LQSSGLAQRIFQRYSLLDGFLSTRICDLSHRIPS ASGIFIQALGSRCENLSTYTMLKKTLCLEGI HLSQGGAVLTLYDRLLCTPFRVLARMYDIL ACRAVEMILAAMLQSSMAQLPMEELNIQEY LQSSGLAQRIFQRYSLLDGFLGSRYALLSALL SWHALHEQIPISLLQCLCCLALQLPGL WSWSSTEPUSLLQCCCLALQLPGL WSWSSTEPUSLLQCCLALQLPGL WSWSSTEPUSLLQGALLGALLVARGYPGFLARAP AREVILARVSGTVQQLAVSHTPOPTLYARMYDIL GULSPERRTNTTWKLSEEGEEVDPNTQNFKYFRIY TAACEMVABMVESLQSVLALGHERNSGVPA FLTFLIRMILISLALPLVSYRLAQURG GESPPEDTERTQNNVLAVQAGTGLVSAMT VPVAGNPAVSCLGQDPRNRJRLALDTRFGRK LSIRGGVPGEIQAMVSKERNIATHHLYQAWD DDRESS PATIGGISIGANSCENLATHHLYQAWD DDRESS PATIGALISHELLGNPEREIGSFY			Ì				SLCSSSYSELGLQLIIDVLILKNSSI WEVKIEL
IRL VPKLFYKCDQQADPVAVARQUSSYYL KLIMHETQPPSIFSSYSTITRYRGYNLLPSITD VTMENNI.SRVIAANSHELITSTIRALTFGCCE ALCLISTAFPVCIWSLGWHGPLSAFDESR KSCTVGMATMILTLISSAWFFLDLSAHQDAL ILAGNILAASARKSLRSSWAFPLDLSAHQDAL ILAGNILAASARKSLRSSWAFPLDLSAHQDAL ILAGNILAASARKSLRSSWAFPLDLSAHQDAL ILAGNILAASARKSLRSSWAFPLDLSAHQDAL ILAGNILAASARKSLRSSWAFPLDLSAHQDAL ANVLDDVAPGPARKAAPSILTSPPSLSPIRKK GKEKEPGEGASVFLSPYKLGSEASAASROSDTS GPVTTSKSSSLGSFYHLPSYLKIDAVIAGHAL ANVLYTLDLQNSTEKFGGFLRSALDVLSQUEL ATLQDIGKCVEELIGYIKSCTSREPMMATVC VQQLKTLRGTNLASQPDGLSSNFSKSQGRA QRLGSSSWAFGLYHYCFMAPYTHIFTQALDA SLRNMVQAEQENDTISGWFDVLQKVSTQLKT NLTSVTKORADKNAHINHIBLFEPLVIKALKQ YTTTTCVQLQKQVIDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYEVGQFRESEAHINFF FLVLLSYERFYHSKQUIGPKIQLCDGIMASGR KAVHAIPALQPIVHDLFVLRGTNKADAGKE LETOKEVVSWALLRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADILLPMLAKQOMHI DSHHALGVLINTLEELAPSERPVDMLIRSMF TPHTMASVSTVQLWISGILALRVLISQSTED IVLSRIGELSFYLJSCTVINTRIRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELIMCLHICHHEKS GMFRRITAAATRLFSDGCGGSFYTLJSCLIMCHHEKS GMFRRITAAATRLFSDGCGGSFYTLJSCLIMCHHEKS GMFRRITAAATRLFSDGCGGSFYTLJSLINLR ARSMITTHAALVLLWCQILLLYNHTDYRWW AEVQQTIKKRISSTKLLISPQMSGEEEDDILA AKLGMCNEUTVRIGALLIFCDYVCQNILDSE HLTWLIVNHODLISSHEEPVQDFISAVHRNS AASGLFIQAIGSRCERLSTYTMLKSTICLEGI HLSQSGAVLTLYDRLLCTPFYVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELINIQEY LQSSGLAQRIGRUTSJLLDFFLSTMQDSLSSS PYVSSHLDGDGHVSLETVSPDKDWYHLVK SQCWTRSDSALLEGAELVNRIPAEDMMAPM MNSEFNLSLLAPCLSLGMSEISGGKSALFEA AREYTLARVSGTVQDLYJNLYRGVPLAVRGVPLAVRG GESPPEDTERSUNVLAVAGLIFLARAQY LVVYSKLPSHLHPPERKERDIVFFVVATLEAL SWILLBEQIPSLDLQAGLDCCLAJQPGL WSVYSSTEFVTHACSTLYQFLUTGENGVPL TAACEMVAEMVPSLQSVLALGHERNSGVPA FLTTLRINIIGSLAALPLVSYTRYPPLVWKLG WSVRSCTPOTHACSLYCVYFTELSAVAQPG EGSPEEDTERTQINVLAVQALIGLALLYQAND DERSIDSTGEGGORMILLANDTRYGEV ATHUR WSVRSTFFTHACSLICHYCVYTLERGVPA FLTTLRINIIGSLAALPLVSYTRYPPLVWKLG WSPKPGGFGTAFFEDVEFLQKEKVYRTEFIYF INTLGWTSRTTGFETWATLLGGLVTQFLVME GESPPEEDTERTQINVLAVQALIGLALANDTRYGEVR LUTGGWTSDSALLGABLUNNFLAALDTRFGRW AUGESPPEEDTERTQINVLAVQALISAMT VPYAGNPAVSCLEQOPRINGLAALDTRFGRW DERSIDSTATLIGGLINGHELIGSNU			1		Ì	1	LETLAEIDFRLVSFLEAKAENLAKOAAATTOL
KLIMHETOPPSHESVSTTIRALTFOCCE ALCLISTAPPVCIWSLGWHCGVPPLASADESR KSCTVGMATMILTLISSAWPTDLISAHQDAL ILAGNILAASAPKSLRSSWASEERANPAATK QEEVVPALGDRALYPMYEQLISHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEGASVPLSPKKGSEASAASROSDTS GPVTTSKSSLGSTYRLPSTLKHDYLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQHEL ATLQDIGKCVEELIGYLKSCTSREPMMATVC VQOLKTLFGTNLASQFDGLSSNPSKSGRA QRLGSSSVRPGLTYLCTMAYTHIFTQALADA SLRNMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVTKNRADKNAHIPHIRLFEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLUQULKVYCLL DSDQVFIGFVLKQFYEYEVGGYESSALIPNIFF FLYLLSYERYHSKQHGPKHQULCDGIMASGR KAVTHAPALQPVPHDLFVLKGTNRADAGKE LETOKEVVVSMLIRLIQYHQVLEMFILVQQ CHKENEDK WRRLSRQLDHLBMALARQOMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILALIRVLSQSTED IVLSRIQELSSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPETFSRFLLQUGHLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLEIDIVT KQLKVEMSEQQHTFYCQELGTLLMCLEIDIVT KQLKVEMSEQQHTFYCQELGTLLMCLEIDIVT KQLKVEMSEQQHTFYCQELGTLLMCLEIDIVT KQLKVEMSEQGISTYLDLSNIRL ARSWITHPALVLLWCQULLLVNHTDYRNW APVQQTFKRISLSSTKLLSPQMSGEESDDLA AKLGMCNRETWRGALLIFCDYVCQNLHDSE HLTWLLNHHDQDLISLSHEPPVODPISAVHRNS AASGLFIQAIOSRCENLSTPTLKKTLQCUCGH HLSQSGAVLTLYVDRLLCTFFRULXGWHDK ARSWITHPALVLLWCQULLTYPHTULKNTLQCLGG HLSQSGAVLTLYVDRLLCTFFRULXGMYBL ACRAVEMLLAANLQSSMAQLPMEELINDICKY LQSSGALARIGNRALSTRIPAEDMMATM MSEFNLSLLAPCLSLGMSEISGGKSALFEA APWSKLNDLGDGHALVSLLEFFRLSTMQDSLSPS PPVSSHLDGDGHVSLETVSPDLWTYVHLVK SQC WTRSDSALLEGABLUKRIPAEDMMATM MSEFNLSLLAPCLSLGMSEISGGKSALFEA APWSKLNDLGDGAALVGSLPTAAYDLL ACRAVEMLLAANLQSSMAQLPMEELINDICKY SQC WTRSDSALLEGABLUKRIPAEDMMATM MSEFNLSLLAPCLSLGMSEISGGKSALFEA APWSKLNDLGDGAALVGSLPTAARAQPL LVVYSKLPSHLHPPEKERDIVKFVVATLEAL SWILHBEIGPISLDLAGALDCCCLALQPGL WSVVSSTEFVTHACSLIVCVFVTALEALAV SQC WTRSDSALLEGABLUKRYVATLEAL SWILHBEIGPISLDLAGALDCCCCLALQPGL WSVVSSTEFVTHACSLIVCVFVTALEALAV UPVSKAPSHLLAPCLSLGMSEISGGKALFER APYWSKLNDLGGDGAALVGSLPTAARAQPI LVVYSKLPSHLLAPCLSLGMSEISGGKALFER PATAGESTOTORPKY TAACEMVERWSCLGQDRINKRENADTH-TURVLU QEESPPEDTERTQINVLAVQAND SPESIPATTGFETWALLGUNTYCRELIKLOFT STATEMENTER STATEMENTER STATEMENTER STATEMENTER STATEMENTER STATEMENTER STATEMENTER STATEMENTER STA							LKLQERVLNNVVIHLLGDEDPRVRHVAAASL
VTMENNISRVIAANSHELITSTITRALINGLES ALCLISTAPPCIWSIG, GWICGYPPLSASDESR KSCTVGMATMILTILISSAWFFLDLSAHDOAL ILAGNILAASAPKSIRSSWASEEANPAATK QEEWPALGDRALVPMYEQLESHLIKVINIC AHVLDDVAPPGARKAAPSITNPPSLSPIRKK GKEKEPOEGASVPLSPKKGSEASAASROSDTS GPVTTSKSSLGSFYHLPSYLTNPPSLSPIRKK GKEKEPOEGASVPLSPKKGSEASAASROSDTS GPVTTSKSSLGSFYHLPSYLTNPPSLSPIRKK GKEKEPOEGASVPLSPKKGSEASAASROSDTS GPVTTSKSSLGSFYHLPSYLTNPSLSPIRKA GKEKEPOEGASVPLSPKKGSEASAASROSDTS GPVTTSKSSLGSFYHLPSYLDVLKANDLOLL ATLQDIGKCVEELIGVIKKSFERPMATVC VQLLKTLEGTNILASQFDGLSSNPSKSGGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA SLRNMVQAEGENDISGWPTVLQKVSTQLKT NLTSYTKNRADKNAHNHIBLEPELVIKALKQ YTTTTTCVQLQKQVILDLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYTEVGGFRESEAHINIFF FLVLLSYERYHSKOQIGPRIJOLCOGIMASGR KAVHAIPALQPIVHDLFVLRGTNKADAGKE LETOKEVVSMULRILQPIQVLLEMFILVLQQ CHIKENEDKWKILSRQIADILLPMLAKQOMHI DSHHALGVLINTLEPLAPSERPYDMLLSSMFB VTPNTMASVSTVQLWISGILALIRVLISQSTED IVLSRQBLSSFYLISCTVINTRIRDGDSTSTLE BESGKORNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELITMCLHIFIKS GMFRITAAATILFSDGCGGSFYTLJACLHITIKS GMFRITAAATILFSDGCGGSFYTLJACLHITIKS GMFRITAAATILFSDGCGGSFYTLJACLHITIKS GMFRITAAATILFSDGCGGSFYTLJACLHITIKS GMFRITAAATILFSDGCGGSFYTLJACLHITIKS ARSMITTHPALVLLWOGILLIVHTIDTRWW AEVQQTFKRISLSSTKLLSPQMSGEEEDSDLA AKLGMCNEEIVRRGALLIFCDTYCCONLINDSE HLTWLIVNHOJDLISSLEFFYOPDISAVHRNS AASGLFIQAIGSRCENLSTPTMLKSTCQLEGI HLSQSGAVATILYDRLLCTPFRVLARMVDLL ACRRVEMLLAANLQSSMAQLPMEELINIQEY LQSSGLAQRINGRYSLLDFFRLSTMQDSLSFS PPVSSHPLDGDGHVSLETVSPDKDWYHLVK SQCWTRSDSALLEGAELVNRIPAEDMMAFM MISEFRI SLLAPCLSLGMSEISGGKSALFEA AREVTLARVSGTVOQLPAHYQFELPAFP AYWSKLNDLFGDAALYQSLPTLARMQSYPA FLTTLRINIISKAALPLYNSTRIPPLVWATLEAL SWILHBGDFISLDLAGALDCCCLALQPGL WSVYSSTFFVHACSTLYQFVTATLEAL SWILHBGDFISLDLAGALDCCCLALQPGL WSVYSSTFFVHACSTLYGVTATLEAL SWILHBGDFISLALAQFULYNTATLAGVTA TAACEMVAEMYESLOSVIALGHERNSGVPA FLTTLRINIISKAALPLYNSTRYPPLVWALG WSPKPGGFGTAFFEDVEFLQEKVFVTATLEAL SWILHBGDFISLALLACLYSTREFIYFLUNKLIG WSPKPGGFGTAFFEDVEFLQEKVFVTATLEAL SWILHBGDFISLALALPLYNSTRYPPLVWALG WSPKPGGFGTAFFEDVEFLQEKVFVTATLEAL SWILHBGDFISLALALPLYNSTRYPPPLVWALG WSPKPGGFGTAFFEDVEFLQEKVFTATLAGAUTPAG	1	}			1		IRLVPKLFYKCDQGQADPVVAVARDQSSV1L
ALCILISTAPPOCIUSACHICOVPICASDESS KSCTVGMATMITILISAS ANFIDLSAHQDAL ILAGNILAASAPKSLRSSWASEEEANPAATK OEEVWPALAGDRALVPMVOQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRKK GKEKEPGEQASVPLSPKSCASAASROSDTS GPVTTSKSSLGSFYHLFSYLKIHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLODIGKCVEELG VILKSCFSREPMMATVC VQQLLKTLFGTNLASCPDGL SSNSPSKOGRA ORLGSSVSPRGLYHYCFMAPYTHFTQALADA SLRNMVQAEQENDTSGWFDVLQKSTQLKT NLTSVTKNRADKNAIHNIRLFEELVIKALKQ YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVPIGFVLKGFEVIEVGPRESEAIPNIFF FLVILSVERYHSKQIIGPKIIQLCDGIMASGR KAATHAPPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLLRLIQYHOVLEMFILVLQQ CHKENEDK WKRLSRQOLADILPMLAKQOMHI DSHBALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTYQLWISGILALLRVLISGSTED IVLSRIQELSFSPYLISCTVINNLRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGLLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYLDISLINK ARSMITTHPALVLIWCQLLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPOMSGEEDSDLA AKLGMCNREIVRRGALHCDYVCQNLHDSE HLTWILVNHIQDLISLSHEPFVORFANH AASGLFIQAJQSRCCHLSTFYTMLKKTLQLEGI HLSQSGAVLTLYVDRLLCTFFRLACLCLEG HLSQSGAVLTLYVDRLLCTFFRLAGDVSLSPS PPVSSHPLDGGGHVSLETVSPDKDWYVHLVK SQCWTRSDSAALLEGGELVNRIFAEDMARFM MNSEFPLSLLAPCLSLGMSEISGGGKSALFEA AREVTLARNVSCHLOGRAPHOFLDRINGEY LOSSGLAGRHQRITSLLDRFRLSTMGDSLSPS PPVSSHPLDGGAHVSLETVSPDKDWYVHLVK SQCWTRSDSAALLEGGELVNRIFAEDMARFM MNSEFPLSLLAPCLSLGMSEISGGGKSALFEA AREVTLARNVSCHLOGLFGAALTVSLFACHTARDDLLSPN TAACEMYARMYDLLCTFFRLARAQDVL SWHJSTSTEVTHACSLIVAFHAEDMARFM MNSEFPLSLLAPCLSLGMSEISGGGKSALFEA AREVTLARNVSCHLOGLGAGLDCCLALQLPGL WSVVSSTEFVTHACSLIVAFHAEDMARFM MNSEFPLSLLAPCLSLGMSEISGGGKSALFEA AREVTLARNVSCHVORFEREKIVNRIFAEDMARFM MNSEFPLSLLAPCLSLGMSEISGGGKSALFEA AREVTLARNVSCHLOGLFFRLSTMGDSLSPS PPUSSHPLLDGGAHVSLCTVFRUFTRAVAVQPG EQLLSPERRTNTPKAISEEEEEVDFNTQNFKY TAACEMYAEMVSSLQSVLALGHKNNSGVPA FLTFLLRNIISLSARPLLVNSTTRVPPLVWKLG WSVVSSTEFFVTHACSLIVANTAEDMARFM VPYAGNFRAVSCLEQOPRINFLKALLDTRIVARVD PUDDS SPATTGALISHEKELLLONFREELGSMS  PUDDS SPATTGALISHEKELLLONFREELGSMS	1	Ì	}	1	1		KLLMHETQPPSHFSVSTTIRIYRGYNLLPSTID
RSCTVGMATMLTLLSSAWFELDSAHQUAL IILAGNILLASAPKSLRSSWASEEEANPAATK OEFWPALGDRALVPMVPQLFSKILLXVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSLGSFYLLFSYLKJENDVLKATHA NYKVTLDLQNSTEKFGGFIRSALDVLSQILEL ATLQDIGKCVEEIG YLKSCFSREPMATYC VQQLKKTLFGTNLASOPGILSSNPSKSQGRA ORLGSSSVRFGLVHYCFMAPYTHTQALADA SLRNMVQAGEORDTSG WPDVLQKVSTQLKT NLTSVTKNRADKANIHNHRJEP-UKALKQ YTTTTCVQLOKQVLDLLAQLVQLRVNYCLL DSQVFIGFVLKQFEVEEVGGPRESAIIPNIFF FLVLLSYERYHSKQIIGGRIQLCDGIMASGG KAVTHAIPALQPIVHDLFVLRGTNADAGKE LETOKEVVVSMLLRLIQYHQVLEMFILVQQ CKKENEDEKWKRLSRQIADIILPMLAKQMHI DSHEALGVLNTLFEILAPSSLRVDMLIRSMF VTPNTMASVSTVQLWSGSFED VLSRIQELSFSPYLISCTVINRLRDGSTSTL EHSEGKQKKIN.PEETFSRFLQLVGILLEDIVT KQLKVEMSEQQHTFVCQELGTLLACHLHFKS GMFRITAAATRIFRSDGCGGSFYTLDSLNLR ARSMITHPALVILWCQULLVNHTDYRWW AEVQQTPKRHSLSTKLLSPQMSGEEEDSDLA AKLGMCNREIVERGGALIFCDYVCQNLHDSE HLTWLIVNHQDLISLSIEPFVQDFISAVHRNS AASGLFQAQSRCENLSSTYLLKKLTQLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDLL CARRYBELLAPLCISGMAQLMEEINRIQES PPVSSHPLDGGOHSTLTMKKKTQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDLL ACRAVEMLLANNLQSSMAQLMEEINRIQES SPPVSSHPLDGGOHSTLTWRKKTQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDLL SQCWTRSDSALLEGAELVNRPAEDMMAPM MNSEFNLSLLAPCLSIGMSEISGGKSALFEA AREVILARNGSTYQQLFAHHVFQPELPAEP AAYWSKLNDLFGBAALYQSLFTLARALAQY ULVVSKLPADGGOHSLLARALAQLG VLVVSKLPATERANINGSLSSF PVSSHPLDGGOHSLETVSPDKDMYYHLVK SQCWTRSDSALLEGAELVNRPAEDMMAPM MNSEFNLSLLAPCLSIGMSEISGGKSALFEA AREVILARNGSTYQQLFAHHVFQPELPAEP AAYWSKLNDLFGBAALYQSLFTVPLKHG ULVSSKLPSTEVTHACSLITYCHFILEANAVQDG EQLLSPERRTNTYKALSEEEEEVPDFINNFKY TAACEMVAEMSENGSVAALGHKRNSGVPA FLITLLINNIISLARLPLVNSYTRVPPLVWLIG WSVYSSTEFVTHACSLITYCHFILEANAVQDG EQLLSPERRTNTYKALSEEEEEVPIFTQNFVLWLIG WSFKSPGGDGGTAFFEIPVEFLQKEVKFEFIY NTTLGWTSSTQPETEWATLLGVLVTQLVLMG WSFKSGOFRAFFEITVEFLQKEVKKEFIY NTTLGWTSSTQPETEWATLLGVLVTQLVLMG UPVSSTSTATTGALISHEKELLLONFREELGSMS PPDASSES PATTGALISHEKELLLONFREELGSMS		1	1			h	VTMENNLSRVIAAVSHELITSTIRALIFGCCE
ILAGNILAASAPKSLRSSWASBELRANPAIN  OEEVWPALGDRALVPMYSQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSSPIRKR GKEKEPGEQASVPLSFKKGSEASAASROSDTS GPYTTSKSSLGSFYHLFSYLKIHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLODIGKCVEELGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNFSKGGRA ORLGSSSVRFGLYHYCFMAPYTHFTQALADA SLRIMVQAEQENDTSGWFDVLQKVSTQLKT NLTSYTKINADKNAIHNIRLFEPLVIKALKQ YTTTTCVQLOKQVLDLLAQLUQLLVNNCLL DSDQVFIGFVLKQFEYEVGGPRESEAIPNIFF FLVLLSVERYFISKQIIGIFKIIQLCDGIMASGR KAVTHAIPALQPIVHIDLFVLRGTTKAAAGGE LETGKEVVYSMLLRLQYHQVLEMFILVLQQ CHKENEDRWKRLSRQLADIILPMAKQOMHI DSHEALGVNTLFEILAFSSLRPVDMLLRSMF VYPNTMASVSTVQLWISGILALRAVLISQSTED IVLSRQELSFSPYLISCTVIRLDGDSTSTLE EHSEGKQKNLPEETFSRFILQLGLLEDIVT KQLKVEMSEQQHTFVCQELGTLLAGLLEDIVT KQLKVEMSEQQHTFVCQELGTLLAGLLHFKS GMFRRTAAATRLFRSDGCGGSFYTLDSLNLR ARSMITHPALVLLWCQLLLVNHTDYRWW AEVQOTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALLHCDYVQNLHDSE HLTWILVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFQAJQSRCENLSTPTMLKKTLQCLGI HLSQSGAVLTLYVORLLCTFRVLARMVQNH ACRRVEMLAANLQSSMAQLPMEELNRIQEY LQSSGLAGRHQRLYSLLDRFRLSTRMQDSLSPS PVSSHPLLDGDGHVSLETVSPDKDMYVHLVK SQCWTRSDSALLEGGELVNRFRALAQV LQSSGLAGRHQRLYSLLDRFRLSTRMQDSLSPS PVSSHPLDGDGHVSLETVSPDKDMYVHLVK SQCWTRSDSALLEGGELVNRFRALAQV LVVSKLPSHLHIPPEKEKDIVKFVVATLEAL SWHLHEQRLSLLAPCLSLGMSEISGGKSALFEA AREVTLARVSGTVQQLPAWHHVFQPELPAEP AAYWSKLNDLFGDALYGSPTLAALAQV LVVVSKLPSHLHIPPEKEKDIVKFVVATLEAL SWHLHEQRLSLDQAGLDCCLALQLPGL WSVVSSTEFVTHACSLTYCHFILBAVAVQPG EQLLSPERRTNITKALSEEEEEVPPLVWLUG WSVVSSTEFVTHACSLTYCHFILBAVAVQPG FQLLSPERRTNITKALSEEEEEVPPLVWLUG WSFKPGGDFGTAFPEPVEFLOEKSVFKEFIY NTLGWTSSRTQFEETWATLLGVLVTQPLVMG QEESPPEEDTERTQINVLAVQLIGHKRNSGVPA FLTFLLRNIISLARLPLVNSYTRYPLVWLIG WSFKPGGDFGTAFPEPVEFLOEKSVFKEFIY NTLGWTSSRTQFEETWATLLGVLVTQPLVMG QEESPPEEDTERTQINVLAVQRICHGEGSMS PVSSTEPTAVSCLLQOFRINFLKALDLTFGRK LSIRGIVSCOEQAMYSKRENIATHLYQAWD PVDSSS PATTGALISHEKELLLONFFEELGGSMS				1	Ì	Į.	ALCLLSTAFPVCIWSLGWHCGVPPLSASDESK
QEEWPALGDRAL VPMVEQLESHLEN VINC AHVLDDVAGPAIKAAL PSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAARGSDTS GPVTTSKSSLGSYHLESYLKLHDVLKATHA NYKVTLDL QNSTEKFGGFLRSAL DVLSQILEL ATLQDIGKCVEEL GYLKSPKEPMAMTVC VQQLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRGL VHYCFMAPYTHTQALADA SLRNMVQAEQENDTSGWTDVLQKVSTQLKT NLTSYTKNRADKNAHNHRIFFTQALADA SLRNMVQAEQENDTSGWTDVLQKVSTQLKT NLTSYTKNRADKNAHNHRIFFTQLVIKALKQ YTTTTCVQLOKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEVIEVGGPRESEAIPNIFF FLVLLSVERYHSKOLIGFRIIQLCDGIMASGR KAYTHAPALQPIVHDLFVLRGTKADAGKE LETQKEVVVSMLLRLIQYHQVLEMFILVLQQ CKENEDE WKRLSRQLADIILPMLAKQOMHI DSHEALGVLNTLFEILAFSSLRVDMLRSMF VTPNTMASVSTVQL WISGLALRVLISQSTED IVLSRIQELSYSPYLISCTVINNLRDGDSTSTLE EISEGKQKIKNIPETFSRFLQLVGILLEDIVT KQLKVEMSEQQHTFVCQELGTLLMCLHHFKS GMFRRTAAATRLFRSDGCGGSFYTLDSLNLR ARSMITHPALVLLWCQLLLVNHTDYRWW AEVQTFKRFLSSTSTLLMCLHHFKS GMFRRTAAATRLFRSDGCGGSFYTLDSLNLR ARSMITHPALVLWCQLLLVNHTDYRWW AEVQTFKRFLSSTSTLJCCUGLLEDIVT KQLKVEMSEQAHTYCQELGTLLACHHFKS GMFRRTAAATRLFRSDGCGGSFYTLDSLNLR ARSMITHPALVLWCQLLLVNHTDYRWW AEVQTFKRFLSSTSTLJCCUGLLEDIVT KQLKVEMSEQAHTYCQELGTLLCHHFKS GMFRRTAATRLFRSDCGGSSFYTLDSLNLR ARSGLFQAQAGSCENLSTFTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDL ACREVEMILAANLQSSMAQLPMEELNRIQES PVSSHPLADGGHONSTTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDL ACREVEMILAANLQSSMAQLPMEELNRIQES SQCWTRSDSALLAFLCSLGMSEISGGKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAPP AAYWSKLNDLFGBAALVQSLFTLARALAQY LVSSKLSTBLAPLCSLGMSEISGGKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAPP AAYWSKLNDLFGBAALVQSLFTLARALAQY UVVVSKLSPHLHIPPEKEKDIVKFVATLEAL SWHLHEQIFLSLDLQAGLDCCLALQLFGL WSVVSSTEFVTHACSLTYCHFILEAVAVQPG EQLLSPERRTNTFKALSEEEEEVPTROPNLYN TAACEMVAEMMESLQSVLALGHKRNSGVPA FLITHLINNIISLARLPLVASYTRVPRIVWLG WSFKPGGDGGTAFFEIPVEFLUWLIG WSFKPGGDGGTAFFEIPVEFLUWLIG WSFKPGGDFTAFFIEVFTLARLLQYVLYLVNLU QEESPPEEDTERTQINVLAVAXGRENIATHLLYQAVD UVVSKLIPSTQPEETWATLLGVLVTTQLVLMG UPDSTS TATTOALISHEKELLLONFFREEKEJ	1		1	i			KSCTVGMATMILTLLSSAWFPLDLSAHQDAL
AHVLDDVAPGPAIKAALPSI.TNPSI.SPIKRG GEKERPEGASVIPJSPKGSEASAASRQSDTS GEVTTSKSSSLGSFYHLPSYLKI.DVLKATHA NYKVTLDLONSTEKFGGFI.RSALDVLSQILEL ATIQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSYRPGLYHVCFMAPYTHFTQALADA SLRNMYQAEQENDTSGWFDVLQKYSTQLK NLTSVTKNRADKNAINHRILFEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEVGGFEESEAIIPNIFF FLVLLSYERYHSKQIIGIPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLLRLQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILHMLAXQQMII DSHEALGVUNTIFELLAPSSLRPVDMILLSSMF VTPNTMASVSTVQLWISGILALRVLISQSTED IVLSRIGGLSFSPYLISCTVINRLRDGDSTSTILE EHSEGKQIKNLPEETFSRFILQLVGILLEDIVT KQLKVEMSEQQHTFVCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSILNIR ARSMITTHPALVLLWCQUILLVHITDYRWW AEVQQTFKRRISLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRGGALLFCDVVCQNLHDSE HTWILIVNHQDLISLSHEPPVQDFFSAVHRNS AASGLFIQAIQSRCENLSTTTMIKKTLQCLEGI HLSQGAVLTLYVDRILLCTFFRVLARMVDIL ACREVENLLAANLQSSMAQLPMEELNRIGEY LQSSGLAQRRIQRLYSLLDFFRTSIMQDSLSPS PPVSHPLDGDCHVSLETVSPDKDWYVHLVK SQCWTRSDSALLBGAELVNIRJREDMNAFM MNSEFINSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDALSGVSALIGHKRNSGVPA FLTPLLRNIISLARLQSVLALGHKRNSGVPA FLTPLLRNIISLARLPLVNSYTRVPPLVWLIG WSVSVSSTFFVTHACSLYCVHFILEAVAVQRG EQLLSPERTNTPKAISEEEEEVDPNTQNRKY TAACGEMVAEMVESLAVARISVLANGVPA FLTPLLRNIISLARLPLVNSYTRYPPLVWLIG WSVSVSSTFFVTHACSLYCVHFILEAVAVQRG EQLLSPERTNTPKAISEEEEEVDPNTQNRKY TAACGEMVAEMVESLAVARISVLAGHRINSGVPA FLTPLLRNIISLARLPLVNSYTRYPPLVWLIG WSVSVSSTFFVTHACSLYCVHFILEAVAVQRG EQLSPERTNTPKAISEEEEEVDPNTQNRKY TAACGEMVAEMVESLOVALGHKRNSGVPA FLTPLLRNIISLARLPLVNSYTRYPPLVWLIG WSPKPGGDFGTAFFEFFVEFLQFEKVKFIYF NTLGWTSRTQFFEET WATLLGVLVTQPLVME QEESPPEEDTERIQNIVLAVQRYGLISVLSAMT VPVAGNPAVSCLEGDQAMVSKRENLATHHLYQAWD BUPUS SPATTGGLISHEKLLLONTPERELGISMS			İ			1	ILAGNLLAASAPKSLRSSWASEEEANPAATK
GREKEPGEQASVPLSPKLGSBASASKNUS GPYTTSKSSLGSFYPLBSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQLELL ATLQDIGKCVEELLGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYHFTQALADA SLRNMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVTKNRADKNAHNHRIFJEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLQVQLRVNYCLL DSDQVFIGFVLKQFEYEVGGFRESEAHPNIFF FLVLLSYBRYHSKQHIGPKHIOLCDGIMASGR KAVTHAHALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLLRLQYHQVLEMFLVLQQ CHENEDEMWRALSRQIADHLPMLAKQOMHI DSHEALGVLNTLFELLAPSSLRPVDMLLRSMF VTPNTMASYSTVQLWISGILALRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGGGGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLYNHTDYRWW AEVQQTFKRISLSSTKLLSPOMSGEEEDSDLA AKLGMCNREIVRRGALDEDVYCQHLHDSE HLTWLIVNHQDLISLSHEFPVQDFISAVHRNS AASGLFIQAIQSRCENLSITTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDIL ACRRVEMLLAANLQSSMAQLFMELNRIQES LQSSGLAQRHQRLYLDEFRISTMQDSLSSS PPVSSHPLDGDGHVSLETVSPDKDWYVHLWK SQCWTRSDSALLEGAELVNRIPAEDMMAFM MNSEFNLSLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLFAVHHYFQFELPAEP AYWSKLNDLFGDAALYQSLTARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGGLOKSLFFAA AREVTLARVSGTVQQLFAVHHYFQFELPAEP AYWSKLNDLFGDAALYQSLTARALAQY LVVVSKLPSHLH.PPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGGLOKSLFFAA AREVTLARVSGTVQQLFAVHHYFQFELPAEP AYWSKLNDLFGDAALYQSLTARALAQY LVVVSKLPSHLH.PPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGGLOKFSTVPPLVWKLG WSVYSSTEFVTHACSLTYCVHFILEAVAVQPG EQLLSPERITNITKAISEEEEUDPHTQNEKY TAACEMVAEMVESLQSVLALGHKRNSGVPA FLITPLLRNIISLARLPLNSYTRYPPLVWKLG WSPKPGGDFGTAFPETVEFLQEKEVKFFIYY NTLGWTSRTQFETWATLLGVLVTOPLVME QEESPPEEDTERIQINVLAVQAITSLVLSAMI VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRGIVEQGDGAMYSKRENLLLONTPERELIGSMS	ı		}	]	1	}	QEEVWPALGDRALVPMVEQLFSHLLKVINIC
GPVTTSKSSSLGSFYHLPSYTKLHDVLKAILH ANYAVTIJLONSTEKFGGFLRSALDVLSQILEL ATLQDIGK CVEEL GYLKSCFSREPMMATVC VQQLKTLFGTHLASQFOGLSSNPSKSGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA SLRNMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVTKNRADKNAINHNHRLFEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEVEGGFESEALINNIFF FLVILSYERYHSKQIIGIPKIIQLCDGIMASGR KAVTHAPPALQPIVHDVLRGTNKADGKE LETQKEVVVSMLIRLIQYHQVLEMFILVLQQ CHKENEDK WKRLSRQLADIILPMLAKQQMHI DSHEALGVUNTJFELLAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILALRVLISQSTEDED IVLSSIGGLSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTPYCQBLGTLLMCLHIFKS GMFRRITAAATRLFRSDGGGSFYTLDSLNIR, ARSMITTHPALVILWCQULLIVHITYDYRW AEVQQTYKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVERGALLIFCDVVCQNLHDSE HLTVILIVNHQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTITMIKKTLQCLEGI HLSQSGAVLTLYVDRILLCTPFRVLARMVDL ACREVEMLLAANLQSSMAQLFMELINIGEY LQSSGLAQRRQRLYSLLDFFRUSTMODSLSPS PPVSSHPLDGDGHVSLETVSFDKDWYVHLVK SQCWTRSDSALLBGAELVNIRAEDMNAFM MISEFINLSLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHYFQPELPAEP AAYWSKLDSLGBAALIQSUSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLDHEQIPISLDLQAGLDCCCLALQLPGL WSVSSTEFVTHACSLIYCVHFLLEAVAVQPG EQLLSPERSTNTPKAISEEEEEDPDFNIQNKSY TACCEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIGLARL,PLVNSYTRYPPLVWKLG WSVSSTEFVTHACSLIYCVHFLEAVAVQPG EQLLSPERSTNTPKAISEEEEEDPDFNIQNKSY TACCEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIGLARL,PLVNSYTRYPPLVWKLG WSVSSTEFVTHACSLIYCVHFLEAVAVQPG EQLLSPERSTNTPKAISEEEEEDPPNIQNKSY TACCEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIGLARL,PLVNSYTRYPPLVWKLG WSPKPGGGDFGTAFPEIPWSFLQSVLALGHKRNSGVPA FLTPLLRNIIGLARL,PLVNSYTRYPPLVWKLG WSPKPGGGDFGTAFPEIPWSFLQSVLALGHKRNSGVPA FLTPLLRNIIGLARL,PLVNSYTRYPPLVWKLG WSPKPGGDFGTAFPEIPWSFLQSVLALGHKRNSGVPA FLTPLLRNIIGLARL,PLVNSYTRYPPLVWKLG WSPKPGGGDFGTAFPEIPWSFLQSVLALGHKRNSGVPA FLTPLLRNIIGLARL,PLVNSYTRYPPLVWKLG WSPKPGGOFGRAFFEIT GARLWALDTHLYQAWD UPVSLSPATTGALISHELLLLONPERERLEGSMS	1	1					AHVLDDVAPGPAIKAALPSLTNPPSLSPIRKK
NYKYTLDLQNSTEKFGGFLRSALDVLSQLIEL  ATLQDIGKCVEELGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSOGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA SLRNMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVTKNRADKNAIHHIRLFEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYTEVGQFRESEAIPNIFF FLVLLSYERYHSKQIIGPKIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTNKADAGKE LETQKEVVSMLLRLQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILPMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQUSGILALIRVLISQSTEDI NLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSGKQKNLPEETFSRFLQLVGLLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGSFYTLDSLNLR ARSMITHPALVLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALLIFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVILTYVDRLLCTPFRVLARMVDIL ACRRVEMLAANLQSSMAQLPMEELNRQEY LQSSGLAQRHQRLYSLLDFFLSTMQDSLSSS SQCWTRSDSALLEGABLVNRPAEDMNAFM MNSEFNLSLLAFCLSLGMSEISGGQKSALFEA AREVTLARAVSGTVQQLPAVHHVFQPELPAEP AAYWSLNDLFGDAALVGSLPTLARALAQPG LVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEOIPLSLOQGLOCCLALQLPGL UVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEOIPLSLOQGLOCCLALQLPGL UVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEOIPLSLOQGLOCCLALQLPGL UVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEOIPLSLOQGLOCCLALQLPGL UVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEOIPLSLOQGLOCALQLPGL UVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEOIPLSLOQGLOCCLALQLPGL UVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEOIPLSLOQGLOCALQLPGL UVSKLSTEFVTHACSLIYCVHFILEAVAVQFG EQLLSPERRITNIFKAISEEEEVDPNTQNFKYI TAACCEMVAEMVPSLQSVLALGHKRNSGVPA FLITPLLRNIIISLARLPLVNSTRVPPLVWKLG WSPKPGGDFGTAFPEFVFLIQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVQHTSLSAMT VPVAGRPAVSCLEQQFRNKPLKALDTRFGRK LSIIRGIVEQEIQAMYSKRENATHHLYQAWD DUPSIS SPATTGALISHEKLLLONFRELGSMS UPDENS SPATTGALISHEKLLLONFRELGSMS UPDENS SPATTGALISHEKLLLONFRELGSMS UPDENS SPATTGALISHEKLLLONFRELGSMS UPDENS SPATTGALISHEKLLLONFRELGSMS UPDENS SPATTGALISHEKLLLONFRELGSMS UPDENS SPATTGALISHEKLLLONFRELGSMS		ŀ					GKEKEPGEQASVPLSPKKGSEASAASRQSDIS
ATLQDIGKCVEELLGYLKSCSREPMANA IV. VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCPMAPYTHFTQALADA SLRNMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVYTKNRADKNAHWHIRLFEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYTEVGGPTEESEALIPNIFF FLVLLSYERYHSKQIIGIPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTNKADAGKE LETQKEVVSMLLRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADILPMLAKQQMHI DSHEALGVLNTLEFLLAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRIR RDGDSTSTLE EHSEGKQKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSILNIR ARSMITHPALVLLWCQULLLVNHTDYXWW AEVQQTPKRSLSSTKLLSPQMSGEEDSDLA KLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHQDLISLSHEEPVQDFISAVHRNS AASGLFQAAJGSCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPRVLARMVDIL ACRRVEMLAANLQSGAVLTLYVDRLLCTPRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIGEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHYSLETVSPBKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAPM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVPOFLPLAPB AYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKKRDIVKFVVATLEAL SWHLDHGQFILSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEEVDPNTQPHKYH TAACEMVAEMVPSLQSVLALGHKRNSGVPA FLITLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEFVEFLQEKEVFKFIYK THALRNIISLARLPLANSTYRPPLVWKLG WSPKPGGDFGTAFPEFVEFLQEKEVFKFIYK NTLGWTSRTQFETWATLLGVLVTQPLVMEL QEESPPEEDTERTQNVLAVQAITSLVLSAMT VPVAGRPAVSCLEQOPRNRPLKALDTRFGRK LSIIRGIVEQEIQAMYSKRENIATHHLYQAWD DDPDSLSPATTGALISHEKLLLONFFERLGAND		Ì	1				GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA
ATLQDIGKCVEELLGYLKSCSREPMANA IV. VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCPMAPYTHFTQALADA SLRNMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVYTKNRADKNAHWHIRLFEPLVIKALKQ YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYTEVGGPTEESEALIPNIFF FLVLLSYERYHSKQIIGIPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTNKADAGKE LETQKEVVSMLLRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADILPMLAKQQMHI DSHEALGVLNTLEFLLAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRIR RDGDSTSTLE EHSEGKQKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSILNIR ARSMITHPALVLLWCQULLLVNHTDYXWW AEVQQTPKRSLSSTKLLSPQMSGEEDSDLA KLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHQDLISLSHEEPVQDFISAVHRNS AASGLFQAAJGSCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPRVLARMVDIL ACRRVEMLAANLQSGAVLTLYVDRLLCTPRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIGEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHYSLETVSPBKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAPM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVPOFLPLAPB AYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKKRDIVKFVVATLEAL SWHLDHGQFILSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEEVDPNTQPHKYH TAACEMVAEMVPSLQSVLALGHKRNSGVPA FLITLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEFVEFLQEKEVFKFIYK THALRNIISLARLPLANSTYRPPLVWKLG WSPKPGGDFGTAFPEFVEFLQEKEVFKFIYK NTLGWTSRTQFETWATLLGVLVTQPLVMEL QEESPPEEDTERTQNVLAVQAITSLVLSAMT VPVAGRPAVSCLEQOPRNRPLKALDTRFGRK LSIIRGIVEQEIQAMYSKRENIATHHLYQAWD DDPDSLSPATTGALISHEKLLLONFFERLGAND	1	İ	į.	İ	Ì		NYKVTLDLONSTEKFGGFLRSALDVLSQILEL
QRLGSSSVRPGLYHYCFMAPYTHI (ALADA SLRMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVTKNRADKNAFINHIRLFEPLVIKALKQ YTTTTCVQLQKQVJUDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYEVGGFRESEAIIPNIFF FLVLLSVERYHSKQIIGIPKIQLCDGIMASGR KAVTHAPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLIRLIQYHQVLEMFILVLQQ CHKENEDK WKRISRQIADIILFMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVILSQSTED IVLSRIQELSFSPVLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVFMSEQQHTFYCQELGTLLMCLHIFKS GMFRRTAAATRLFRSDGCGGSFYTLDSLNLR ARSMITHPALVLLWCQILLVNHITDYRWW AEVQOTPKRHSSTKILLSPMGSGEEDSDLA AKLGMCNREIVRGGALLFCDVVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKILQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDIL ACRYEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSSS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVPOPELPAR AYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPFEKEKDIVKFVATLEAL SWHLHEEPIRSTAGSTVQQLPAVHYPOPELPAR AYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPFEKEKDIVKFVVATLEAL SWHSLHEEPIRSATSGTVQCLPAVHTVPOPELPAR AYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPFEKEKDIVKFVVATLEAL SWHLHEEPIRSAISEGEGEVENTOPHYNPKY TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWNLG WSVVSSTEFVTHACSLLTYCVHFILEAVAVQPG EQLLSPERRTNITFKAISEEEEEVDPNTOPHKY TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWNLG WSFKPGGDFGTAFFEIPVEFLQKEVKKEFIYF NTILGWTSRTOFEETWATLLGVLVTQPLVME QEESPPEEDTERTQIONVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRGIVEQEIQAMVSKRENIATHHLYQAWD DVZSSLSPALSHELLLINGNFERELGSMS		1	ł	1	Ì	İ	ATI ODICK CVEET GYLKSCFSREPMMAT VC
QRLGSSSVRPGLYHYCFMAPYTHI (ALADA SLRMVQAEQENDTSGWFDVLQKVSTQLKT NLTSVTKNRADKNAFINHIRLFEPLVIKALKQ YTTTTCVQLQKQVJUDLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYEVGGFRESEAIIPNIFF FLVLLSVERYHSKQIIGIPKIQLCDGIMASGR KAVTHAPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLIRLIQYHQVLEMFILVLQQ CHKENEDK WKRISRQIADIILFMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVILSQSTED IVLSRIQELSFSPVLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVFMSEQQHTFYCQELGTLLMCLHIFKS GMFRRTAAATRLFRSDGCGGSFYTLDSLNLR ARSMITHPALVLLWCQILLVNHITDYRWW AEVQOTPKRHSSTKILLSPMGSGEEDSDLA AKLGMCNREIVRGGALLFCDVVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKILQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDIL ACRYEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSSS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVPOPELPAR AYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPFEKEKDIVKFVATLEAL SWHLHEEPIRSTAGSTVQQLPAVHYPOPELPAR AYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPFEKEKDIVKFVVATLEAL SWHSLHEEPIRSATSGTVQCLPAVHTVPOPELPAR AYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPFEKEKDIVKFVVATLEAL SWHLHEEPIRSAISEGEGEVENTOPHYNPKY TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWNLG WSVVSSTEFVTHACSLLTYCVHFILEAVAVQPG EQLLSPERRTNITFKAISEEEEEVDPNTOPHKY TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWNLG WSFKPGGDFGTAFFEIPVEFLQKEVKKEFIYF NTILGWTSRTOFEETWATLLGVLVTQPLVME QEESPPEEDTERTQIONVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRGIVEQEIQAMVSKRENIATHHLYQAWD DVZSSLSPALSHELLLINGNFERELGSMS			1	1	1		VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA
NLTSYTKNRADKNAHNIRLEPEY NIKALKQ YTTTTCVQLQKQVJLLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYIEVGQFRESEAIPNIFF FLVILSYERYHSKQIIGIPKIQLCDGIMASGR KAVTHAPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLIRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILFMLAKQOMHI DSHEALGYLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISIGIALIRVILSQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQLGTLLMCLHIFKS GMFRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQULLLVNHITDYRWW AEVQQTPKRRSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRGAALILFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLTLYVDRLLCTPFRVLARMVDIL ACRRVEMILAANIQSSMQLPMEELINRIQEY LQSSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMILAANIQSSMQLPMEELINRIQEY LQSSGLAQRHQRLYSLLDFRFLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAGEDMAFM MNSEFNLSLLAPCLSLGMSEISGGGKSALFEA AREVTLARVSGTVQQLPAVHHVPQPELPAEP AAYWSKLNDLGGDAALYQSLPTLARLAQY LVVVSKLPSHLHPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL UNVYSKLPSHLHPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL UNVYSKLPSHLHPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL UNSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLESPERTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTFLLRNIIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRPA FLTFLLRNIISLARLPLVNSYTRVPPLVWRLSALSAMT VPVAGNPAVSCLEQQPRNKPLKALDTTFGRK LSIRGIVEGEIQAMVSKRENIATHHLVQAWD DPZBSI SPATTGALISHEKLLLOGDFFEREGSMS			ŀ	1			ORI GSSSVRPGLYHYCFMAPYTHFIQALADA
NLTSYTKNADKNAHNIRLEPEY NIKALKQ YTTTICVQLQKQVJLLLAQLVQLRVNYCLL DSDQVFIGFVLKQFEYIEVGQFRESEAIPNIFF FLVILSYERYHSKQIIGIPKIQLCDGIMASGR KAVTHAPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLIRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILFMLAKQQMHI DSHEALGYLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISIGIALIRVILSQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQLGTLIMCLHIFKS GMFRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQULLLVNHITDYRWW AEVQQTPKRRSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRGAALILFCDJYVCQNLHDSE HLTWLIVNHIQDLISLSIEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPMLKKTLQCLGGI HLSQSGAVLTLYVDRLLCTFRVLARMVDIL ACRRVEMILAAANLQSSMAQLPMEELINRIQEY LQSSGLAQRHQRLYSLLDFRFLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAGDMAFM MNSEFNLSLLAPCLSLGMSEISGGGKSALFEA AREVTLARVSGTVQQLPAVHHVPQPELPAEP AAYWSKLNDLGGDAALYQSLPTLARLAQY LVVVSKLPSHLHPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCLALQLPGL UNVSKLPSHLHPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWFL SQCBPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEJQAMVSKRENIATHHLYQAWD DYPSI SPATTGALISHEKLLLOQINFERELGSMS			-				SLRNMVQAEQENDTSGWFDVLQKVSTQLKT
TTTTTCVQLQKQVI.DLAQLUQLKNYCLL  DSDQVFIGFLXQFEYEVGGFRESEAIIPNIFF FLVLLSYERYHSKQIIGPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLLRIQVHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILPMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGRQUKNLPEETFSRFLIQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHFALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCERLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQFY LQSSGLAQRHQRLYSLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGKSALFEA ARRYTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLJTLARALAQY LVVVSKLPSHLLIPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLTYCVFTLEAVAVQPG EQILSPERRITNITPKAISEEEEEVDPNTQNFKY TAACEMVAEMVESLQSVLALGHKRNSGYPA FLTPLLRNIIISLARLLVNSTTRQLPCK WSVSSTEFVTHACSLTYCVFTLEAVAVQPG EQILSPERRITNITPKAISEEEEEVDPNTQNFKYI TAACEMVAEMVESLQSVLALGHKRNSGYPA FLTPLLRNIIISLARLLVNSTTRPLVWKLG WSVPSTEFVTHACSLTYCVFTLEAVAVQPG EQILSPERRITNITPKAISEEEEEVDPNTQNFKYI TAACEMVAEMVESLQSVLALGHKRNSGYPA FLTPLLRNIIISLARLLVNSTTRPLVWKLG WSVPSTEFVTHACSLTYCVFTLEAVAVQPG GCILSPERRITNITPKAISEEEEEVDPNTQNFKYI TAACEMVAEMVESLQSVLALGHKRNSGYPA FLTPLLRNIIISLARLLVNSTTRPLVWKLG WSVPSTEFVTHACSLTYCVFTLEAVAVQPG GCILSPERRITNITPKAISEEEEEVDPNTQNFKYI NTLGWTSRTOFEETWATLLGVLVTQPLVME QEESPPEEDTERTQNVLAVQAITSLUVSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKERNIATHHLYQAWD DVDSTSPATTGALISHEKLLLONFEREELGSMS	i						NI TSVTKNRADKNAIHNHIRLFEPLVIKALKŲ
DSDQVPIGFVLKQFEYEVGQIRESEAIIPNIF FLVLLSYERYHSKQIGIPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTTNKADAGKE LETQKEVVVSMLLRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILPMLAKQQMHI DSHEALGVLNTLFELAPSSLRPVDMLLRSMF VYPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HTWLIVNHQDLISSHEPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQESY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSILAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRITNTFKAISEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHRRNSGVPA FLTPLLRNIISLARPLVNSYTRVPPLVWKLG WSPKPGGDFGTAPPEPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVMML QEESPPEEDTERTOINVLAVQATISLUSMM VPYAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRGIVEQEIQAMVSKERNIATHHLYQAWD PVPSISPATTGALISHEKLLLQNTPEERLGSMS			1				VTTTTCVOLOKOVLDLLAQLVQLRVNYCLL
FLVLLSYERYHSKQIIGPKIIQLCDGIMASGK KAVTHAPALQPIVHDLFVLRGTNKADAGKE LETQKEVVSMLLRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILPMIAKQQMHII DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFSPYLLISCTVINRLINGDSTSTLE EHSEGKQIKNL PEETFSRFILQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEDSDLA AKLGMCNREIVRRGALLIFCDYVCQNLHDSE HLTWLIVNHQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMILAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRRAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLFAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQACLDCCCLALQLPGL WSVVSSTEFVTHACSLTYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNFKY TAACEMVAENVSSLQSVLALGHKRNSGVPA FLTPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYM INTLGWTSRTQFEETWATLLGVLVTQPLVMG QEESPPEEDTERTQNVLAQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKERNIATHHLYQAWD PURSI SPATTGALISHEKLLLQNTPEGRE		1					DSDOVFIGEVLKOFEYIEVGQFRESEAIIPNIFF
LETQKEVVVSMLRLRQYMQVLEMFLVLQQ CHKENEDK WKRLSRQLADIIL PMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTYOL WISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTTYCQELGTILMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLINLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKILSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVQDNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMYDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDFFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKINDLFGDAALVQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHBEQIPLSLDLQAGGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQOF EQLLSPERRTNTPKAISEEEEEVDPNTONPKYI TAACEMVAEMVSELQSVLALGHKRNSGVPA FLITPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF NTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQNVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PUPPLS SPATTGALSISHCLLLONPERELGSMS		100	1	1	i		FIVE I SYFRYHSKOIIGIPKIIQLCDGIMASGR
LETQKEVVVSMLRLRQYMQVLEMFLVLQQ CHKENEDK WKRLSRQLADIIL PMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTYOL WISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTTYCQELGTILMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLINLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKILSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVQDNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMYDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDFFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKINDLFGDAALVQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHBEQIPLSLDLQAGGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQOF EQLLSPERRTNTPKAISEEEEEVDPNTONPKYI TAACEMVAEMVSELQSVLALGHKRNSGVPA FLITPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF NTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQNVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PUPPLS SPATTGALSISHCLLLONPERELGSMS	1					1	KAVTHAIPALQPIVHDLFVLRGTNKADAGKE
CHKENEDKWKRLSRQIADIILPMLAKQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILALIRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITHFALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKILLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLFAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHJPEKEKDIVKFVVATLEAL SWHLHBEIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQFG EQLLSPERRTNIFKAISEEEEEVDFNTQNFKYI TAACEMVAEMVESLQSVLALGHKRNSGYPA FLTPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYY INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRIKPLKALDTRFGRK LSIRGIYGEGEIQAMVSKRENIATHHLYQAWD BYPSI SPATTGALISHEKLLLONPERELGSMS			ì		ĺ		I ETOKEVVVSMLLRLIQYHQVLEMFILVLQQ
DSHEALGVLNTLFEILAPSSLRPVDMLLKSMIF VTPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEFTSRFILQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTILMCLHIFKS GMFRRITAAATRLFRSDGCGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALLIFCDYVCQNLHDSE HLTWLIVNHQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTFFRVLARMYDIL ACRRVEMLLAANLQSSMAQLPMEELNRIOEY LQSSGLAQRHQRLYSLLDFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQOLPAVHHVFOPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRINTPKAISEEEEEVDFNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGYVA ELTPILLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAPPEPVEFLQEKEVFKEFIVM NTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRIKPLKALDTRFGRK LSINGGVFGEIQAMVSKRENIATHHLYQAWD BYDESI SPATTIGALISHEKLLLONPERELGSMS		1	1		1	1	CHKENEDKWKRLSRQIADIILPMLAKQQMHI
IVLSRIQELSFSPYLISCTVINRLRDGDSISTUS EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYQQLGTLLMCLHIIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRGALLIFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAJQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSFS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVPQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD DPSSI SPATTGALISHEKLLLONPERELGSMS	1						DSHEALGVINTLFEILAPSSLRPVDMLLKSMF
IVLSRIQELSFSPYLISCTVINRLRDGDSISTUS EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYQQLGTLLMCLHIIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRGALLIFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAJQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSFS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVPQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD DPSSI SPATTGALISHEKLLLONPERELGSMS			1	1			VTPNTMASVSTVOLWISGILAILRVLISQSTED
EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVI KQLKVEMSEQQHTFYCQELGTLLMCLHIJFKS GMFRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HILTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMILAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSFS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHIPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLTYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNFK YI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKFGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFFETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSLSPATTGALISHEKLLLOINPERELGSMS	1						IVI SRIOELSESPYLISCTVINRLEDGDS1S1LE
KQLKVEMSEQQHTFYCQELGTLLMCLHIFKS GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALLIFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSGNPATTGALISHEKLILLONPERELGSMS	1						FHSEGKOIKNLPEETFSRFLLQLVGILLEDIVI
GMFRRITAAATRLFRSDGCGGSFYTLDSLNLK ARSMITHPALVLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF NNTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRGIVEQEIQAMYSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLQINPERELGSMS	İ				İ		KOLKVEMSEOOHTFYCOELGTLLMCLIHIFKS
ARSMITTHPALVLLWCQILLLVHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLTYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF NTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRRGIVEQEIQAMVSKRENIATHHLYQAWD BYDSLSPATTGALISHEKLLLOINPERELGSMS		İ	- (				GMERRITAAATRLFRSDGCGGSFYTLDSLNLK
AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNFKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVDSI SPATTGALISHEKLLLQINFERELGSMS	1					Ï	ARSMITTHPALVLLWCQILLLVNHTDYRWW
AKLGMCNREIVRRGALILFCDYVCQNLHUSE HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD BYDSI SPATTGALISHEKLLLOINPERELGSMS		1					AFVOOTPKRHSLSSTKLLSPQMSGEEEDSDLA
HLTWLIVNHIQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPTMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMYDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRGIVEQEIQAMVSKRENIATHHLYQAWD DYDELSPATTGALISHEKLLLOINPERELGSMS			1		1		AKI GMCNREIVRRGALILFCDYVCQNLHDSE
AASGLFIQAIQSRCENLSTTTMLKKILQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD DVPSI SPATTGALISHEKLLLQNYPERELGSMS		1		1	1	j	LIT TWI IVNIHIODI ISL SHEPPVODFISAVHRNS
HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS			ł				A ASCI FIGATOSECENT STPTMLKKT LUCLEGI
ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQATISLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD BYDSI SPATTGALISHEKLLLQINPERELGSMS			}	1			HISOSGAVITLYVDRLLCTPFRVLARMVDIL
LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSYS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS				-	1		A CREVENT I A ANT OSSMAOL PMEELNRIQEY
PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSILAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS						1	LOSSCI AORHORI YSLLDRFRLSTMQDSLSPS
SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS		-	l				DDV66HPI DGDGHVSLETVSPDKDWYVHLVK
MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS		]	1		1		SOCWTRSDSALLEGAELVNRIPAEDMNAFM
AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS							MAISEENT SLLAPCLSLGMSEISGGOKSALFEA
AAYWSKLNDLFGDAALYQSLPITARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS		İ	1			1	APEVIT ARVSGTVOOLPAVHHVFOPELPAEP
LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS					1		A AVWSKI NDLEGDA ALYOSLPTLARALAUY
SWHLIHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS			J		1	1	I VVVSKI PSHLHLPPEKEKDIVKFVVATLEAL
WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS							SWIJI THEOTPL SLDLOAGLDCCCLALQLPGL
EQLLSPERRTNTPKAISEEEEEVDPNTQNPKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS			1		1		WELVESTEFVTHACSLIYCVHFILEAVAVQPG
TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS	1		- [				FOLL SPERRINTPK AISEFEEEVDPNTONPKYI
FLTPLLRNIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS			1				TAACEMVAEMVESI OSVI AI GHKRNSGVPA
WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIYF INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS					1		EL TOLL DAILIST A DI PI VASYTRAPPI VWKI G
INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS	I	-	1	ł	1	1	TELEPHOCODEGE A EDETOVEFI OF KEVEKEFIYR
QEESPPEEDTERTQINVLAVQAITSLVLSAMI VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS				1		1	WSPKPUUDFUTAFFEIT VEIT VERT VTOPI VMF
VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSI SPATTGALISHEKLLLOINPERELGSMS				1			INILGWISKIQFEETWAILLGYLYTQFEYWE
LSIIRGIVEQEIQAMVSKRENIATHHLYQAWD  PVPSI SPATTGALISHEKLLLOINPERELGSMS	1	1					GEESPPEED LEKT QUANTA V QALISE V LOADE GOV
PVPSI SPATTGALISHEKLLLOINPERELGSMS	ļ						VPVAGNPAVSCLEQQPKNKPLKALDIRFORK
PVPSLSPATTGALISHEKLLLQINFERELGSMS YKLGQVSIHSVWLGNSITPLREEEWDEEEEEE				J		1	LSIIRGIVEQEIQAMVSKKENIAI AHLLI QAWD
YKLGQVSIHSVWLGNSITPLREEEWDEEEEE		{				-	PVPSLSPATTGALISHEKLLLQINPEKELGSMS
							YKLGQVSIHSVWLGNSITPLREEE WDEEEEEE

					1 5 1 1 - d	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of,	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	1=Isoleucine, K=Lysine, L-Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
-	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ł	,	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	İ		Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ	1		Joquener	/=possible nucleotide deletion, \=possible
	1		1	peptide		nucleotide insertion
			·	sequence	<u> </u>	ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL
		<b>†</b>		T		ADAPAPSSPP1SPVNSRRIHOTO VDIIISOOQID
			1			LELYSRWILPSSSARRTPAILISEVVRSLLVVS
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Į.	}	1	1	}	}	PVISDYLLSNLKGIAHCVNIHSQQHVLVMCA1
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<b>[</b>		1		1		FDRIRKGFPCEARVVARILPQFLDDFFPPQDIM
	l		1	l		NKVIGEFLSNQQPYPQFMATVVYKVFQTLHS
		1				TGOSSMVRDWVMLSLSNFTQRAPVAMATWS
		1	1	1		LSCFEVSASTSPWVAAILPHVISRMGKLEQVD
]	1	1	1			VNLFCLVATDFYRHQIEEELDRRAFQSVLEV
1	1		1			VAAPGSPYHRLLTCLRNVHKVTTC
	1.			<del></del>	430	NSRPSPSAALVEVLLRSGSTFPHTVSGGWAA
428	1778	Α	3449	3	430	WGPWSSCSRDCELGFRVRKRTCTNPEPRNGG
		1		<u> </u>	ļ	LPCVGDAAEYQDCNPQACPVRGAWSCWTS
1		1		Ì	[	LPCVGDAAE YOUR PORTOR PROCESS A PERCEDICI
1		1	1	1	1	WSPCSASCGGGHYQRTRSCTSPAPSPGEDICL
1	1	1	1	,		GLHTEEALCATQACPEGWS
120	1779	A	3464	583	3	DALDRRYLERCHPAAGGWVGEGE*ALCQKT/
429	1779	1^	3404	1 3 3 3	]	RFSGVLEPPLPSLKDGGRFPAWT*RSCSKSLR
1	1		1	[	ļ	A A FTSOFFPSRRSRASPGSAP\GNGQNLTEQHP
	l	1				CPGSCDPOVLSASWM*VEHRSKFRPPP*NST1
1	1				İ	PPES/RS*QGGTVQTGQHSSGREAGSWRARGR
,		ì	- 1		ļ	NAGRR*KGGGKIGTKQGAVRARKECRGEMA
1			1			SGETDSE
1	1		1			FRMRIFLHCPWNQQMWKIWNLLETSLESCKA
430	1780	A	3473	2802	270	FKWKIFLHCPWIQQMWKIWIEDDIODDOOLD
1.50						HLSIQKLLKER\Q\QLPVFKHRDSIVETLKRHR
l l		1			ļ	VVVVAGET\GSGKSTQVPHFLLEDLLLNEWE
1		1		İ		ASKCNIVCTQPRRISAVSLANRVCDELGCENG
Į	ļ					PGGRNSLCGYQIRMESRACESTRLLYCTTGV
1	l		ļ	1	i	LLRKLQEDGLLSNVS/HMFIVDEV\HER\SVQS
1	İ	-				DFLLIILKEILOKRSDLHLILMSATVDSEKFST
İ		ł	<u> </u>	Ì		VETHCPILRISGRSYPVEVFHLEDHEETGFVLE
l l	. ]	1	1	1	-	KDSEYCQKFLEEEEEVTINVTSKAGGIKKYQE
	'			1		YIPVQTGAHADLNPFYQKYSSRTQHAILYMN
ļ		1			1	PHKINLDLILELLAYLDKSPQFRNIEGAVLIFL
				1		PGLAHIQQLYDLLSNDRRFYSERYKVIALHSI
				I	!	LSTQDQAAAFTLPPPGVRKIVLATNIAETGITI
1	ł		1	1	1	LSIQUQAAAFILFFFGVAALVLAINADIGII
				Į.	:	PDVVFVIDTGRTKENKYHESSQMSSLVETFVS
1		-	1			KASALQRQGRAGRVRDGFCFRMYTRERFEG
						FMDYSVPEILRVPLEELCLHIMKCNLGSPEDF
			1		1	I SKALDPPOLOVISNAMNLLRKIGACELNEPK
1		-	1			LTPLGOHLAALPVNVKIGKMLIFGAIFGCLDP
Ì	i i	}	1			VATLAAVMTEKSPFTTPIGRKDEADLAKSAL
						AMADSDHLTIYNAYLGWKKARQEGGYRSEI
					!	TYCRRNFLNRTSLLTLEDVKQELIKLVKAAGF
					1	SSSTTSTSWEGNRASQTLSFQEIALLKAVLVA
						22211212 MEDIAWA STEDI YOUNETYOOK
		ļ				GLYDNVGKIIYTKSVDVTEKLACIVETAQGK
,	1	1	1			AQVHPSSVNRDLQTHGWLLYQEKIRYARVY
		i	1			LRETTLITPFPVLLFGGDIEVQHRERLLSIDGW
1		ł		1		TYFOAPVKIAVIFKQLRVLIDSVLRKKLENPK
1			}	1		
				{		MSI ENDKILOIITELIKTENN
				<u> </u>	441	MSLENDKILQIITELIKTENN  FR PAPGHVOP*GGSSAAAGGGLLSHPRPCQQ
431	1781	A	3474	1	441	MSLENDKILQIITELIKTENN FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ PCPPAPAPSRPRSLGSLGORVPAALATAAQEL
431	1781	A	3474	1	441	MSLENDKILQIITELIKTENN FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ PCPPAPAPSRPRSLGSLGORVPAALATAAQEL
431	1781	A	3474	1	441	MSLENDKILQIITELIKTENN  FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ PCPPAPAPSRPRSLGSLGQRVPAALATAAQEL PATI GGDGGKPALTAGEAALPGLHRSGVPAA
431	1781	A	3474	1	441	MSLENDKILQIITELIKTENN FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ PCPPAPAPSRPRSLGSLGORVPAALATAAQEL

		1 3 4	1 000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ì	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	914	ng to first	acid residue	O=Ghitamine, R=Arginine, S=Serine,
uence	1	{	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	'sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		i	ĺ	1	sequence	/=possible nucleotide deletion, \=possible
		1	1	peptide		nucleotide insertion
			1	sequence	ļ	QLRRLTLPNFKTY/YSS*IIEIAWH**KNMQID
432	1782	Α	3478	416	23	QWFRRESPEIDLCKYS*LSFDKEAKAIK/WKE
	i					CSLFNKWC/YKNWM/LHVQKKRI*VQTLHPS
	Į	}		}		QKLK\SKWIKDLNVECRITKLLDQEYPGDLGY
	Ĭ	1	1		ì	
	1				l	SRALNSGSR
433	1783	A	3504	1876	552	CLAPCSPQPEKNGMQPLLLLLPPLLYQQLLHS
733	1.05	1		ļ		SLGAPGESTLLVRTSKLLVGLGLQLLVWLLL
			j	)	1	QTRSLLALQLHLTSSAPLLAAPTAVCSCSRCS
	1		1	1		APRSRCVARPAARTGLPTPAPASSPAPAASPA
	1	ļ	1	1		PAASPAPAESTA\PQPLILLPKP/PPAPGAPPPRP
	1					GAPPPRPAASPSPAASPAPPAASPVLTASPPLP
	1		1		1	AASPSPAASPAPPAASPVLTASPPLPAASPSPA
	1	1	j	1		ASPAPPAASPVLTASPPLPAASPALAASPVHT
	[	-				ASPPVHVASPPVHTASPPVHVASPPVHTASPP
·	1		Ì	1		VHVASPPVHTASPHVHVASPPVHVASPPVHV
	1	İ	1			ASPPVHTASPPVHVASPPVHTASPHVHVASPP
		Ì	1			VHTASPPVHVASPPVHVASPPVHVAYPPVHV
	i	1	l			ASPPVHVASPPVHVASPPVSCSGDSTSDCFPP
		ĺ		Į.		OPGAVEPHSLAPSLGGWSHLVAALP
			10016	142	590	GGVNRPRSETEOVKTPVLISSWDYRHPPPRPA
434	1784	A	3516	142	390	SFFVFLV*TGF\TALARMVLISWPCDLPTSASQ
	-	1	1	Ì		SAGITGVRHHA\RLLYFEOESHSVTQAGW\VQ
	1	1				WHNLGSLQPLSLEDRLSPGVLGCSALCRSGV
			1			RTKFGINMVTSRERGTTRLPKEG
						MSLVRAALEALDELDLFGVKGGPQSVIHVLA
435	1785	Α	3529	1	3161	DEVQHCQSILNSLLPRASTSKEVDASLLSVVS
		1	1			FPAFAVEDSQLVELTKQEIITKLQGRYGCCRF
	j	- [	ł			LRDGYKTPKEDPNRLYY/ENPAELKLFENIEC
	i	l	-		}	EWPLFWTYFILDGVFSGNAEQVQEYKEALEA
	1			ļ		VLIKGKNGVPLLPELYSVPPDRVDEEYQNPHT
	1	1	1	ì		VDRVPMGKLPHMWGQSLYILGSLMAEGFLA
	- (		İ			PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS
						SKSPSHQCTIISIRTTRKITAPVSILAETEEIKTIL
	j	-		1		KDKGIYVETIAEVYPIRVQPARILSHIYSSLEIF
	1	l	1	1	Ì	LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK
		1		Ì		LPFLNSVSGCNNKMKLSGRF I KHING V EGTER
		-	1	1		LYDIRKTIFTFTPQFIDQQQFYLALDNKMIVE
	1	i			i	MLRTDLSYLCSRWRMTGQPTITFPISHSMLDE
	1	- 1	ł			DGTSLNSSILAALRKMQDGYFGGARVQTGKL
l			İ	Į.		SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN
		1				YDYLESGNWMNDYDSTSHARCGDEVARYL
					1	DHLLAHTAPHPKLAPTSQKGGLDRFQAAVQT
	ì					TCDLMSLVTKAKELHVQNVHMYLPTKLFQA
	1	-	1	1	1	SRPSFNLLDSPHPRQENQVPSVRVEIHLPRDQ
				1		SGEVDEKALVLOLKETSSLOEQADILYMLYT
1			1			MKGPDWNTELYNERSATVRELLTELYGKVG
ļ						FIRHWGLIRYISGILRKKVEALDEACTDLLSH
1		1			1	OKHLTVGLPPEPREKTISAPLPYEALTQLIDEA
-	1					SEGDMSISILTOEIMVYLAMYMRTQPGLFAE
						MFRLRIGLIIQVMATELAHSLRCSAEEATEGL
1	}	1				MNLSPSAMKNLLHHILSGKEFGVERSVRPTD
		1				SNVSPAISIHEIGAVGATKTERTGIMQLKSEIK
1		1	1			QSPGTSMTPSSGSFPSAYDQQSSKDSRQGQW
1				1		QRRRRLDGALNRVPVGFYQKVWKVLQKCH
		1		1		GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL
	İ	İ		1		NRVPQPEYRQLLVEAIL\VLTMLADIENHSIGS
				1		NKVPQPETKQLLVEALLVETWILADIENTISIOS
			i	1		IIAVEKIVHIANDLFLQEQKTLGADDTMLAKD
						PASGICTLLYDSAPSGRFGTMTYLSKAAATY
						VOEFLPHSICAMO
436	1786	A	3546	73	393	VQEFLPHSICAMQ  CP*LTWELLEVKKAEVLQDSLDGRYSTPSSCL EQPDSCRPYGRSFYALEEKHVIFSLDVGETDN

WO 01/57188

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
IO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	•	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		ł	{	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		]	1	peptide	ļ	nucleotide insertion
	1	1	l	sequence		KGKGKTIRGI*TFKGRKGGTYQREHDANPLA
				}	ļ	PYSARSCWMRKG
					2939	TAYBAFPGI FELSSGLRAHSPSATTVCEPEAQU
137	1787	Α	3554	5157	2939	L SASGCRYA AHPHWGLGGAAAAGGSWEPQPP
		1		,		PROCEPAGEGEPHPPAAPESPLLPGSKKKPHA
			-			AOPGARARTSPPPASARNMAARPAATLAWSL
			1			I I I SSALLREGCRARFVAERDSEDDGEEPVVF
	Ì					PESPLOSPTVLVAVLARNAAHTLPHFLGCLER
			ł		,	LDVPKSRMAIWAATDHNVDNTTEIFREWLK
	-	1	1	1		NVORLYHYVEWRPMDEPESYPDEIGPKHWP
		1	Ì	1		TODEAHVMKIROAALRTAREKWSDYILHUV
						DNEI TNPOTI NLLIAENKTIVAPMLESKULYS
		Į			,	NEWCGITPKGFYKRTPDY\VOIREWKKIGCFF
		ľ	1	1		VPMVHSTFLIDLRKEASDKLTFYPPHQDYIW
		1	1	\	İ	TEDDITVEAESSROAGIOMYLCNREHYGYLPI
	]		}	1		I K PHOTI OFDIENLIHVOLEAMIUKPYMEPSQ
	1		İ	1		YVSVVPKYPDKMGFDEIFMINLKRRKGQGGI
		1	<b>\</b>			RWLRTLYEQEIEVKIVEAVDGKALNTSQLKA
	1	Ì	1	1		LNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSV
			1			WKEVIDRELEKTLVIEDDVRFEHQFKKKLMK
		ì	1			LMDNIDQAQLDWELIYIGRKRMQVKEPEKA
	-	1		1		VPNVANLVEADYSYWTLGYVISLEGAQKLV
	1	1	ł	İ	i	GANPFGKMLPVDEFLPVMYNKHPVAEYKEY
		1			1	YESRDLKAFSAEPLLIYPTHYTGQPGYLSDTE TSTIWDNETVATDWDRTHAWKSRKQSRIYSN
				1	j	TSTIWDNETVATOWDRITTAWROIG COLORS
		1	1			AKNTEALPPPTSLDTVPSRDEL  IFFNSSSLFCRVFCLFLRWSFTLVAQARVQ*C
438	1788	A	3563	130	527	NLSSLQPLPPGFK*FSCLSPPRS*DYRRPPPRPA
150	1 2,755		1	1	İ	NFLYF**RQGFTVLGQAGLELLT/S/GDPPTSA
		1				SQSAGITGVSHRAWPVHAISTHISLVKTRPSL
						TLG
					1834	LI OPAMRK SPGLSDCLWAWILLLSTLTGRSY
439	1789	Α	3565	446	1834	GOPSI ODELKONTTVFTRILDRLLDGYDNKL
			1			RPGLGERVTEVKTDIFVTSFGPVSDHDMETT
		1	1	}		DVFFROSWKDERLKFKGPMTVLRLNNLMAS
		Ì	Ì	1	1	KIWTPDTFFHNGKKSVAHNMTMPNKLLRIII
		l	1		1	DOTE I YTMRI TVR\AECPMAFGKDFPM\U\A
				1	\	ACPI KEGSYAYTRAEVVYEWTREPAKSV V V
Ì		1				AEDGSRI NOYDLLGOTVDSGIVQSSTGEYVV
		. }	1	1		MTTHEHI KRKIGYFVIOTYLPCIMIVILSQVS
	1				1	UT NDESVPARTVEGVTTVLTMTTLSISAKNS
				}		PKVAVATAMDWFIAVCYAFVFSALIEFATVI
	1	Ţ		Į.	1	VETKRGYAWDGKSVVPEKPKKVKDPLIKKN
1						NTVAPTATSYTPNLARGDPGLATIAKSATIE
}		}	1	1	1	KEVKPETKPPEPKKTFNSVSKIDRLSKIAFPLI
		}				FGIENT VYWATYLNREPOLKAPTPHQ
ļ			25/0	<del>-  </del>	350	STSSCEPAAAAAIMREIVHLOAGQCGNQIGA
440	1790	A	3568	1 1	330	EWEVISDEHGIDPTGTYHGDSDLOLERINVY
		1			i	NEATGEAPVPSPTALRGPRGPCLG*RPPVPAG
1		- 1			1	GKYVPRAVLVDMEPGTMDSV
L	1,==		3569	2	1751	FVAVAGAUSGEPLVHWCTOOLRKTFGLDV
441	1791	A	3309	12	1751	EEDOVUI SIESAEEIREYVIDLLOGNEGKKG
1				1		FIFELITKWOKNDOELISDPLQQCFKKDELL
	1			)	1	OVECTHI KRGRKKGRNROEVPAFTEPULLA
	1	1	[	- !	1	VKTPFDLAKAOENSNSVKKKTKFVNLYTRE
					į	ODDI AVI I PGRHPCDCLGOKHKLINNCLICO
1 1		ı	l l	ł	1	RIVCEQEGSGPCLFCGTLVCTHEEQDILRGD
		J	1	t t		MACE OF OFFICE A
			Ì			MKSQKLLKKLMSGVENSGKVDISTKDLLPF QELRIKSGLEKAIKHKDKLLEFDRTSIRRTQ

				Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	1	USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	i	09/496	correspondi ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence		1	914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
		i		amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
	1			residue of	sequence	/=possible nucleotide deletion, \=possible
	1	-		peptide		nucleotide insertion
	<b>\</b>			sequence		DDESDYFASDSNQWLSKLERETLQKREEELR
					1	ELRHASRLSKKVTIDFAGRKILEEENSLAEYH
			Ì			ELRHASRLSKKVIIDPAURKILEEENSERII GVI
			1			SRLDETIQAIANGTLNQPLTKLDRSSEEPLGVL
		ĺ			į	VNPNMYQSPPQWVDHTGAASQKKAFRSSGF
		1				GLEFNSFQHQLRIQDQEFQEGFDGGWCLSVH
	ì	1	ì	1	1	QPWASLLVRGIKRVEGRSWYTPHRGRLWIAA
	1	1		ļ		TAKKPSPQEVSELQATYRLLRGKDVEFPNDY
	Į.		1		ì	PSGCLLGCVDLIDCLSQKQFKEQFPDISQESDS
	i			ì	}	PFVFICKNPQEMVVKFPIKGNPKIWKLDSKIH
	1	1	1			OGAKKGLMKONKAV
			-	<del> </del>	2019	MPRSHTGERLCEGKEGSOCAENFSPNLSVTK
442	1792	A	3576	1	2017	KTAGVKPYECTICGKAFMRLSSLTRHMRSHT
	1		1	1		A IR A IVEK PYK CKEC\GRAFSLSQILSK\HERSH
					1	TGEKPYKCKQCGKTFIYHQPFQRHERTHIGEK
						PYECKQCGKALSCSSSLRVHERIHTGEKPYEC
		1			1	KQCGKAFSCSSSIRVHERTHTGEKPYACK\EC
		1				GKAFIS\TTSVLTHMITHNGDRPYKCKECGKA
	1	1	1			FIFPSFLRVHERIHTGEKPYKCKQCGKAFRWS
	1	i i	1			TSIQIHERIHTGEKPYKCKECGKSFSARPAFRV
	1	1				HVRVHTGEKPYKCKECGKAFSRISYFRIHERT
				ļ		HVRVHTGEKPYKCKECGKATSKISTT KITEKT
	1		1	1		HTGEKPYECKKCGKTFNYPLDLKIHKRNHTG
	1	1		Į.		EKPYECKECAKTFISLENFRRHMITHTGDGPY
	1	1	f		ļ	KCRDCGKVFIFPSALRTHERTHTGEKPYECKQ
	Ī	ļ.	Į.	ł		CGKAFSCSSYIRIHKRTHTGEK\PYECKECGK
		1	1			AFIYPTSFQGHMRMHTGEKPYKCKECGKAFS
		-	1		·	LHSSFR\RHTRIHNYEKPLEC*Q\CGKAFSVSTS
			1	ļ	İ	LKKPMRNAQSDRKLY/KCEK*EKVFNSNRCF
			İ	1		OSCENSH*REKSCOCK*YRKRDTR*FMYSQV
				1		PHNHVSVSNGPYR/CGSPIRLYNT*NISINKNL
	}	1		-		VAVVTP*CSTLFKCLWCWCKRAALSVV*/IVQ
		1	1		1	DSGRGRWLTPVIPALWEAKAGGSRGQEIKTII
	Ì	1	ł	Į		ANTVKPHLY
					114	DFYERKFEQFIEGHKQIVNKWRDLLCSWKRK
443	1793	Α	3578	287	114	LSIIKKSVLQNNL*FSAASMRFQKVFF
		<u> </u>			1000	HLFFSLFLAAMAMTGSTPCSSMSNHTKERVT
444	1794	Α	3582	3335	1909	MTKVTLENFYSNLIAQHEEREMRQKKLEKV
						MEEEGLKDEEKRLRRSAHARKETEFLRLKRT
	ĺ	Ì				RLGLEDFESLKVIGRGAFGEVRLVQKKDTGH
	1			i		KUULEULESIN AIGNOALGE AKT AGANTAIT
	Į.	1		ļ		VYAMKILRKADMLEKEQVGHIRAERDILVEA
	1	- 1	}	1		DSLWVVKMFYSFQDKLNLYLIMEFLPGGDM
				1		MTLLMKKDTLTEEETQFYLAETVLAIDSIHQL
					,	GFIHRDIKPDNLLLDSKGHVKLSDFGLCTGLK
			1			KAHRTEFVRNI.NHSLPSDFTFONMNSKRKAL
				1		TWKRNRROLAFSTVGTPDYLAPEVFMQTGY
1		- 1		<b>\</b>	i	KI CDWWSLGVIMYEMLIGYPPFCSETPQETY
		1				KKVMNWKETLTFPPEVPISEKAKDLILRFCCL
1		l				WEHRIGAPGVEEIKSNSFFEGVDWEHIRERPA
	1	1				AISIFIKSIDDTSNFDEFPESDILKPTVATSNHP
1					}	TDYKNKDWVFINYTYKRFEGLTARGAIPSYM
	1				i	
1	1					KAAK RTRGIEKRFAYSFLQQLIRYVDEAHQYILEFD
445	1795	A	3584	1	6169	KIKULEKKATSTLQQLIKT VDEALQTILLID
773	••••	1				GGSRGKGEHFPYEQEIKFFAKVVLPLIDQYFK
!						NHRLYFLSAASRPLCSGGHASNKEKEMVTSL
1						FCKLGVLVRHRISLFGNDATSIVNCLHILGQT
1		İ		1		LDARTVMKTGLESVKSALRAFLDNAAEDLE
į		]	1			KTMENI KOGOFTHTRNOPKGVTOINYTTVA
İ		1				I I PMI SSLIFEHIGOHOFGEDLILEDVQVSCYR
				- 1		I TSLVALGTSKSIYVERORSALGECLAAFAGA
ļ						FPVAFLETHLDKHNTYSIYNTKSSRERAALSL
1			1	1		
			1			TNVEDVCPNIPSLEKLMEEIVELAESGIRYTQ

NO: of Nonucl-peotide se	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of N nucl- protide seq- u	NO: of ceptide seq-	hod	)	beginning	nucleotide	D=Aspartic Acid, E=Glutainic Acid,
nucl- eotide se seq-	eptide seq-	{	in (			n ni delecie G-Chroine H-Histidine
eotide se	seq-	ļ	•	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine, l=Isoleucine, K=Lysine, L=Leucine,
seq- u	uence		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
- 1		i	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
		j	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		. 1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
				sequence		MPHVMEVILPMLCSYMSRWWEHGPENNPER
					l	AFMCCTALNSEHMNTLLGNILKIIYNNLGIDE
		<u> </u>			1	GAWMKRLAVFSOPIINKVKPQLLKTHFLPLM
1		1				FKIKKKAATVVSEEDHLKAEARGDMSEAEL
l l		[				LILDEFTTLARDLYAFYPLLIRFGDYNRAKWL
ì		l				KEPNPEAEELFRMVAEVFTYWSKSHNFKREE
		Ì	\	ł		ONEVVONEINNMSFLITDTKSKMSKAAVSDQ
				}	}	ERKKMKRKGDRYSMQTSLIVAALKRLLPIGL
		Ì		}	•	NICAPGDQELIALAKNRFSLKDTEDEVRDIIRS
		1		}		NIHLQGKLEDPAIRWQMALYKDLPNRTDDTS
		1		1	1	DPEKTVERVLDIANVLFHLEQKSKRVGRRHY
		1	-	1	1	CLVEHPORSKKAVWHKLLSKORKRAVVACF
1		1	}	1	1	RMAPLYNLPRHRAVNLFLQGYEKSWIETEEH
<b>,</b>		1	1			YFEDKLIEDLAKPGAEPPEEDEGTKRVDPLHQ LILLFSRTALTEKCKLEEDFLYMAYADIMAKS
1 1		Ì	1	Ì		CHDEEDDDGEEEVKSFEEKEMEKQKLLYQQ
[ ]			1	\	]	ARLHDRGAAEMVLQTISASKGETGPMVAAT
1		1	İ	1		LKLGIAILNGGNSTVQQKMLDYLKEKKDVGF
1		1		1		FQSLAGLMQSCSVLDLNAFERQNKAEGLGM
1 1				1	1	VTERGSGEKVI ODDEFTCDLFRFLOLLCEGH
1 1			,	1		NSDFONYLRTOTGNNTTVNIIISTVDYLLKVQ
j l		}		1	1	FRIEDEVWYYSGKDVIDEOGORNESKAIQVA
1		1	i	1		KOVENTITEYIOGPCTGNQQSLAHSRLWDAV
1 1		1	1			VGELHVEAHMOMKLSODSSQIELLKELMULQ
		l	1	1	1	KDMVVMLLSMLEGNVVNGTIGKQMVDMLV
1		l		l l		ESSNNVEMILKFFDMFLKLKDLTSSDTFKEYD
		1	1	1		PDGKGVIFKRDFHKAMESHKHYTQSETEFLL
1			-	1	1	SCAETDENETLDYEEFVKRFHEPAKDIGFNVA
		1	j	1		VLLTNLSEHMPNDTRLQTFLELAESVLNYFQP FLGRIEIMGSAKRIERVYFEISESSRTQWEKPQ
1 [		1	]			VKESKRQFIFDVVNEGGEKEKMELFVNFCED
1 1	ĺ	1	1			TIFEMQLAAQISESDLNERSANKEESEKERPEE
		1	1		1	QGPRMAFFSILTVRSALFALRYNILTLMRMLS
1		l	1.	İ	[	I K ST K K OMKK V K K M T V K DM V T AFF 55 Y W 51
		1	1		ľ	FMTLLHEVASVFRGFFRIICSLLLGGSLVEGA
1	1			Ì		KKIKVAELLANMPDPTODEVRGDGEEGERKP
		100		1	1	I FAAL PSEDLTDLKELTEESDLLSDIFGLDLKK
		{	}	)	1	FGGOVKLIPHNPNAGLSDLMSNPVPMPEVQE
	1					KEOFOKAKEEEKEEKEETKSEPEKAEGEDGE
	1	1		1		KEEKAKEDKGKQKLRQLHTHRYGEPEVPESA
	1					FWKKIIAYQQKLLNYFARNFYNMRMLALFV
1	}			1		AFAINFILLFYKVSTSSVVEGKELPTRSSSENA
	}				1	KVTSLDSSSHRIIAVHYVLEESSGYMEPTVRIL
			\	1		PILHTVISFFCIIGYYCLKVPLVIFKREKEVARK
		1		1		LEFDGLYITEQPSEDDIKGQWDRLVINTQSFP NNYWDKFVKRKVMDKYGEFYGRDRISELLG
	1	1	{	1		MDKAALDFSDAREKKKPKKDSSLSAVLNSID
1	1		1	1		VKYQMWKLGVVFTDNSFLYLAWYMTMSVL
1				1		GHY/NNFFFAAHLLDIAMGFKTLRTILSSVTH
	1			}	}	NGKQLVLTVGLLAVVVYLYTVVAFNFFRKF
				1		YNKSEDGDTPDMKCDDMLTCYMFHMYVGV
	[			1		RAGGGIGDEIEDPAGDEYEIYRIIFDITFFFFVI
	1	1				VILLATIOGLIDAFGELRDOOEOVKEDMETKC
	1			1	1	FICGIGNDYFDTVPHGFETHTLQEHNLANYLF
}	1		1	l		FLMYLINKDETEHTGQESYVWKMYQERCWE
	j	l	Į		1	FEPAGDCFRKOYEDOLN
	1	<del></del>	2502	<del> </del>	355	AGLELL NSDDPPALASOSAGITGVTRTPSLFF*
446	1796	A	3592	1	333	DTVLLCCSGWSAVAPSRLTAALFS*AQAVCL
	1	1	1	- {		SLPRSWDYRRW/PPHPANFCIFCRDE/SLA/ML
		Į	1	(		PRLVSNSWTQAILLPRPPKMLGLQV

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	İ	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		{	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uciico	}	1	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ì	)	ļ	residue of	sequence	/=possible nucleotide deletion, \=possible
		1	}	peptide		/=possible nucleonde deletion, \-possible
		1	1	sequence		nucleotide insertion
447	1797	A	3598	1202	1070	LFVGGGPICPEGASGFAPGPAPAPRVGVDAEV
441	1757	1 '	1		Í	GR*V*GAAASQGA/GSLRPRPTGPGHPGAWL
	İ	1		ļ		QVWGAAAVCAGPAM*/AVRAKRGPRAG*EP
		ì	1		}	NSPWRSGVLAA\RAVGAGPWP*P*PGCS*ARG
	1	ĺ	ı		}	PSSRSAPGLASGPAAPLLQGVHSSAGPLLCYI
	1	1	[	ļ	1	NIGIT ALGUKP**AWGWGEWRPKG
			12604	2116	557	ERREGGGEREDEGAGLKYNSRHEKVNGLEE
448	1798	A	3604	3115	337	GVEEL PVNNVKKVEKHGPGRWVVLAAVLIG
	1	1	l	1		LILLVILGIGELVWHLOYRDVRVQKVFNGYM
	-	1	Ì			RITNENFVDAYENSNSTEFVSLASKVKDALKL
	1		1	1	1	LYSGVPFLGPYHKESAVTAFSEGSVIAYYWSE
			ì	1	[	FSIPQHLVEEAERVMAEERVVMLPPRARSLKS
		1	1	1	<b>\</b>	FVVTSVVAFPTDSKTVQRTQDNSCSFGLHAR
:		1	j	<b>)</b>		GVELMRFTTPGFPDSPYPAHARCQWALRGD
	1		1	ļ		ADSVLSLTFRSFDLASCDERGRHLV\TVYNT\L
	1	-	ì	ì	1	SPMEPHALL VQLCGTYPPSYNLTFHS\S\QNVL
	1	1	ł			LITLITNTERRHPG/FEATFFQLPRMSSCGGRL
	1	}	1	1	(	RKAQGTFNSPYYPGHYPPNIDCTWNIEVPNN
			ł	1		QHVKVRFKFFYLLEPGVPAGTCPKDYVEING
	1	1	<b>\</b>	) -		QHVKVKFKFF YLLEPOVFAGTCT KDT VEITO
İ		- {	-		İ	EKYCGERSQFVVTSNSNKITVRFHSDQSYTDT
	1	1	l	1	ļ	GFLAEYLSYDSSDPCPGQFTCRTGRCIRKELR
	ļ	1	l	ł	1	CDGWADCTDHSDELNCSCDAGHQFTCKNKF
]	}	- }	1	Į.	Ì	CKPLFWVCDSLNDCGDNSDEQGCSCPAQTF
	1	1	1		1	RCSNGKCLSKSQQCNGKDDCGDGSDEASCP
	ì		1	Ì		KVNVVTCTKHTYRCLNGLCLSKGNPECDGK
	1		(			EDCSDGSDEKDCDCGLRSFTRQARVVGGTD
ļ		1			1	ADEGEWPWQVSLHALGQGHICGASLISPNWL
]	j ,	1	}	1	1	VSAAHCYIDDRGFRYSDPTQWTAFLGLHDQS
Ì	}	1	j			QRSAPGVQERRLKRIISHPFFNDFTFDYDIALL
1	- 1	1	1		Ì	FIFKPAEYSSMVRPICLPDASHVFPAGKAIWV
1	- [	1	.		1	TGWGHTQYGGTGALILQKGEIRVINQTTCEN
1	1	ļ	1	(	Į.	1 I POOITPRMMCVGFLSGGVDSCQGDSGGPL
	1	1				SSVEADGRIFQAGVVSWGDGCAQRNKPGVY
	1	- )	1	}	l	TO DE FROMIKENTGV
					613	FVSGSPWRMDGSTERLEARRPAGRLPWSSRQ
449	1799	A	3618	2	013	EMTRRPSLMAGROHGWSAQQSATVANPVPG
		1			1	ANPOLLPHELGEPEDVYIVKNKPVLLVCKAV
			1	1	1	PATOIEFK CNGEWVROVDHVIERS I DGSSGLI
		}			1	TMEVRINVSRQQVEKVFGLEEYWCQCVAWS
		}			1	SSGTTKSQKAYIRIAYLRKNFEQEPLAKEVSL
1		-		}	1	EQGIVLPCRPPEGIPPAE
		1				MEPSLGQGMDLTCPFGVSPACGAQASWSIFG
450	1800	A	3620	1	2676	ADAAEVPGTRGHSQQEAAMPHIPEDEEPPGE
1 750		1		}		ADAAE V POI KONSQUEAA VIF HIT EDELIT OF
1			1			PQAAQSPAGQQGPPTAGVSCSPTPTIVLTGDA
			1			TSPEGETDKNLANRVHSPHKRLSHRHLKVST
1	1	1	{		1	ASLTSVDPAGHIIDLVNDQLPDISISEEDKKKN
1		1				LALLEEAKLVSERFLTRRGRKSRSSPGDSPSA
		1				VSPNLSPSASPTSSRSNSLTVPTPPEGDEADVS
İ		)				SPHPGEPNVPKGLADRKQNDQRKVSQGRLAI
	1	1		1		PPPPVEKSKEJAJEOKENFDPLOYPETTPKGLA
		Ì		l.		PVTNSSGKMALNSPOPGPVESELGKQLLKTG
		1				WEGSPLPRSPTODAAGVGPPASOGRGPAGEP
1	1					MGPEAGSKAELPPTVSRPPLLRGLSWDSGPE
				1		PGPRIOKVLAKLPLAEEEKRFAGKAGGKLAK
	1					APGLKDFQIQVQPVRMQKLTKLREEHILMRN
	İ			1	1	AL OUADI VIV. A TRANSPORT OF A IEEE
		Ì	1	t	i	ONIT VOLKI POLSEAAFOEKGI PSELSTALEEE
						ONLYGLKLPDLSEAAEQEKGLPSELSPAIEEE
						FSKSGLDVMPNISDVLLRKLRVHRSLPGSAPI
						ESKSGLDVMPNISDVLLRKLRVHRSLPGSAPI I TEKEVENVFVOLSSAFRNDSYTLESRINQAE
						FSKSGLDVMPNISDVLLRKLRVHRSLPGSAPI

						Amino scia senticine (A-Adminic C-C) stories
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine R=Arginine, S=Serine,
uence	1 1		914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	[ ]	Ì		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ		peptide .	Joquence	/=possible nucleotide deletion, \=possible
		İ			1	nucleotide insertion
	·	<b></b> _	ļ	sequence	ļ	VROEKRMSKATEVMMQYVENLKRTYEKDH
		ł				A EL MEEKKLANONSSRSCGPSEDGVLRTARS
	ł	}			{	MSI TI GKNMPRRRVSVAVVPKFNALNLPGQ
	1	<b>\</b>	1	ł		TRESSSIPSI PALSESPNGKGSLPVTSALPALLE
	1	1				MGKTNGDPDCEASAPALTLSCLEELSQETKA
		1		1		DMEERAVSKGFOEGLKKTKELODLKEELELU
		1	1	1		VSESPEEPEEVEETEEEEKDPRSSKLEELVHIL
	1	1	1			OVMYPKI COHWOVIWMMAAVMLVLIVVL
	1	1	1	i		GLYNSYNSCAEQADGPLGRSTCSAAQKDSW
	1	1				WSSGI OHEOPTEO
		<del></del>	10/22	504	198	QLIQHQTVHTGRKLYECKECGKAFNQGSTLI
451	1801	Α	3623	304	1,50	PHODIHTGEKPYECKVCGKAFRVSSQLKQHQ
		1			1	RIHTGERPYQCKELKGRGAEMLAVLAVKEQ
	1	1		1	ł	NOTOVNIVCK
		<del>                                     </del>	3628	2	195	MTCI HSAKAFHY*SSCSFSCEEGFALIGPEVV
452	1802	A	3020	4	1	OCTAL GVWTAPAPVCIAVQCQHLEALNEGI
	1	1				MG*DYPFTAFAYGSSCKYECHTVYRVRGLD
	ł	1				MLHSRGCYLWNGHFTT*EAISCEPLERPCH*S
						V*CSFSCEEGFALIGPEVVQCTALGVWTAPAP
	}			1		VCIAVOCOHI EALNEGTMG
	1.000		3637	662	142	1QAKGLGIWHVPNKSPMQHWR\KGSLLRYRT
453	1803	Α	3037	002		DTGFLQTLGHNLLGIYQKYPVKYGEGKCWT
1	1	ļ			{	DNGPVIPVVYDFGDAQKTASYYSPYGQREFT
	1	1			1	AGFVQFRVFNNERAANALCAGMRVTGCNTE
1	1	l		}		HHCIGGGGYFPEASPQQCGDFSGFDWSGYGT
1	1	1			_	\HVGYSSSREITE\AAVLLFYR
454	1804	A	3641	1	362	TOVHPAMLGLDELGRSGCGHCTQADLRFGD
434	1807	1		1		AAGRDPGQDNDRNTAEPAFPPPPRVMAAAA ALRAPAQSSVTFEDVAVNFSLEEWSLLNEAQ
ļ			l l	1	Ì	ALRAPAOSSVIFEDVAVNISLEEWSEENEN
}	1	L				TO THE PARTY OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF
1						CCT VHDVMLETLTLISSLGKVLILNCULS
455	1805	A	3646	2	414	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEOGRRVGLGSRAH
455	1805	A	3646	2	414	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTENSCOVSSOPPRVAGLGLPLKHEPS
455	1805	A	3646	2	414	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS PROPPSPRGPRTVRAGVPGAHPQDTPCPEFVR
455	1805	A	3646	2	414	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE
455	1805	A	3646			GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE
		A	3646	396	414	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  OVSENSYLTLYTKNNLKSMKDLNVNTEMIK
455	1805					GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW
						GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW PRIJKJKSFCSI.SDTJKKMKROTIVWEQTFIIHI
						GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK
			3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK
						GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAII SRAPWSLOSVNPGLKTNSSKEPKF
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TVCPSPERFTFSCHWTDEVHHGTKNLGPIQLF
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TVCPSPERFTFSCHWTDEVHHGTKNLGPIQLF
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSETSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEGGRAFVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSETSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTILLNVSLTGIHADIQVRWEAPRN
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVIHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVSKQRNSGNY GESFVI_YVTLPOMSOFTCEEDFYFPWLLIIIF
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDILIKEGKLEEVNTILAIHDSYKPEFHS
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPYYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPYYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGGGGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPVPVPVKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTESSDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGGGGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH SPYNDACPATOOPSVIOAEKNKPOPLPTEGAE
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGGGGGRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCTSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEQGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGEGGRRVGLGSRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS VVLSPGQKNKAGMSQCDMHPEMVSLCQENF
456	1806	A	3656	396	8	GCLYHDVMLETLTLISSLGKVLILNCDLS  AAAGRGASGALTGEGGGGGGGRAH SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE SRVRAPSYDDIT  QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK F  SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF YTRRNTQEWTQEWKECPDYVSAGENSCYFN SSFTSIWIPYCIKLTSNGGTVDEKCTSVDEIVQ PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN ADIQKGWMVLEYELQYKEVNETKWKMMDP ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE

			1 050	D 31-4-4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Mct	SEQ	Predicted	i e	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	Ì	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ļ	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	,	}	)	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
{	!	1	1		Soquene	/=possible nucleotide deletion, \=possible
ĺ	1	1	1	peptide		nucleotide insertion
1	ļ	l	l	sequence		PVPDYTSIHIVQSPQGLILNATALPLPDKEFLS
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458	1808	A	3663	154	462	TRAPASGRSGAGLALSANAPDSGGHPGATEG
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l			<del> </del>		135	LGKYNTSMALFDFVLHNSTGEIRYITEDDVIQ
459	1809	A	3664	902	133	SQNALGKYNTSMALFESNSFEKTILESPYYVD
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460	1810	A	3670	850	557	LGILMSPQVEAGEI*ALLTPPPGCMQFSPLTL/P
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461	1811	Α	3671	24/2	2000	TSAFRIAGTTSVHHHPQLTFFFFWIETGSHCV
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462	1812	A	3672	394	110	VKPVNGESKRD*GADTQTCEGEADEQLQT\N
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463	1813	A	3673	348	1	KSSFSRDQDVW*SQAVPKRQ*QRNPFSAGHP
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464	1814	A	3070	2233	320	KVFOLLPSFPTLTRSKSHESQLGNRIDDVSSM
		1	1			RFDLSHGSPQMVRRDIGLSVTHRFSTKSWLS
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			}	1	)	VYLQEWDIPFEQVELGEPIGQGRWGRVHRGR
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		1	1			WHGEVAIRLLEMDGHNQDHLKLFKKEVMN
1	1	1	1			YRQTRHENVVLFMGACMNPPHLAIITSFCKG
	1	l	- 1	1	1	RTLHSEVRDPKTSLDINKTRQIAQEIIKGMGY
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1	1	[				VSLGKEVSENLSACWAFDLQERPS\FSLLMD
}			1	1	1	MLEKLPKLNRRLSHPGHF*KSADINSSKVVPR
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L					1002	IPSPAWWNSTWADTFSLLLALAVALYLGYY
465	1815	A	3679	8	803	WACVLQTHRAFCASNTEDLETVVNHIKHRYP
				1	1	WACVLUIRIATCABNIEDLEI VYNIIAIANI
1	1		ĺ	1		QAPLLAVGISFGGILVLNHLAQARQAAGLVA
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	ļ		1	1		GLCQLVERLSY/E*DLQARTIRQFDERYTSVA
L	1					

	ero m	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	hod	ID NO:	beginning	nucleotide	D-Accordic Acid F=Glutamic Acid,
10: of	NO: of peptide	lloa	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
eq- ience	daice	l	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
ichc		}		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			ļ	residue of	sequence	/=possible nucleotide deletion, \=possible
		Ì	1	peptide		nucleotide insertion
			l	sequence		PGYODCYTYYKAASPRTKIDAIRIPVLYLSAA
					1	DDDFSTVCALPKOAAOHSPYVALLITARGGHI
	1	1				GFLEGLLPWQHWYMSRLLHQYAKAIFQDPE
		l	Ì		1	CL DDI PALI PSEDRNS
		<u> </u>	1		307	CCOVIVOSKTKIFI * AAREKO/RHTCRRFSIRLS
466	1816	A	3684	3	307	ANISSOTGEARGOWPSVFKVLKEKKLOIKKO
		1	1	1		FGQK*GR\RKTFPDKQK/LREFDTTRPTIQEML
			1	1		TCVI OG
		<b>_</b>	3687	2465	837	ELPTPLIAAHQLYNYVADHASSYHMKPLRMA
467	1817	A	3087	2403	[ 03.	DECOPEHNEYALVSAWHSSGSYLDSEGLKING
				1	1	L DDEDVSI I VCHCAAPFEEOGEAEKHVLKLQI
	1	-	1			TYVI TSOREL FPRI TADMRRFRK PPRLPPEPE
	1	1	1	1		A DCSC A CSPGFASGI II APGPAPLEPPLAAE VU
			1			MARARLAQLVRLAGGHCRRDTLWKRLFLLE
		1				PPGPDRLRLGGRLALAELEELLEAVHAKSIGD
		1				IDPOLDCFLSMTVSWYQSLIKVLLSRFPQSCR
	1	1			)	HFQSPDLGTQYLVVLNQKFTDCFVLVFLDSH LGKTSLTVVFREPFPVQPQDSESPPAQLVSTY
	}				]	HHLESVINTACFTLWTRLL*GSGLDH*MSLFL
		1	1			ESWAYQIACQRQD*PALLGPRASQTLSDTKG
		l				FVTMS*GSAAPAWQQEPPSPNTHSH*PIQDSR
	1	٠.				ESGQPRGPLGPFWGTPFGPPGRVSGVHTGWC
		1	ŀ	1		TPPRAPLPESCPL\PLTTVSHLCPLSLRVFTSHL
	ļ	1	ł	İ		DITAGHSHRDDTWVPIPALPLKHLRPPSSPFA
	1		1			LGPWVSHPLMRWVQKLSHLHSNPGTGFSMC
						CKOORN
				1 250	499	OTCDVDVD A IVPHEONE MNEIKAI*SGTGGI
468	1818	A	3691	960	499	OCEHSONDSAFFFFLFLLETEFCSAA/IVQWI
			1	1	1	DELSMOPPPPGFKOFTCLSLLSSWNIKKUFF
<b>,</b>		1	1		}	PGNF\*FLVKTGFPHVGQTGFELLISSDLAPLA
ł	l		}	1	)	CONGGITGMSPCAWPFFFFFFFGLC
l			3714	4747	495	TAAVSWOTDPNPNESHEKOYEHQEFLIVNQP
469	1819	Α	3/14	4/4/	175	TIESSOUSI GEDOIVDEISGKIPHYESELDEN IF
{				ĺ		VDTAPKWDSTGHSLNEAHOISLNEFISKSKE
ļ		- 1				SWHOVSKAPAIGFSPSVLPKPUNINKECOWC
1				1	į .	SPIGKHHGADDSRFSILAPSFTSLDKINLEKEI
1		1		1		ENENHNYHIGFESSIPPTNSSFSSDFMPKEEN
Į.	1	}	}	1	}	RSGHVNIVEPSLMLLKGSLQPGMWESTWQK
İ	ļ		1		1	NIESIGCSIQLVEVPQSSNTSLASFCNKVKKIR
1		l		1	j	ERYHAADVNFNSGKIWSTTTAFPYQLFSKT
İ		ı	i	ļ	1	FNIHIFIDNSTQPLHFMPCANYLVKDLIAEILI
1		- (				FCTNDQLLPKDHILSVWGSEEFLQNDHCLGS
į.			1	Ì		HKMFQKDKSVIQLHLQKSREAPGKLSRKHE
1		- 1	ł	į		DHSQFYLNQLLEFMHIWKVSRQCLLTLIRKY
		1	1	1	1	DFHLKYLLKTQENVYNIIEEVKKICSVLGCV
] .		j	1		1	TKQITDAVNELSLILQRKGENFYQSSETSAK LIEKVTTELSTSIYQLINVYCNSFYADFQPVN
	1	1	1	1	1	PRCTSYLNPGLPSHLSFTVYAAHNIPETWVF
1	1			j		INFPLEIKSLPRESMLTVKLFGIACATNNANL
1		-	1	1		AWTCLPLFPKEKSILGSMLFSMTLQSEPPVE
1				1	1	ITPGVWDVSQPSPVTLQIDFPATGWEYMKP
			1	1		SEENRSNLEEPLKECIKHIARLSQKQTPLLLS
1				1		EKKRYLWFYRFYCNNENCSLPLVLGSAPGV
		1	1			DERTVSEMHTILRRWTFSQPLEALGLLTSSF
1	1	1			1	DERTVSEMHTILRRWTFSQLEEALSDD
].	i		- 1	ł	Į.	KFEWNLESPLVQLLLHRSLQSIQVAHRLYW
1	}	1		1	1	LKNAENEAYFKSWYQKLLAALQFCAGKAL
1	1	- 1	ı	l l	ı	LKNAENEA ITASW I VALLAMEVI CHOME
1	{	ì		1		PRESENTANT OF CHICEDIVES A SUHURUEV
						DEECK FOR I IKIT GDIGERVKSASDHQKQEV
						DEFSKEQKLIKILGDIGERVKSASDHQRQEV KKEIGRLEEFFQDVNTCHLPLNPALCIKGID DACSYFTSNALPLKITFINANLMGKNISIIFK

WO 01/57188

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	l	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	] -	09/496	correspondi	to last amino acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		İ	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
		1		amino acid	of peptide sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	İ	(		residue of	sequence	/=possible nucleotide deletion, \=possible
	}	1		peptide	1	nucleotide insertion
		<u> </u>		sequence	<del> </del>	GDDLRQDMLVLQLIQVMDNIWLQEGLDMQ
			]	Ì	}	MILYRCLSTGKDORLVQMVPDAVTLAKIHKH
		1	1		j	SGLIGPLKENTIKKWFSOHNHLKADYEKALR
	1	1			1	NEFYSCAGWCVVTFILGVCDRHNDNIMLTKS
		1			i	GHMFHIDEGKELGHAOTEGGIKRDRAPFIETS
		}	}			FM/EYFITEGG/KNPOHFODFV/ELCCRAYNUR
		ļ		}		KHSOLLL\NLL\EMMLYAG\LPELSGI\QDLKY
		1				VYNNLRPQDTDLEATSHFTKKIKESLECFPVK
		1				LNNLIHTLAQMSAISPAKSTSQTFPQESCLLST
		1	1			TRSIERATILGFSKKSSNLYLIQVTHSNNETSL
			ì	1	1	TEKSFEQFSKLHSQLQKQFASLTLPEFPHWW
	}	1	1		1	HLPFTNSDHRRFRDLNHYMEQILNVSHEVTN
l		1		1	1	SDCVLSFFLSEAGQQTVEESSPVYLGEKFPDK KPKVQLVISYEDVKLTILVKHMKNIHLPDGSA
l						PSAHVEFYLLPYPSEVRRKTKSVPKCTDPTY
	-	•	Ĭ	1		NEIVVYDEVTELQGHVLMLIVKSKTVFVGAI
	1	1		[	•	NIRLCSVPLDKEKWYPLGNSII*PLLLFSSFGM
İ	1	}		1		KSLEKDEFVGGMLLSNPIW
				120	75	SHGSISILNLHOGCVFLPSLPAQGLRCYRCLA
470	1820	Α	3718	430	13	VI_EGASCSVVSCPFLDGVCVSQKVSV/CWQ*/
			<b>\</b>	1	}	CPWGARAEGRLSAVVDSQISCCKGDLCNAV
						VLAAGSPWALCVQLLLSLGSVFLWALL
471	1821	A	3723	891	494	LRQSL/NSVPQAGVQWRDSSLQAPPPRFTPLS
4/1	1021	1	3723		{	CLSLPSSWDYRRLPPCLANFLYF**RRGFTML
	1	1		l	1	ARMVLIS*PRDPPASASQ\STEITGGSHRAQHP
		1		ł		TDSRDHSERSVKKSHEVISELRMKVIKCKVAF
1		1				SKNPI GFIET*NFCVSKDTSKKLS/RLPTKWKNVFAN
472	1822	A	3734	443	251	*ISDKGLVSRICQELLRHLDAEQVSSTAGLSL
		1				THASGGARSGAGWAGRGVRAGTEAGRGGIF
473	1823	Α	3746	3	500	LTLSILRTRDLPSGAMSEGVDLIDIYADEEFNQ
,				· I		DPEFNNTDOIDLYDDVLTATSQPSDDRSSSTE
						PPPPVROEPSPKPNNKTPAILYTYSGLRNRKA
	}	- 1				AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV
1	1	1		ļ	}	KEAENRAK
15.	1824	- A	3753	2	5262	RPLFAREGGIYAVLVCMQEYKTSV\LVQQAG
474	1024	^ _	3733	-		LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ
1		-		1	1	MTREIFASIDSATRPGSESLLLTVPAAVILMLN
		- }	ļ	{	1	TEGCSSAARNGLLLNLLLCNHHTLGDQUTQ
- ]	1	1		Ì		ELROTLFRHSGIAPRTEPMPTTRTILMMLLNR
į		1	1	Į.		YSEPPGSPERAALETPIIQGQDGSPELLIRSLV GGPSAELLLDLERVLCREGSPGGAVRPLLKRL
						QQETQPFLLLLRTLDAPGPNKTLLLSVLRVIT
1		- 1	İ	1		RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE
		- 1	1	1		IVQELTCFLHRLASMHKDYAVVLCCLGAKEI
}	İ		1		1	LSKVLDKHSAQLLLGCELRDLVTECEKYAQL
l		- 1				VSNI TSSII AGCIOMVLGOIEDHRRTHQPINIP
i				)		FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN
		1			1	PHRASKLTDHNPKTYWESNGSTGSHYITLHM
		(	1	1		HRGVLVROLTLLVASEDSSYMPARVVVFGG
-						DSTSCIGTELNTVNVMPSASRVILLENLNRFW
		1				PUOTRIKRCOOGGIDTRVRGVEVLGPKPTFWP
1	1	- (				I FREGI CRRTCLEYTIRAOAWSRDIAEDHRRL
1	j	- /		1	1	LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL
	İ		Ì		i	LOUCING THE ANY AND THE PROPERTY OF THE
						GKTCWEALVSPLVONITSPDAEGVSALGWLL
						GKTCWEALVSPLVQNITSPDAEGVSALGWLL DOYLEORETSRNPLSRAASFASRVRRLCHLL
						GKTCWEALVSPLVQNITSPDAEGVSALGWLL DQYLEQRETSRNPLSRAASFASRVRRLCHLL VHVEPPPGPSPEPSTRPFSKNSKGRDRSPAPSP
						GKTCWEALVSPLVQNITSPDAEGVSALGWLL DOYLEORETSRNPLSRAASFASRVRRLCHLL

			1000	TO a dilate of	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	1=1501eucine, K-Lysine, L-Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
delice		1		arnino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	peptide	304	/=possible nucleotide deletion, \=possible
	1	İ		,		nucleotide insertion
				sequence		ALRSGFSGALLQQSFLTAAHMSEQFARYIDQ
						ALKSGFSGALLQQSFLTAAHWSEQFAKTIDQ
	ł		1	}	Ì	QIQGGLIGGAPGVEMLGQLQRHLEPIMVLSG
	[	1	ì			LELATTFEHFYQHYMADRLLSFGSSWLEGAV
		ļ	1	}		LEQIGLCFPNRLPQLMLQSLSTSEELQRQFHLF
					}	OLORLDKLFLEOEDEEEKRL*EEEEEEEEA
	1	ì	1		ĺ	EKELFIEDPSPAISILVLSPRCWPVSPLCYLYHP
	1	1	1			RKCLPTEFCDALDRFSSFYSQSQNHPVLDMG
			1		}	PHRRLQWTWLGRAELQFGKQILHVSTVQMW
	1	1	1	ļ		PHKKLQW I WLGKAELQFORQILITYS I YQM W
		1	ļ	Į		LLLKFNQTEEVSVETLLKDSDLSPELLLQALV
		ļ				PLTSGNGPLTLHEGQDFPHGGVLRLHEPGPQ
1	1	1				RSGEALWLIPPOAYLNVEKDEGRTLEQKRNL
	1	i	1	1	1	LSCLLVRILKAHGEKGLHIDQLVCLVLEAWQ
1		1	1			KGPNPPGTLGHTVAGGVACTSTDVLSCILHLL
1	l	1	1	1	i	GQGYVKRRDDRPQILMYAAPEPMGPCRGQA
1	1	1	1			DAMEGOGGET CARDET AND THE THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE T
1	1	1	1	1		DVPFCGSQSETSKPSPEAVATLASLQLPAGRT
1	1	1		1	1	MSPQEVEGLMKQTVRQVQETLNLEPDVAQH
	1			1	1	LLAHSHWGAEQLLQSYSEDPEPLLLAAGLCV
l			ł		1	HQAQAVPVRPDHCPVCVSPLGCDDDLPSLCC
ł		ľ	ł		1	MHYCCKSCWNEYLTTRIEQNLVLNCTCPIAD
1		1	- 1	ì		CPAQPTGAFIRAIVSSPEVISKYEKALLRGYVE
l.		1	1	i	1	SCSNLTWCTNPQGCDRILCRQGLGCGTTCSK
1	1			Į.		CGWASCFNCSFPEAHYPASCGHMSQWVDDG
1	]		1	ł	1	GYYDGMSVEAQSKHLAKLISKRCPSCQAPIE
1			i	ļ	1	GYYDGMSVEAQSKILKKLISKKCI SEQIRIB
i			1			KNEGCLHMTCAKCNHGFCWRCLKSWKPNH
		ļ				KDYYNCSAMVSKAARQEKRFQDYNERCTFH
1	-		1	1		HOAREFAVNLRNRVSAIHEVPPPRSFTFLNDA
		1	Ì	1		COGLEOARKVLAYACVYSFYSQDAEYMDVV
i	1	}	)	1		EQQTENLELHTNALQILLEETLLRCRDLASSL
	l l	1		1		RLLRADCLSTGMELLRRIQERLLAILQHSAQD
			- 1		l	FRVGLQSPSVEAWEAKGPNMPGSQPQASSGP
l	<b>\</b>		l l		!	FKVGLQSF3VEAWEAKOI WIN GSQI QILSSGI
1			1			EAEEEEDDEDDVPEWQQDEFDEELDNDSFS
	ł	-	İ			YDESENLDQETFFFGDEEEDEDEAYD
475	1825	A	3754	1093	96	GTSRNQHSPKTHA*RSS/WPQPPPLFLPPLQPQ
4/3	1025	Α.	1 3,31	1000		ATGRRRRTRTQQRTAALLTDGTTKTGAAW
ļ			1	1	1	SRRPSLCWPSRTTGAPGAK*AVLVRSATPTTN
1	1		İ			PPNPQSPTGAAGKLRAPGNRAG/SEPSSQEPPP
Į.	- 1	- [				DGTR/RPASITGVAQSPATRATPSLPCLHVPAP
			1	1		SRGQTLGVRTTGRASRLTVDRSRLSWPGRSA
	J				1	RSGGGRWRPNAPRGRWPRAP*SWEPGSWTE
	ì		1	1	1	KSGGGK WKTNAFKGK WFKAF 'S WELGSWIE
	ļ			1	1	PWRWPFPAAESPPHRCIYCTNHVSPAGPARPS
1	1		1	ĺ		HVYIIRATINSISHPLCRAQSSPWEAAGVWRR
1	1		1	[		PAQPAPTSDVNINLLRKPRVKRHDLIYQFLGN
1				1		TI.WEEGRORPPETLOPAR
				1003	621	FFFGNGVSPCPQAGV*WHDLDSLQNLPPGFK
476	1826	A	3758	901	521	RFSYLSLPSSW\DYRHVPPRQANFCIF/M*RRG
						TO I AD AIGIC PODDI DAI A COCACITO CHIL
	1	1	1			FTMLARMVSIS*PRDLPALASQSAGITGVSHH
1			1			APPOMDFTFALLCFAPKGCLPRQKEGGTLNLI
100	1937	- <del> </del> -	3761	843	575	GVISAHCNLRL/CHLPGSSNSPASASQVAGTIG
477	1827	A	3/01	545	1	ARTTPS*IFVFLVETGFHHVSQDGLDLL/NFVI
1	1			1		RPRRPLKVLGLQACTRARLPSPLKEL
1		_1_			1010	HLLSFHLWSASLDCLEQLSQERHVKGMLLGP
478	1828	A	3763	267	1240	PPVNESTKPSPSPWKLTPPMCSIPPVFPPKSGS
1 .			1			PPVNESI KPSPSP WKLIPPMCSIFF VFF KSOS
1	1	- 1	1			PTTSWS/PSGHSKLEVERAQTGPFCLHIYCP*P
1			1		1	GVTDNTTSLLHYIPFPRL\SGLVCFPAH*FPSY
	1	1	. [			WTGHSFASQAWLRQVPEVSKHLQCPSAESLL
		1	l l			TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG
1				1		PDEHPQDTDARDADGEAREREP/RRPSFAA*P
				1		PUENTQUI DARDADGEAREREFIRM SI AA I
}		- 1	}			VWGQP\ESPLPEASSAPPGPTLGTLPEVETIRA
1	1	- 1	ı	4		CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE
1	l l					
	1	ì	İ			QTPIITQSTNGPLPSPCHHEHPLSSVEGEAPPA

					7 1: A. d. and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uenœ	ĺ		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
,	ļ	ļ	1	peptide	Soquene	/=possible nucleotide deletion, \=possible
		1		sequence	Ì	nucleotide insertion
	L	<del> </del>		sequence		EGSDHIG
		ļ	3766	2	2152	VSPIRILEVCVPLPKIFIKROAPLKVSLLQDLK
479	1829	Α	3/00	2	2152	DFFOKVSOVYVAIDERLASLKTDTFSKTREEK
	!		}			MEDIFAOKEMEEGEFKNWIEKMQARLMSSS
			1	1		VDTPOOLOSVFESLIAKKQSLCEVLQAWNNR
	1	-		1		LODLFOOEKGRKRPSVPPSPGRLRQGEESKIS
	0	1			ļ.	AMDASPRNISPGLONGEKEDRFLTTLSSQSST
				1	ł	SSTHLOLPTPPEVMSEQSVGGPPELDTASSSE
	}		1		1	DVFDGHLLGSTDSOVKEKSTMKAIFANLLPG
				1		NSYNPIPFPFDPDKHYLMYEHERVPIAVCEKE
	1	Y				PSSILAFALSCKEYRNALEELSKATOWNSAEE
		1	1			GLPTNSTSDSRPKSSSPIRLPEMSGGQTNRTTE
						TEPOPTKKASGMLSFFRGTAGKSPDLSSQKRE
	Ĭ					TLRGADSAYYQVGQTGKEGTENQGVEPQDE
		1		1		VDGGDTQKKQLINPHVELQFSDANAKFYCRL
					ļ	YYAGEFHKMREVILDSSEEDFIRSLSHSSPWQ
1		1	1	1		ARGGKSGAAFYATEDDRFILKQMPRLEVQSF
						LDFAPHYFNYITNAVQQKRPTALAKILGVYRI
]	ĺ	1		1		GYKNSQNNTEKKLDLLVMENLFYGRKMAQ
ļ		]				VFDLKGSLRNRNVKTDTGKESCDVVLLDENL
ļ	)			}	1	LKMVRDNPLYIRSHSKAVLRTSIHSDSHFLSS
	1				i	HLIIDYSLLVGRDDTSNELVVGIIDYIRTFTWD
						KKLEMVVKSTGILGGQG*MPTVVSPELYRTR
		1				FCEAMDNYFLMVPDHCTGLGLNC
480	1830	A	3777	251	3	QGCGSAGTLIHY**ECKMVQLLWKTV*QFLI
700	1000			{		KLNIKDPAITLDVYPNEVKNYVRTKTYTQMF
						I/ANFIMAKSWKQPTHPSVRT EAAIRQPEPNILDVNQIFKDLAMIIHDQGDLID
481	1831	A	3779	333	3	SIEANAESSEVLVERAPGQLQRPA\YYQKKSR
10.		1		1		KKMCLVVLVQTAIILICERIM*VVYTTKWSPPI
				1		VLPVSCFQGQKFN
1		ì	i			TGGRQGKNDHTSITEKPSRDFNRHLITQNI*M
482	1832	A	3780	2	371	PNQDMKSSSNSLIIRKVQIKPTILYHHIFTRKA
		1		}		KMKTTDKTKYR*GFKAITTLIHCSQDCKLQ*S
1						/L*ENHFMIFPKAEQHITYDTTIPFLR
}		1				LMKDLSPYVMETHYILNRLNER/RSMWRHIIG
483	1833	A	3787	43	448	KLPNTKDQEKILKAIRGRREVIQGS/RQQYRR
						PAAFSAAEKARRLWCS/VFNIERRNL/CEYPTK
		- (				LSFNIKGEMTFSDKTEFTTNRPSLKMLLKDRI
1		1		1		QEEGKMF*KEKCFKRKE
					727	FFFFETESRSVAQAGVQWCNLGSLQALPPGF\
484	1834	A	3798	1	727	SHSPASASRVAGTTGTRH*ARLIFYIFSRDGVS
				1	l	PC*PGWS*SPDLVIRPP\RLPKCWDYRREPPRP
			1	1		A*FFVFLVE\OGFTMLARMVSIS*PQ/CDLPAS
1				1		VSQNAGITGVSHCAWPCLHFCFFGFFFEMESC
		}	1	J		SVAOAEVOWHDLRSLOAPPPGFTPFSCLSLPG
		- 1	1	İ		SWDYRRPPPRPANF\CIFSRDGVSPC*PGWSRS
	1					PDLVIRPPRPPKVLGLQA
					220	FFFFEMECLTVSQAGVQWYNLHSLQPLPPGF
485	1835	Α	3802	1	239	KOFSC\LSLPSSWD*RVPTSRPAKF/CVIF*DGV
		}		1	1	SHCQPGWSAVVQPPLH
						RYD*SSQSENIP\QKEFLLKYP*CTATLGMRN
486	1836	A	3811	378	98	MSIMKKKSIFSAEFYKVSLPSLLLVHLLAIEWG
						FHIEIQLTIHQHFLNYELESDFVHIVEYM
			1			FDPDWTRAAGIRHEKKPKALAYRRENSPGDL
487	1837	A	3814	771	320	PPPPLPPPEEEASWAL/GAEGSRQHVLPGAGA
1			-			QWGEESGPGRAPGSPAGAPPR*RGLAP\NSRP
1			1	1		CARGESOLOWALOSLYOUTLY, KORVI ILOIN
ĺ						
		1		1		SFLSRGQGTSTCSTAGSNSSRGSSSSRGSRGPC RSRSRSQSRSQSQRPGQKRREEPR

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SED_ID   SEQ_ID   Mod   ID NO:   hold   ID NO:   hold   ID NO:   hold   ID NO:   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hold   hol							Amino acid sequence (A=Alanine C=Cysteine,
NO. of NO. of In Inculation and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent and Incurrent an	L GEO ID	SEOID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alamine C=Cystoling)
auch peptide entitle in a stammor of the peptide of the peptide of peptide entitle of peptide sequence per per per per per per per per per pe			hod	ID NO:			E=Phenylalanine, G=Glycine, H=Histidine,
conide of sequence when the corresponding of the sequence peptide sequence peptide sequence peptide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se		peptide	1			location	I-Icoleucine K=I vsine L=Leucine,
uence    914	eotide	seq-				to last amino	M=Methionine, N=Asparagine, P=Proline,
amino seid recible of peptide sequence peptide sequence peptide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se		uence	Ì		no to first	acid residue	O-Glutamine R=Arginine, S=Serine,
488 1838 A 3818 1 781 FRANCE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P	uence		1	914	amino acid		T=Threonine, V=Valine, W=Tryptopnan,
### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence   ### Poptide sequence		1		1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
TRACILLEIPYAPTISWITACPPAMAGIRGLE   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing   Tracing		1		1			/=possible nucleotide detetion, (~possible
488   838   A   2818   LICLLAFCLAGFSFWRGQVLFWGLDWITH FLYCTSCAMKQTCFSGWTRELPDQTGDCC YFVQLGGSWYSMSGCRRKCKQVVQKACG GYWGSRCHECTGGAETTCMGHGTCLDGMDR NGTCVCQNFRGSACGEQDPNRFGDPCQSY GSCWHOVCHGFRGDSGCLCFAGYTGPHCD QELPWQELGFPQNNFPLRKAFNCKCLPGFP RIGILATIPICCEP RIGILATIPICCEP RIGILATIPICCEP ASSA'S AGTIGACHAQLIFVELVETGHHVG QDGLDLLAMHPPRPPKVLGFQA ASSA'S AGTIGACHAQLIFVELVETGHHVG QDGLDLLAMHPPRPPKVLGFQA ASSA'S AGTIGACHAQLIFVELVETGHHVG QDGLDLLAMHPPRPPKVLGFQA ASSA'S AGTIGACHAQLIFVELVETGHHVG QDGLDLLAMHPPRPPKVLGFQA ASSA'S AGTIGACHAQLIFVELWIMAFESL XSFQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ			1		sequence		nucleotide insertion
HIVECTSCAAKKQTCPSGWKRELFUQITQUACCE GYWGSRCHECPGGAETPCNGHGTCLDOMDR NGTCVCQENFRGSACGQCQDVRNFGPDCQSV CSCVHOVCHGPRGDGSCLCFAGYTGPHCD QEDVWGLGFPGNPRELKAPNGKCLPG*H RNGLIATPNCRP RNGLIATPNCRP RNGLIATPNCRP ASAS*VAGTIGACHHAQLIFVELVETGFHHVG DOGLD LIAIMHPPPRPVLGFGPA ASAS*VAGTIGACHHAQLIFVELVETGFHHVG DOGLD LIAIMHPPPRPVLGFGPA ASAS*VAGTIGACHHAQLIFVELVETGFHHVG DOGLD LIAIMHPPPRPVLGFGPA GCGCGCWFAWFELRRGFASAGAALLGRKAPA GLFGRVODGPLRGFYLFRRAFTAPVLSGA ASRPEASDCRAGRETAMATLEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQQQPPPPP PPPPPRQFQFQQQQQQQQQQ	488	1838	A	3818	1	781	I CLI ARCIA GESEVRGOVI FKGCDVKI I I VI
YEVQLGGSMYSMSGCRRCKRQVVQSRCB GYWGSRCHECTGGGETTPCMGGTCLDOMDR NGTCVCQENFRGSACGECQDPNRTGPDCQBC CSCVHQVCNHGFRGSACGECQDPNRTGPDCQBC GCVWCVCNGFRGSACGECQDPNRTGPDCQBC PRIGIATNIPCRP RNGLATNIPCRP 490 1840 A 3822 934 669 FFFSEMSRSYVTRLECSGAISAHLRLLGSSNSP ASAS'VAGTIGACHHAQLIFVELVETCFHHVG QDGLDLLNMHPPRPPKVLIFQA 490 1840 A 3825 79 9748 GCGSCWPAWFRLRKRGPASGARLGRKAPW GLPGRVODGRPLRTCFYLFRAPFTAFVLSGA ASRFASDICKAGRFTAMATLEKLIKAKAFESL KSFQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	100		1		1	1	TRIPOTEC A ATKKOTCPSGWLKELPDQIIQDCK
A				1		1	L VEVOT GGSMVSMSGCRRKCRKUV VVAACUL
NOTCYCQENFRGSACQEQUINNEGDSCLCEAGYTOPHOLO	1	1	1		ŀ	1	- CVWGSDCHECPGGAETPCNGHGICLDGMDR
CSCVHGVCNIGREGOSSCLLFAGT IGHEN GELEVWOELGFFQNNPRLEKARNCKCLPGH RNGLLATPHORP  489 1839 A 3822 934 669 FFESEMESRSVTRIECSGAISAHLRILIĞSSNSF ASAS*VAGTIGACIHAQLIFVFLVETGFHHYG OGLDLIALIMIPPRPRVLJEGGA  490 1840 A 3825 79 9748 GCOSCWPAWPELRREGYASAGARIJGRKAPW GLPGRVQDGRPLRFCFYLRRAPHAPVLSGA ASRPEASGDCRAGRETAMATLEKLIKKARAPW GLPGRVQDGRPLRFCFYLRRAPHAPVLSGA ASRPEASGDCRAGRETAMATLEKLIKARAPSL KSFQQQQQQQQQQQQQQQQQQQQQQQQPPPP PPPPPPPQLPPPPQAQPLLPQPQPPPPPPPPPP			1			1	I NOTOVOCENERGSACOECUDPNREGEDCQ3 V I
RNGLIATFNICH  489 1839 A 3822 934 669 FFFSEMESKYTRLECSGAISAHLRILGSSNSP ASAS YAGTIGACHHAQLIFYFLVETGHTWG QUEDLIANIMIPPRPRYVLGQA  490 1840 A 3825 79 9748 GCOSCWPAWPRILRIRGPASAGARIGKAPW GLIPGR NODGRIPARCPYLARPAPIAPVLSGA ASBFEASGDCRAGRETAMATLEKIMAFESI. KSFQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	1		1		ļ	ļ	1 COCVUCYCNTIGPRGDGSCLCFAGY IGFACD
489 1839 A 3822 934 669 FFFSEMESRSYTRLECSGAISAHLRUSSNSY- ASS-VAGTIGACHHAQLIPYTLVETGFHHYG QDGLDLLANLMIHPPRPKVLGFQA  490 1840 A 3825 79 9748 GCQSCUPA-WPRILRERGASAGARLGRKAPW GLPGRVQDGRPLRFCYLRPRAPFLAPVLSQA ASSPEASODCRAGRETAMATILEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQQQQPPPP PPPPPPPQLPQFPPQAPPLPPPPPPPPP GPAVAEPLHHPKKELSATKKDRVNHCLTIC ENIVAQSVRNSPEFQKLLGIAMELFILGDDA ESDVRWANDECLNKVIKALMDSNLPRLQLEL YKEIKKNGAPRSLRAALWRFAELAHLVRQK CRPYLVNLIP-CLTRTSKRFESVQETLAAAVP KIMASFGWFANDNEIKVLLKAFIANLKSSSPIT RRTAAGSAVSICOHSRRTOKYFYSWLLNVLLG LLVPVEDEHSITLLLGVLLTLRYLVPLLQQQV KDTSLKGSFGVTREMEWSPSADOLVYVSL THHTUHQDHNVVTGALELLQOLFRTPPEL LQTILTAVGGIGQLTAAKESGGRSRSGSIVELI AGGGSSCSPVLSRKQKKVLLGEEEALEDDS ESRSDVSSAALTASVKDEISGELAASSGVSTPG SAGHDITTEGPRSQHTLQABVDLASCDLTSS ATDGDEEDLSHSSSQVSAVFSDRAAMDLNDG TQASSFINDSSQTTTEGPBSAVTFSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGLTDBASSA FRNSSMALQAHLLKNMSHCRQFSSSVDKF VLRDEATERGDGENKPCRRGDIGGSTDDDS APLUHCWRLSASFLLTGGNVLVPDDVNV SVKALALSCVGAAVALHESSFFSLKYVPLD TTEYPEGVVSDLNYUDDDPQVRGATALLC GTILCSLSRSRPHVGDWMGTTRTLTGMTFSL ADCIPLLRKTILKDESSVTCLACACTAVRNCVM SLCSSSYSELGQLIDVITIRNSSYWL VRTEL LETLAEDFRLVSSLEAKAENLHRGAHTYGL LKLGERVINNVYHLLGDPPVRHVAAASL RLVPKLFYKCDQGQADPVVAVARDQSSVYL KLLMEETGPPSHSVSTITIRYRGYNLLPSHD VTMENNLSRVLAAVSHELITSTTRALTGCCE ALCLLSTAPVCUWSLGWHCGYPPLSASDESR KSCTVGMATMITLLSSAWSPEDLSHQDAAL RLAGRENDARGAWSAVSKELERSTTRALTGGCCE ALCLLSTAPVCUWSLGWHCGYPPLSASDESR KSCTVGMATMITLLSSAWSEEEANPAAATK QEEVWPALGDBALVPMVEQLFSHLLKVNIC AHVLDDVARGFRAKAALPSLTNPPSLSPRRK GKEKEPGGASVFLSKKGSEASAASRQSDTS AVVSVLDLONSTEKEFGGFLRSALDVLSQILEL ATLQDIGKCVEELLGYLKSCSSEPSMAATKC VQOLLKTLGTGNASSPROHAATVC VQOLLKTLGTGNASSPROHAATVC VQOLLKTLGTGNASSPROHAATVC VQOLLKTLGTGNASSPROHAATVC VQOLLKTLGTGNASSPROHAATVC VQOLLKTLGTGNASSPROHAATVC VQOLLKTLGTGTLASSPOGLASSPROHAATVC VQOLLKTLGTGTLASSPOGLASSPROHAATVC VQOLLKTLGTGTAASOPGGLSSNPSNAGVCBLY				1		ŀ	QELPVWQELGFPQNNPRLKKAFNCKCEI G 11
ASAS VAGTIGACHHAQLIPVI-VEIGHAY  QUEDLILANIMIPPRPREVI-GROA  490 1840 A 3825 79 9748 GCOSCWPAWPRIERRGPASAGARICREAW GLEGRWODGRIPLRCEYLRPAPFIAPVI-SGA ASREASGDCRAGRETAMATLEKIMAFESI KSSQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	1	1	-			1	RNGLIATPNPCRP
490 1840 A 3825 79 9748 GCGSCWPAPRIRRERGPASAGARIGRKAFW GLPGRVQDGRILRCYLRPRAPIAYUSGA KGPGSCWPAPRIRRERGPAFVUSGA GLPGRVQDGRILRCYLRPRAPIAYUSGA KSPQOQQQQQQQQQQQQPPP SPPPPPPQLPQPPPQPPPPPPPPPP	480	1839	A	3822	934	669	ASASAVAGTIGACHHAOLIFVFLVETGFHHVG
490 1840 A 3825 79 9748 GCOSCWPAWPILRRRGPASAGALGRANAY GLIGRAVQDGRIPLEGFCYLBRAAPTIAPVLSGA ASKPEASGDCRAGRETAMATILEKLMKAFESL KSTOQQOQQQQQQQQQQQQQPPP PPPPPPPQLQPPPQAQPILIPQPQPPPPPPPPP GPAVAEEPILRPKKELSATKKDRVSHCLTIC ENIVAGSWRSFEEPGKLIGIAMELFILCSDDA ESDVRMVADECLNKVIKALMOSNLPRLQLEL YKEIKKNGAPRSLRAALWFAELAHLVRPGK CRPYLVHLIPCLTRTSKEPESVQETLAAAVP KIMASFGRANDMEIKVLIKAFIANIKSSSPTI RRTAAGSAVSICOHSRRTQYFYSWLINVLLG LLVPVEDEDHSTLILIG VLUTIRVLVELQQQV KDTSLKGSFQVTRKEMEVSPSAEQUVQVYGL TLHHTQHQDHNVTTALBELQQLFRTPPPEL LQTITANVGIGQLTAAKEESGGRSSGSIVELI AGGGSSCSPVLSKKQKGKVLLGEEEALEDDS ESRSDVSSSALTASVKDEISGELAASSGVSTPG SAGHDITTEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TOASPISDSSQTTTEGPDSAVTTSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQQAHLLKNMSHCRGPSDSSVDKK VLRDEATEPGDOENKPCRIKGDIGGSTDDDS APLVHCVRLLSASFLLTGGKNVLVPDRDVRV SVKALALSCVGAAVALHTESFFSKLYKVPLD TTEYPEERGYVSDLINVIDHODPQVRGATAILC GTILCSILSRSRFHVGDWGMTGTITGTTGTSNTSL AGCPILKRIKDESSVTCKLACTAVRNCVM SLCSSSYSELGLQLIIDVLTLRNSSYWLVRTEL LETLAEIDFELVSFLEARDLHRGAHTYGL LKLQERVLNNVVIHLLGEEDPRVRHVAAASL IRLVPKLFYKCDQQADPVVAVARDQSSVYL KLLMHETQPSHFSVSTTRITATIFGCCC ALCLSTAFPVCIWSL,GWHCGVPPLSASDESR KSCTVGMATMILTLISSAWPFLDLSAHQDAL ILGKLAASAPKSLEG,GWHCGVPPLSASDESR KSCTVGMATMILTLISSAWSEELANPAATK QEEVWPALGDRALVPMYEQLFSHLKVNIC AHYLDDVAPGPAKASHSLTNPPSLSPRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKDSLAAHDAL NAVYTLDLQNSTEKRFGGFLRSALDVLSQLEL ATLQDIGKCVEEILGYLKSCFSREPMATVC VQULKTLEGTITLASOFDGLSSNPSKSQGKA QRLGSSSVRPGLYHCCPMAPYTHTTQALAA	407	1037	1				LODGI DI LAN MIHPPR PPK VLGPUA
GLFGRVQDGRPLRFCFYLRRFATHATATATATATATATATATATATATATATATATATAT		ì				0740	- CCOCCUPA WPRI RRRGPASAGARLGRAAPW
ASRPEASODCRAGRE I AMAILEA, MICKATORY OR STROQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	490	1840	A	3825	79	7/48	CI DODVODGRPI RECEYLKPKAPTIAT V DOUA
KSFQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ			1		1	1	A CODE A CODOR A GRETAMA LENLIVINATE DE 1
GPAVAEPLHRVKELSAINADR VINDED ENIVAGSVRINSEPGKILGIAMELFILCSDDA ESDVRMVADECLNKVIKALMDSNLFRLQLEL YKEIKKNGAPRSLRAAL WRFAELAHLVRPOK CRPYLVNLLPCLITRTSKRPEESVQETLAAAVP KIMASFGNFANDNEIKYLLKAFIANLKSSPTI RRTAAGSAVSICOHSRRTQYFSWILLNVILLG LLVPVEDEHSTILLILGVLTIRYLVPILQQQV KDTSLKGSFGVTRKEMEVSPSAEQLVQYYEL LQTILTAVGGIGQLTAAREESGGRSSGSIVELI AGGGSSCSPVLSRKGKGKVLLGEEEALEDDS ESRSDVSSSALTASVKDEISGGLAASSGVSTPG SAGHDITEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TOASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYTGLQIGOPQDEDEEATGILPDEASEA FRNSSMALQQAHLLKNMSHARCRPSDSSVDKF VLRDEATEPGDQENKPCRIKGDIGGSTDDDS APLVHCVRLLSASFLLTGGKNVLVPDRDVRV SVKALALSCVGAAVALHPESFFSKLYKVPLD TTEYPEGQYSDILNYIDHODPQVRGATAILC GTLICSLLSRSRPHVGDWMGTRITLGNTTSL ADCIPILRKTLKDESVTCLLACTAVRNCVM SLCSSSYSELGLQIIDVLTLRNSSYWLVRTEL LETLAEIDFRLVSFLEAKABNLHRGAHHYTGL LKLQERVLNNVFULLBGEDPRVRHVAAASL RLVPKLFYKCDQGQADPVAVARDQSSVYL KLLMHETQPSHFSVSTIRTRRGVILLPSITD VTMERNLSRVLAASHELITSTTRALTFGCCE ALCLLSTAPPVCIWSLGWHGQVPPLSASDESR KSCTVGMATMILTLLSSAWFPLDLSAHQDAL LLAGRLLAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPMVQQLFSHLKVNILC AHVLDDVAGPGAHKAALPSLTNPPSLSSPIRK GKEREPGGQASVPLSPKKGSGASAASRQSDTS GPVTTSKSSSLGSFYLISPSYLLSHIDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEELCYLKSCFSREPMMATVC VQULLKTLFGTNLASOFDGLSSNPSKSQGRA QRLGSSSVRGLYHYCYMAAYTHETLOALDA	İ	}	1			-	- $1$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$
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YKEIKKNGAPRSLRAAL WA AVA CRPYVNILPCLTRTSKRPEESVQETLAAAVP KIMASFGNFANDNEIKVILKAFIANI KSSSPTI RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG LLVPVPDEHSTILLIGVLLTLRYLVPLLQQV KDTSLKGSFGVTRKEMEVSPSAEQLVQVYEL TLHHTQHODHNVTGALELLQQLFRTPPPEL LQTLTAVGGIGQLTAAKEESGGRSRSGIVELI AGGGSSCSPVLSRKQKGKVLLGEEALAEDDS ESRSDVSSALTASVKDEISGELAASSGVSTPG SAGHDITTQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSPDAMDLNDG TQASSIBDSSQTTTEQPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEATGILPDEASEA FRNSSMALQQAHLLKNMSHCRQFSDSSVDKF VLRDEATEPGDQENKPCRIKGDIGQSTDDDS APLYHCVRLLSASSFINGKNVLLYPDRDVRV SVKALALSCVGANLHESFFSKLYKVPLD TTEYPEGQYSDLWYDDRDVRV SVKALALSCVGAVALHESFFSKLYKVPLD TTEYPEGQYSDLWHVTLTGKTFL GTLICSILSRSRPHVGDWMGTRTLTGNTFSL ADCTPLIRRTLKDESSVTCKLACTAVRNCVM SLCSSSYSELGLQLIIDVLTRNSSYWLVRTEL LETLAEIPFLVSFLEAKAENLHRGAHHYTGL LKLQERVLNNVIHLLGDEPRVRHVAAASL RLVFKLFYKCDQQADPVAVARDQSSVYL KLLMHETQPPSHSVSTITRYRGYNLLPSITD VTMENNLSRVIAAVSHELITSTTRALTFGCCE ALCLLSTAFPVCIWSLGWHCGYPLSASDESR KSCTVGMATMILTLLSSAWFPLDLSAHQDAL ILAGNILAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPWVEQIFSHLLKVINIC AHVLDDVAFQPAIKAALPSLTNPSLSPIRRK GKEKEPGQASVPLSPKKGSEASAASRQSDTS GPVTTSNSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDICKCVEEILGYLKSCFSREPMMATVC VQQLIKTLFGTNLASOFDGLSSNPSKSQGRA QRLGSSSVRPGLYHKYCFMAPYHLFVALABL				1	Ì		TODAD MANADECT NK VIK ALMUSNUTAL QUUL
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LQTLTAVGGIGGLTAAKESGGRASUSVENG AGGSSCSPVLSRQQKKVLLGEEEALEDDS ESRSDVSSSALTASVKDEISGELAASSGVSTPG SAGHDITTEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIQPQDEDEEATGILPDEASEA FRNSSMALQQAHLIKNMSHCRQPSDSSVDKF VLRDEATEPGDQENKPCRIKGDIGGSTDDDS APLVHCVRLLSASFLLTGGKNVLVPDRDVRV SVKALALSCVGAAVALHESFFSKLYKVPLD TTEYPEEQYVSDILNYIDHGDPQVRGATAILC GTLICSILSRSRPHVGDWMGTTRILTGNTFSL ADCIPLIKKTI.KDESSVTCKLACTAVRNCVM SLCSSSYSELGLQLIIDVLTILRNSSYWLVRTEL LETLAEIDFRLVSFLEAKAENLHRGAHHYTGL LKLQERVLNNVVHLLGDEDRRVRHVAAASL IRLVPKLFYKCDQGQADPVAVARDQSSVYL KLLMHETQPPSFISVSTITTRYGYNLPSITD VTMENNLSSRVIAAVSHELITSTTRACTRILFIGCCE ALCLISTAFPVCIWSLGWHCGVPPLSASDESR KSCTVGMATMILTLLSSAWFPLDLSAHQDAL ILAGNILAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPMVEQLFSHLLKVNIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRKS GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREFMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHTTQALADA			i		{	1	THUTOHODHNVVTGALELLOOLFRTPPPEL
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IRLVPKLFYKCDQGQADPVVAVARDQSSVTL KLLMHETQPPSHFSVSTITRIYRGYNLLPSITD VTMENNISRVIAAVSHELITSTTRALTFGCCE ALCLLSTAFPVCIWSLGWHCGVPPLSASDESR KSCTVGMATMILTLLSSAWFPLDLSAHQDAL ILAGNLLAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPMVEQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRIGSSSVRPGLYHYCFMAPYTHFTQALADA GRINDAVIOAEOFNDTSGWFDVLOKVSTQLKT				ļ	1		I VI OEDVI NNVVIH LGDEDPRVRHVAAASU
KLLMHETQPPSHFSVSTITRIYRGYNLLFSITD VTMENNLSRVIAAVSHELITSTTRALTFGCCE ALCLLSTAFPVCIWSLGWHCGVPPLSASDESR KSCTVGMATMILTLLSSAWFPLDLSAHQDAL ILAGNLLAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPMVEQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA	1	1	1		1		mi voki EAK CDOGOADBAAYAKAASSA in 1
VTMENNLSRVIAAVSHELITST TRALIFGCCE ALCILSTAFPVCIWSLGWHCGVPPLSASDESR KSCTVGMATMILTLLSSAWFPLDLSAHQDAL ILAGNLLAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPMVEQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA CLINDAGOEOFNDTSGWFDVLOKVSTQLKT			1		1		VI I MUETOPPCHESVSTITRIYKU YNLLESII D
KSCTVGMATMILTLLSSAWFPLDLSAHQDAL ILAGNLLAASAPKSLRSSWASEEEANPAATK QEEVWPALGDRALVPMVEQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA GLBSSVRPGLYHYCFMAPYTHFTQALADA	}		l				VENEZINI SEVIA AVSHELITSTI RALIFUCCE
ILAGNLLAASAPKSLRSSWASEEEANFAATK QEEVWPALGDRALVPMVEQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA GENDALVOAFGFNDTSGWFDVLOKVSTQLKT			Į.	Ì		}	ALCLLSTAFPVCIWSLGWHCGVPPLSASDESK
QEEVWPALGDRALVPMVEQLFSHLLKVINIC AHVLDDVAPGPAIKAALPSLTNPPSLSPIRKK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA GENDALVOAFGFNDTSGWFDVLOKVSTQLKT						}	KSCTVGMA1MILILLSSAWFEDLSAMQDFU
AHVLDDVAPGPAIKAALPSLTNPPSLSPIRRK GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA GENDAUGAEGENDTSGWFDVLOKVSTQLKT		{	{		1		OFFICE ALCOP AL VPMVFOLFSHLLKVINIC
GKEKEPGEQASVPLSPKKGSEASAASRQSDTS GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA GENDAUGAEGENDTSGWFDVLOKVSTQLKT			1		1		ALDER DOMADGRAIK A ALPSI TNPPSLSPIKKK
GPVTTSKSSSLGSFYHLPSYLKLHDVLKATHA NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA GCDANDUSGAFOFNDTSGWFDVLOKVSTQLKT			}				CVEVEDGEOASVPI SPKKGSEASAASKQSDIS
NYKVTLDLQNSTEKFGGFLRSALDVLSQILEL ATLQDIGKCVEEILGYLKSCFSREPMMATVC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA GRANDWOAFGFNDTSGWFDVLOKVSTQLKT			1		}		CONTROVERSI GREVHI PRYLKLHUVLKA I DA
ATLQDIGKCVEEILGYLKSCFSREPMMAT VC VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA GLBDAGGENDTSGWFDVLOKVSTQLKT			1		l		NOVETTI DI ONSTEKEGGELRSALDVESQUELL
VQQLLKTLFGTNLASQFDGLSSNPSKSQGRA QRLGSSSVRPGLYHYCFMAPYTHFTQALADA			1				TI ODIGECVEEILGYLKSCHSKEPMMAI VC
CT DATACOAEOFNDTSGWFDVLUK VSIQLAI			l				UCOLI PTI EGTNI ASOFDGLSSNPSKSQGKA
SLRNMVQAEQENDISGWIDVEQRV3IQERI NLTSVTKNRADKNAIHNHIRLFEPLVIKALKQ				1		į	QRLGSSSVRPGLYHYUFMAF I INF I QALADA
NLISVIKNKAUKNAIIIVIIIGA 21212			1			-	SLRNMVQAEQENDISOWEDVEQRASIQUE
						L	NL194 I MANAGEMENT TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE

55.15	CEOTO	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
iO: of ucl-	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-	•	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
oa.cc ≥q-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
	}		İ	peptide		nucleotide insertion
		L		sequence	ļ	VTTTTCVOLOKOVLDLLAOLVOLRVNYCLL
			1	1	ļ	DSDOVFIGEVLKOFEYIEVGQFRESEAIIPNIFF
				1		FLVLLSYERYHSKOIIGIPKIIQLCDGIMASGR
	1	1	i	1		KAVTHAIPALQPIVHDLFVLRGTNKADAGKE
						LETQKEVVVSMLLRLIQYHQVLEMFILVLQQ
			1	l l		CHKENEDKWKRLSRQIADIILPMLAKQQMHI
					•	DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF
			ļ	•		VTPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE
			l			EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT
		1				KQLKVEMSEQQHTFYCQELGTLLMCLIHIFKS
	1	1				GMFRRITAAATRLFRSDGCGGSFYTLDSLNLR
			1			ARSMITTHPALVLLWCOILLLVNHIDYKWW
		1				AEVOOTPKRHSLSSTKLLSPQMSGEEEDSDLA
						AKI GMCNREIVRRGALILFCDYVCQNLHDSE
					-	HI TWI IVNHIODLISLSHEPPVODFISAVHRNS
			Ì	1		AASGLFIQAIQSRCENLSTPTMLKKTLQCLEG
		1	1	}		HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL
	1	[	ĺ	1	1	ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS
		1		1		PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK
	1					SQCWTRSDSALLEGAELVNRIPAEDMNAFM
	1			1		MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA
	-					A DEVIT ARVSGTVOOLPAVHHVFQPELPAEP
	-		1	1		AAYWSKI NDLFGDAALYQSLPILAKALAQY
		1	1			I VVVSKLPSHLHLPPEKEKDIVKFVVAILEAL
			İ	1		SWHITHEOIPLSLDLOAGLDCCCLALQLPGL
	1	1	ł	1		WSVVSSTEFVTHACSLIYCVHFILEAVAVQPC
			l		1	EQLLSPERRINTPKAISEEEEEVDPNTQNPKY
					1	TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG
						WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFIY
		į.		ł		INTLGWTSRTQFEETWATLLGVLVTQPLVME
		-		1		QEESPPEEDTERTQINVLAVQAITSLVLSAMT
	1	-				VPVAGNPAVSCLEOOPRNKPLKALDTREGRE
		- [		1		I SURGIVEOEIOAMVSKRENIATHHLYQAWL
		- 1		ì		DUDGE CDATTGALISHEKLLLOINPERELGSMS
			1			VKI GOVSTHSVWLGNSTTPLREEEWDEEEEE
		1			\ '	ADADADSSPPTSPVNSRKHRAGVDIHSUSQFL
			1			LELYSRWILPSSSARRTPAILISEVVRSLLVVS
				1	Ì	DLFTERNQFELMYVTLTELRRVHPSEDEILAG
		1				YLVPATCKAAAVLGMDKAVAEPVSRLLEST
		1	1	1	}	RSSHLPSRVGALHGVLYVLECDLLDDTAKQI IPVISDYLLSNLKGIAHCVNIHSQQHVLVMCA
		1		1	i L	TAFYLIENYPLDVGPEFSASIIQMCGVMLSGS
			1	Į.	İ	EESTPSIIYHCALRGLERLLLSEQLSRLDAESL
				1		VKLSVDRVNVHSPHRAMAALGLMLTCMYT
		1	1	1		GKEKVSPGRTSDPNPAAPDSESVIVAMERVS
		1		1		VI EDRIRKGEPCEAR VVARILPOFLDDFFPPQ
				1		DIMNKVIGEFLSNOOPYPOFMATVVYKVFQ
	1	ļ				L HSTGOSSMVRDWVMLSLSNFTQRAPVAM
				Ì		TWSLSCFFVSASTSPWVAAILPHVISRMGKL
		]		}		OVDVNLFCLVATDFYRHQIEEELDRRAFQSV
		1			1	T EVV A APGSPYHRLLTCLRNVHKVTTC
401	1841	A	3826	469	302	SNPPASASRVAGITGVHQHAWLIFVFLVEME
491	1041	1	3020	1		HHVGQAVLKLLISGDLPVSASQSA
492	1842	A	3836	392	88	VAPSPMIMPDLYFYRDPEEIEKEE*AAAEK\E
1 432	1042	11		}		FQSEWTAVV/P/EFTATQSEVADWFKDMQVF
1				Į.		SVPIQQFPTEDWST*PTMNDWSATSTAQTTE
				1		WVRITTEWP

EC ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid. F=Glutamic Acid.
NO: of nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-	 	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
ed-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eri-	dance		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
Cucc		ļ		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	<b>\</b>	1		residue of	sequence	Y=1 yrosine, X=0 nkilowii, '-stop codori, /=possible nucleotide deletion, \=possible
		ì		peptide		/=possible nucleotide defetion, (~possible
				sequence		nucleotide insertion TPSDMNRAFETDTQSIGEKNRSPSEPDYFERK
193	1843	A	3838	19	380	KFKRS*EKAHIRYKIDQPEDIPLK\EFLCKHSK
.,,	1	1	1	}		CTATLSMRNMSLMKKKCSFSEEF\LAFFPSLL
		1				VCHLLAIKLGFYIEIHLTTFNNTF
		}				FFFLRRSL/DSVAQAEAQWL\ELGLLQAPPPGF
494	1844	A	3845	2	352	KPISLP\GLPSSWDYGRPPPCPANFCIF/M*RRG
171	10	}				FTVLARMVLIS*PCDPPTLASQGTAITGMSYH
	Ì	1				ARPQDIDFLYAHQGRCWFRLL
		1				DIFFRRAKEGMGQDEAQFSVEMPLTGKAYL
495	1845	A	3847	1774	40	WADKYRPRKPRFFNRVHTGFEWNKYNQTHY
177		i		1		DFDNPPPKIVQGYKFNIFYPDLIDKRSTPEYFL
		1	}		1	EACADNKDFAILRFHAGPPYEDIAFKIVNREW
		į.				EYSHRHGFRCQFANGIFQLWFHFKRYRYRR*
		ļ			}	RPWGTAGRCPRGHSKGASVKLVVTPGPLSGL
			}	)		QGRGFTSHLRPHLSFARPQFPPI*KGGHH*AC
				ì		UCEL PRHWDRLA*GPDATEGALGASFEHEG
		1	}	Ì		COOPPADLTVOADTLHRPSARLGGAHRACPK
			1			PRPHRVI WRWARGAWAWRCQAREKQEIQG
	j	1		Ì	1	ODCUITCHPI GREAFPA AAGAAPALAHKPPF
		1			1	ARTGSTE\PGPCWRPIRHCRRDPLWTP1LCKD
	Ì	1				WIDDLING AGGVHFPAAG/IGGCVEVPVSVN
			- 1		}	VMCTKSH*AVLPPPPSTGPGGOGLPEGWOLE
	(	1	i	1		VGEGI PPGIPPPGLLTGPW\SMRPVTPSFAHIK
		1		1	J	TVAPSHSPESGOEGRGPHGCHSPGR\SUP\AGK
		1		1		I VI OHPTGTSPTEAKRKVPPGPPEGHP1SPV1
		- 1	1			SPRPPTAPPRHPASSGNSSVCFSKKTCRWEKK
Ì		- 1			]	CEVI MET AVWODRMEF
	1046		3849	830	442	AKSPLPLG*IQWR/NLGSLKLRLPGFK*FTCLG
496	1846	Α	3049	050		LLSSWDYRSLPPRPVNFCILVELGFHHVDQAG
ĺ		-		ŀ		LKLLTSSALPALASQSAEITGMSHRIWPLPLLR
İ				}		RPPVIRIRAPPQRLPFNLITSLKALSPNMATF
497	1847	A	3859	2	393	ALRKTRRDGIARTGAQPAASWKGTNNYPWR
497	1047	1.	1 2 2 2 2	1		LEMAGRPGSQEQSKDRGTGSLPPPSQRPLGPS
1		ì				PEGAGPSPPPPGIPRGGGSSSSEGP/PQLLFVPR
ĺ		- (			İ	RFPAPKKGLPSDTPHSKAPPTPHLILGGEDSQ
		1				VPIL VACAGE I DWG ALVAGAG
498	1848	A	3860	253	634	KNASTVYSSQGDPKSFFFLLRWSLALVAQAG
470	1040	1 ' '				EQ*RDLSSLQPPPGFK*FSCLSLPSSWD\YRCI
	1	1				LPCLANFA*FLVETGFHHVGQADLKLLTSGDP
1		ł				PTSASESAGITGVSHRAWPRIHFLYWKTFFL
499	1849	A	3863	423	263	APSQISVAFLYAA/DKLFEKEI*KKIPFIIAS/DK
477	1049	( ' '	1		1	KIGINLTKEVKYLYTENYITLMKEIK/DTDKW KDILY*WIGKINI*KMSTPPKAIYRFNAIPTKIP
		1	.		}	KDILY*WIGKINI*KM51*FKAI1KFNAII KII
1		1		1		MTFFTEIEKSIIKFIWNHKKPPNTQSNIEQKE*S
					Ì	FCSILLWVFGGFLWFHMNFMIDFSISVKNVIG
	1	1				LVGIALNI.
500	1850	A	3865	2	15246	LPRGCLWCLQRSPTPARPQPSRPARSPLPLFP  LPRGCLWCLQRSPTPARPQPSRPARSPLPLFP  LPRGCLWCLQRSPTPARPQPSRPARSPLPLFP
300	1050	''				DLRPWASDLDIMGDAEGEDEVQFLRTDDEV
		1	1		(	VLQCSATVLKEQLKLCLAAEGFGNRLCFLEP
1		1				TSNAQNVPPDLAICCFVLEQSLSVRALQEML
	Ì	1	1			ANTVEAGVESSQGGGHRTLLYGHAILLRHAI
1	1	1	j			SRMYLSCLITTSRSMTDKLAFDVGLQEDATGI
1	1					ACWWTMHPASKQRSEGEKVRVGDDIILVSV
1		]		1		SERYLHLSTASGELQVDASFMQTLWNMNPK
		1		1		SRCEEGFVTGGHVLRLFHGHMDECLTISPAD
		}				DDQRRLVYYEGGAVCTHARSLWRLEPLRIS
1	1	[	}			WSGSHLRWGQPLRVRHVTTGQYLALTEDQX LVVVDASKAHTKATSFCFRISKEKLDVAPKR
	ı	1		t .	1	L L MANDA SK A HTK ATSFCFRISKEKLUVAPKK
1	į.	1	1	i	1	DVEGMGPPEIKYGESLCFVQHVASGLWLTY.

					B 15	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Oldraine Acid,
nucl-	peptide		l in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	, -	{	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		1	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	Ì	ì	914		of peptide	T=Threonine, V=Valine, W=Tryptophan,
ì	1	ļ	1	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
Ì	ł	1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
}	}			peptide		
1	İ		1	sequence		nucleotide insertion
	<del> </del>	<del> </del> -	1			APDPKALRLGVLKKKAMLHQEGHMDDALSL
1	1	l	i			TRCQQEESQAARMIHSTNGLYNQFIKSLDSFS
1	1	1				GKPRGSGPPAGTALPIEGVILSLQDLIIYFEPPS
1		1	İ		1	EDLQHEEKQSKLRSLRNRQSLFQEEGMLSMV
1		Į.	1			LNCIDRLNVYTTAAHFAEFAGEEAAESWKEI
1		i		1		VNLLYELLASLIRGNRSNCALFSTNLDWLVS
	1	1	1	1		VNLL I ELLASLIKONASNOALI SINED WEVE
	i		1		ļ	KLDRLEASSGILEVLYCVLIESPEVLNIIQENHI
1	1			\		KSIISLLDKHGRNHKVLDVLCSLCVCNGVAV
1	1	1	1			RSNQDLITENLLPGRELLLQTNLINYVTSIRPN
Ì	•		1		}	IFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQ
1	1		1			ATHLRVGWALTEGYTPYPGAGEGWGGNGV
4		1				GDDLYSYGFDGLHLWTGHVARPVTSPGQHL
1	1			1		LAPEDVISCCLDLSVPSISFRINGCPVQGVFESF
	1	1	1		1	NLDGLFFPVVSFSAGVKVRFLLGGRHGEFKF
1	1	1	1		1	LPPPGYAPCHEAVLPRERLHLEPIKEYRREGP
1						DON'T HODER OF CHILDENDONDATION DOD
		1	1		1	RGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPH
	ì	Ì		Ì		LERIREKLAENIHELWALTRIEQGWTYGPVRD
	1		1		j	DNKRLHPCLVDFHSLPEPERNYNLQMSGETL
1	1	(	1	· ·		KTLLALGCHVGMADEKAEDNLKKTKLPKTY
1	1	ŀ				MMSNGYKPAPLDLSHVRLTPAQTTLVDRLAE
			1			NGHNVWARDRVGQGWSYSAVQDIPARRNPR
			Į.	,	)	LVPYRLLDEATKRSNRDSLCQAVRTLLGYGY
i			1			NIEPPDQEPSQVENQSRCDRVRIFRAEKSYTV
	1				1	QSGRWYFEFEAVTTGEMRVGWARPELRPDV
				1		ELGADELAYVFNGHRGQRWHLGSEPFGRPW
	į	1	- }			QPGDVVGCMIDLTENTIIFTLNGEVLMSDSGS
1	1		-			ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD
1	1				1	VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS
	1		İ			KGLPQFEPVPLEHPHYEVSRVDGTVDTPPCLR
	1					LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR
	- 1				1	LIHKI WOOQNOLVENILI ENEADA AEPDPDVE
- 1						CTAGATPLAPPGLQPPAEDEARAAEPDPDYE
1			- {			NLRRSAGGWSEAENGKEGTAKEGAPGGTPQ
	ł	1	ł	1	1	AGGEAQPARAENEKDATTEKNKKRGFLFKA
		ŀ	1		1	KKVAMMTQPPATPTLPRLPHDVVPADNRDD
1	İ		l			PEILNTTTYYYSVRVFAGQEPSCVWAGWVT
ŀ			- 1	i		PDYHQHDMSFDLSKVRVVTVTMGDEQGNV
	}	ł	İ		[	HSSLKCSNCYMVWGGDFVSPGQQGRISHTDL
		1		1	1	VIGCLVDLATGLMTFTANGKESNTFFQVEPN
1		1				TKLEPAVEVLPTHONVIOFELGKOKNIMPLSA
I		1	1			AMEOSER KNPAPOCPPRLEMOMLMPVSWSR
						MPNHFLQVETRRAGERLGWAVQCQEPLTMM
		]				ALHIPEENRCMDILELSERLDLQRFHSHTLRL
1					j	YRAVCALGNNRVAHALCSHVDQAQLLHALE
						I KA VCALUMNK VARALCSITY DOAQUEITADE
						DAHLPGPLRAGYYDLLISIHLESACRSRRSML
		}	1		1	SEYIVPLTPETRAITLFPPGRSTENGHPRHGLP
				1		GVGVTTSLRPPHHFSPPCFVAALPAAGAAEAP
}		1	1			ARLSPAIPLEALRDKALRMLGEAVRDGGQHA
l	i				1	RDPVGASVEFQFVPVLKLVSTLLVMGIFGDE
j .		-		1	1	DVKOILKMIEPEVFTEEEEEEDEEEGEEEDEE
1		1		1	1	FKEEDEEETAOEKEDEEKEEEEAAEGEKEEG
1				1		LEEGLLOMKLPESVKLOMCHLLEYFCDQELQ
1		l	1	1	1	HRVESLAAFAERYVDKLOANORSRYGLLIKA
1		1	Ì			FSMTAAETARRTREFRSPPQEQINMLLQFKDG
İ			1	1	1	TDEEDCPLPEEIRQDLLDFHQDLLAHCGIQLD
-		- [		1	1	GEEEEPEEETTLGSRLMSLLEKVRLVKKKEEK
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1				1	1	PEEERSAEESKPRSLQELVSHMVVRWAQEDF
					1	VQSPELVRAMFSLLHRQYDGLGELLRALPRA
		1	1			YTISPSSVEDTMSLLECLGQIRSLLIVQMGPQE
		ļ		- 1	1	ENLMIQSIGNIMNNKVFYQHPNLMRALGMHE
	1	1	1	1		TVMEVMVNVLGGGESKEIRFPKMVTSCCRFL
L						

				<b>*</b> ***********************************	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid F=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	1	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	1	l	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	İ	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	Ì		residue of	sequence	/=possible nucleotide deletion, \=possible
1		)		peptide	{	/=possible flucteonide detection, \ possible
	ļ	İ		sequence		nucleotide insertion CYFCRISRQNQRSMFDHLSYLLENSGIGLGM
<b></b>	<del>                                     </del>	┼──	ļ ———			CYFCRISKONORSMIFDHEST LEENSGIGDEN
		1	ļ			QGSTPLDVAAASVIDNNELALALQEQDLEKV
}	1	-	1	1		VSYLAGCGLQSCPMLVAKGYPDIGWKPCGG
ì		i	]	)	}	ERYLDFLRFAVFVNGESVEENANVVVRLLIR
	1	1	1	l		KPECFGPALRGEGGSGLLAAIEEAIRISEDPAR
i	1	1	1	}		DGPGIRRDRRREHFGEEPPEENRVHLGHAIMS
1	1		İ	1	1	FYAALIDLLGRCAPEMHLIQAGKGEALRIRAI
1	1	1		1		LRSLVPLEDLVGIISLPLQIPTLGKDGALVQPK
ł	1		1	1	•	MSASFVPDHKASMVLFLDRVYGIENQDFLLH
1		1	1			VI DVGFI PDMRAAASLDTATFSTIEMALAY
	1	1				NRYLCLAVLPLITKCAPLFAGTEHRAIMVDS
ŀ		1	1		1	MLHTVYRLSRGRSLTKAQRDVIEDCLMSLCR
1	1				Ì	YIRPSMLQHLLRRLVFDVPILNEFAKMPLKLL
	l	ŀ	İ	1		TNILVERCWKYYCLPTGWANFGVISEEELHL
-		1	1	{		TRKLFWGIFDSLAHKKYDPELYRMAMPCLC
l	1					ALAGAL PPDYVDASYSSKAEKKATVDAEGNE
	1					DODDOVETI NVIIPEKLDSFINKFAEYTHEKWAF
	1					DKIONNWSYGENIDEELKTHPMLRPYKITSE
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		1	İ	}		FERTERKKTAKISOSAOTYDPREGYNPQPPDL
	j.	1	}			SAVTI SRELOAMAEOLAENYHNI WUKKKKU
	1				ļ	FIRANGGGTHPILVPYDTLTAKEKARDKEKA
	1	1			1	OF LIKELOMNGYAVTRGLKDMELDSSSIEKK
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}				1		FKSPHEOEIKFFAKILLPLINQYFTNHCLYFL
	1	}	}	1	1	TPAKVI GSGGHASNKEKEMITSLFCKLAALV
		1				RHRVSLEGTDAPAVVNCLHILARSLDARI VM
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		-		Ì		KVSOARTOVKGVGONLTYTTVALLPVLTILF
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-	1					ALTEKSKLDEDYLYMAYADIMAKSCHLEEG
						LCENCEARREVEVSFFEKOMEKORLLYQQAKL
						HTRGAAEMVLQMISACKGETGAMVSSTLKL
			ļ			GISILNGGNAEVQQKMLDYLKDKKEVGFFQS
1		1				IQALMQTCSVLDLNAFERQNKAEGLGMVNE
}	1	1	}	1		DGTVINRQNGEKVMADDEFTQDLFFFLQLLC
		1		ì	1	DGTVINRQNGEKVMADDEFTQDEFN EQELE EGHNNDFQNYLRTQTGNTTTINIICTVDYLL
		1				EGHNNDFQN I LKTQTGN I I INNIECT V TEE
		1				RLQESISDFYWYYSGKDVIEEQGKRNFSKAM
						SVAKQVFNSLTEYIQGPCTGNQQSLAHSRLW
-	1			1		DAVVGFLHVFAHMMMKLAQDSSQIELLKEL
1	{					LDLQKDMVVMLLSLLEGNVVNGMIARQMV
	1					DMLVESSSNVEMILKFFDMFLKLKDIVGSEAF
		1				QDYVTDPRGLISKKDFQKAMDSQKQFSGPEI

		1364	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	1	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in	location	corresponding	I=Isolencine, K=Lvsine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	\	09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	1	914	ng to first	of peptide	T=Threonine V=Valine, W=Tryptophan,
	1			amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	İ			residue of	sequence	/=possible nucleotide deletion, \=possible
)		}	}	peptide	1	nucleotide insertion
	1			sequence		OFLLSCSEADENEMINCEEFANRFQEPARDIG
	T			1		FNVAVLLTNLSEHVPHDPRLHNFLELAESILE
						YFRPYLGRIEIMGASRRIERIYFEISETNRAQW
Ì		1				YFRPYLGKIEIMGASKKIEKI ITEISETTIGIQU
}	1			1	İ	EMPQVKESKRQFIFDVVNEGGEAEKMELFVS
	1					FCEDTIFEMQIAAQISEPEGEPETDEDEGAGA
ļ	l			1	Ì	AEAGAEGAEGAAGLEGTAATAAAGATARV
		1	}		}	VAAAGRALRGLSYRSLRRRVRRLRRLTAREA
1		1	1			ATAVAALLWAAVTRAGAAGAGAAAGALGL
	1				1	LWGSLFGGGLVEGAKKVTVTELLAGMPDPT
ļ	1					SDEVHGEQPAGPGGDADGEGASEGAGDAAE
	ļ	İ				GAGDEEEAVHEAGPGGADGAVAVTDGGPFR
		}				PEGAGGLGDMGDTTPAEPPTPEGSPILKRKLG
1	1			ļ		VDGVEEELPPEPEPEPEPELEPEKADAENGEK
						FEVPEPTPEPPKKOAPPSPPPKKEEAGGEFWG
	1		1	1		ELEVORVKFLNYLSRNFYTLRFLALFLAFAIN
				1		FILLFYKVSDSPPGEDDMEGSAAGDVSGAGS
	1		ŀ			GGSSGWGLGAGEEAEGDEDENMVYYFLEES
ļ			Į.	1		TGYMEPALRCLSLLHTLVAFLCIIGYNCLKVP
	İ					LVIFKREKELARKLEFDGLYITEQPEDDDVKG
1	}				1	QWDRLVLNTPSFPSNYWDKFVKRKVLDKHG
		1				DIYGRERIAELLGMDLATLEITAHNERKPNPP
İ	1				ļ	PGLLTWLMSIDVKYQIWKFGVIFTDNSFLYLG
1				1		WYMVMSLLGHYNNFFFAAHLLDIAMGVKTL
1			ļ	1		RTILSSVTHNGKQLVMTVGLLAVVVYLYTVV
	1	-		1		RTILSSVIHNGKQLVMI VOLLAVVVILITVV
Ì	Į.		ļ			AFNFFRKFYNKSEDEDEPDMKCDDMMTCYL
ł		ì	i			FHMYVGVRAGGGIGDEIEDPAGDEYELYRVV
l l	1		1	1		FDITFFFFVIVILLAIIQGLIIDAFGELRDQQEQV
ŀ		-				KEDMETKCFICGIGSDYFDTTPHGFETHTLEE
	j			İ		HNLANYMFFLMYLINKDETEHTGQESYVWK
1						MYQERCWDFFPAGDCFRKQYEDQLS
	1051		3869	467	665	VIVAIYCQLIFDKGAKTIQ*PFQQIAL/CKRMK
501	1851	Α	3609	107	1 332	LGPCFTPCGKINSEWIRELSVRVKTIKHLEIGV
		Ì		1		่ง
				1042	724	SGMOWRDLTPLOPLPPRFKQFSCLSLPGSWD
502	1852	A	3888	1042	124	VRHAP\PLI.TNF\*FLVEMGFCYVGQAGRKLL
		1	ļ	ł	ł	ASSDQSALASQSAGITGISTAPGPPFFFLNFEA
1	1		İ	į		GSCSVAQAGVQ
					1102	EVDSQSGVQ*QAPGSLQLQTPGLK/VSCLLSR
503	1853	A	3891	1773	1193	QDYRSSLPHLASCCYYYYYY/VFL*RRGLTTL
		1	1		1	VQGGLKLLPSSNPFASAP*TAGITGMSHCAGP
1				1		HFNF*MFRKISCIRE*F*HTRIYDIPFLILFFKET
		l				WVLLCYPGWPQIPGLKPSSCLRLLSSWDHRC
1			1	1	į.	APPCPASFFIFHVDRVSPPCPGLVSITFKMLLL
		1		-	1	
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504	1854	В	3896	279	70	MVSKSKSILMSYNHVELTFSDMKKMPEAFRR
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	}	J	}	1		OKEYYENO*
			2000	2	1396	EPGVPTKKTWFDKPDFNRTNSPGFQKKVQFG
505	1855	A	3899	4	1370	NENTKLELRKVPPELNNISKLNEHFSRFGTLV
		1			1	NI.OVAYNGDPEGALIQFATYEEAKKAISSTEA
	1					VI NINRFIK VY WHREGSTOOLOTTSPK V MQPL
						VQQPILPVVKQSVKERLGPVPSSTIEPAEAQS
		Ì			}	ASSDLPQVLST\LLA*QKQCIIQLL\WKAAQKT
-		1				LLVSTSAVDNNEAQKKKQEALKLQQDVRKR
		1				KOEILEKHIETQKMLISKLEKNKTMKSEDKAE
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1		1				IMKTLEVLTKNITKLKDEVKAASPGRCLPKSI
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			}		1	RRKYTELQLEAAKRGILSSGRGRGIHSRGRGA
				- [		VHGRGRGRGRGRGVPGHAVVDHRPRALEIS
	ı	1	1	1		

PCT/US01/03800 WO 01/57188

	_				Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-Assertic Acid F=Glutarnic Acid,
O: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	1	in		corresponding	1-teoleucine K=1 vsine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	Glutamine R=Arginine, S=Serme,
ence	}	l	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	, '		1	amino acid	of peptide	V=Tyrnsine, X=Unknown, *=Stop codon,
	1		l i	residue of	sequence	/=possible nucleotide deletion, \=possible
		}	1	peptide		nucleotide insertion
		1		sequence	<u> </u>	AFTESDREDLLPHFAQYGEIEDCQIDDSSLHA
	<del> </del>		<del> </del>			VITEKTRAEAEAAAVHGARFKGQDLKLAWN
	ł		1		l	VITEKTRALALAAAVHOARIROQUIA
	1	1	1	l		KPVTNISAVETEEVEPDEEEQREIIIA
	1055	<del> </del> -	3911	1952	919	DAELSGTLSLVLTQCCKRIKDTVQKLASDHK
06	1856	Α	3511	1,722		DIHSSVSRVGKAIDKNFDSDISSVGIDGCWQA
		ì	1			DSQRLLNEVMVEHFFRQGMLDVAEELCQES
	1	1	1		Ì	L CT CVDDCOVEDEVEL NRILEALKVKVLKPALE
	1	1	1	1	ļ	WAVENDEMI JAONSSLEFKLHRLYFISLLMO
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	1	1	1	1	1	DDACATIGI SVESPI SVSFSAGCVALPALINIA
		1		1		AVIEQRQCTGVWNQKDELPIEV\DLG*KSAGY
		1				HSIFACPILRQQTTDNNPPMKLVCGHIISRDAL
	1	1	1	}	1	HSIFACPILKQQI IDRINFI WILL VOCAMBLE
		1	1			NKMFNGSKLKCPYCPMEQSPGDAKQIFF
	1000	+	3936	439	18	SHPFSPAPGICPDAPPPLPRPSKGLGHPGTAGA
507	1857	A	3930	435		PGSGARCHPPSTCSPSWASPG*GAKASPALPR
	ł		1	1		SHGVTLLCKAQAHLCRGEDSKDASGSTSQA
	1	1	1	l		WEPG*GAWGMPRCQGPALGSCFCPPGTTVQ
		1	1			DDAKODDKRNRHI.GR
					412	WCPACTI DEPGPOEMVILEIEVMNULNHKN
508	1858	A	3944	120	412	IOI VA AIFTPHEIVI FME\YECPK-W-ULGGG
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	1	1			1	LTKTPSPREKGRGVLSVLLMMI*KCRVIFVKI
600	1859	A	3949	31	392	MVFFLQNFC/RIILNVA\WTGD*PNTL*KEQRC
509	1039	1 ^	23			MVFFLQNFC/KIILNVA/WIGD TITTE TELEVIO/ERN
	1	1	İ			ITFSDSKS*YKATKIKTMWYCHKNRYID/ERN
	1	- 1				RIEIPEINPCICDKIIFRKLSMTTQ
			3954	1013	885	FSETRACCPRLEHSGRIEAHCSLNIPGSSDPPT
510	1860	A	3934	1013		SASSVAATTG
				<del>-   1</del>	1054	PPAWAPRSPLIWAPTSGRHPCRAALPWSTSS
511	. 1861	Α	3956	1 1	1051	PWOPSEKOPPPPAHRGPADSLSIAAGAAELS
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		- 1		1		FHHGL*AWLWCPELLLQGQARRH*RSPPS/F
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l		1		- [	1	CPATLSLTAWSQTKRLRSQFLLLPWL*RAL*
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1 213	1,000	1.		1		VKLEILPHHQTRLALKGPDHVKIQRSDRQL
1	<b>\</b>					VKLEILPHHQI KLALAGI DII VAGAMDAQ2
	1			1	1	WDSWASNHSSLHTNHHYNTYHPDHCRVPA TFPKAPPPNSPPALVSSSFSPTSMSAYSLSSL
		1	1	1	1	TERM APPRISPHAL VSSSESPI SMOAT SLOSL
1	1	- 1	- 1	1		MGTLPRSLYSTSPRGTMMRRRLKKKDFKS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
ence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
		ł		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
	1			peptide		
	<b>\</b>	1	_	sequence		nucleotide insertion SLASSTVGLAGQVVHTETTEVVLTADPVTGF
					1	GIQLQGSVFATETLSSPPLISYIEADSPAERCG
	ŀ	1	]		}	VLQIGDRVMAINGIPTEDSTFEEASQLLRDSSI
		}		1	1	TSKVTLEIEFDVAESVIPSSGTFHVKLPKKHN
		Ì				VELGITISSPSSRKPGDPLVISDIKKGSVAHRT
		i				GTLELGDKLLAIDNIRLDNCSMEDAVQILQQC
		1				EDLVKLKIRKDEDNSDEQESSGAIIYTVELKR
	1		}	Ì	}	YGGPLG\ITISGTEEP\FDL*IISSLTKGGLAERT
						GAIHIGDRIL\AINSSSLKGKPLSEAIHLLQMAG
		}				ETVTLKIKKQTDAQSASSPKKFPISSHLSDLGD
	1	1		1		VEEDSSPAQKPGKLSDMYPSHGCPSVDSAVD
	1	1		1		SWDGSA\IDTS\YGTEGT\SFQASGY\NFNTYD
	1					WRSPKORGS\LSPVT\KPRSQTYPDVGLSYED
		ļ		K)		WDRSTASGFAGAA\DSAETEQEENFWSQALE
	1	1		1	1	DIETCGOSGILRELEATIMSGSTMSLNHEAPT
		1			1	PRSPAGSDRPSFOERSSSRPHYSQTTRSNTLPS
					1	DVGRKSVTLRKMKOEIKEIMSPTPVELHKVI
		1				LYKDSDMEDFGFSVADGLLEKGVYVKNIRPA
		1				GPGDLGGLKPYDRLLQVNHVRTRDFDCCLV
	1					VPLIAESGNKLDLVISRNPLASQKSIDQQSLPG
	ì					D*SEQNSAFFQQPSHGGNLETREPTNTL
514	1864	A	3967	833	800	LEKQGYSGMATKRLARQLGLIRRKSIAPANG NLGRSKSKQLFDYLIVIDFESTCWNDGKHHH
		İ		1		SQEIIEFPAVLLNTSTGQIDSEFQAYVQPQEHPI
	1	ł		1		LSEFCMELTGIKQAQVDEGVPLKICLSQFCK
		1				WIHKIQQQKNIIFATGISEPS/DF*SKIMCICYL
						VR*RISYTY*SKHKSKGC
				100	182	CRFWGISTHCDTCDPLSPQTTEG**EGDLWSL
515	1865	Α	3969	492	182	DLLGPEFLARKPLFKTKTYQSTF*SISKNE/FTC
		1			l .	PNFIIEEGTDLIF/*QVKHNPCHRLTPEEGTVQL
	ì	į.		ì		NRADS
	1000	+	3977	12	1357	KMLC/QKESNYIRLKRAKMDKSMFVKIKTLG
516	1866	A	3377	12	1.00	GAFGEVCLARKVDTKALYATKTLRKKDVLL
		1		1	1	RNQVAHVKAERDILAEADNEWVVRLYYSFQ
-						DKDNLYFVMDYIPGGDMMSLLIRMGIFPESL
	į	1		1		ARFYIAELTCAVESVHKMGFIHRDIKPDNILID
				}	1	RDGHIKLTDFGLCTGFRWTHDSKYYQSGDHP
!	1					RODSMOFSNEWGDPSSCRCGDRLKPLERRAA
						RQHQRCLAHSLVGTPNYIAPEVLLRTGYTQL
1			1		1	CDWWSVGVILFEMLVGQPPFLAQTPLETQM
1		1		1		KVINWQTSLHIPPQAKLSPEASDLIIKLCRGPE DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS
		1	1			DRLGKNGADEIKAHPIF*NQFDF3Q*FED3R3 AFKQFP*NHTTPTDTSNFDP\VDPDKLWSDDN
		]				AFKQFP*NHTTPTDTSNFDF(VDFDKLWSDD) EEENVNDTLNGWYKNGKHPEHAFYEFTFRRI
		1				FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD
		1				QNTGSEIKNRDLVYV
1					1,000	FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY
517	1867	A	3980	1358	1022	VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD
j		1	1		1	*RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA
1						QAIFQPQPPKVLGLQV
				107/	166	SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F
518	1868	A	3986	974	666	SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH
1		1		- [		VGQAGLELLTSGDLPALASQSAGITG\SHRAR
		- 1				PENGEENIE
			2001	751	126	NOGLRHVGLCRTCLVNOMFASSILGKSHHHS
		A	3994	751	120	LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC
519	1869	1		1		LISINOGHNAL WKAAGIFLFERAGI CIQSI SI C
519	1869	)			}	DSLKYG\SWDEKDLTVPORDTHKRSVLRWIS
519	1869					DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV HLFSSEMGE\NRPMVG\ARHVYSNAALLSFTP

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid F=Glutamic Acid,
10: of	NO: of	hod	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
lence		Ì	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ł	ĺ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	l	ł		peptide	50425005	/=possible nucleotide deletion, \=possible
	l		1	sequence		avalentide incertion
				sequence	<del> </del>	LRCLGGEKHKSGLHARPVIVPSLELHYDMDSI
	ļ		1			AUNTADI I LIITLPSYYIPFC
				000	698	OSFRI SLLSSWDYRHM*PRLANF*T\FFCRDRV
520	1870	Α	3999	882	090	STATEPREVSNSWPOAILPPRPPKVLULQI
	1				1178	FFF*ETVSCSAS*AGVRSHDNSSLQPPSPG\SSN
521	1871	Α	4011	1346	1178	DDTG A SHV AGATGTHHHAWLLSV
	Ì					QGIALLTRMGESVKHVTGGYKLRTRPLEFAA
522	1872	A	4015	2	377	IGDYLDTFALKLGTIDRIAQRIIKEEIEYLVELR
		1				EYGPVYSTWSALEGELAEPLEGVSACIGNCST
	ì		l			AL*ELTDDMTEDFLFVLREYILYSDSMK
	1		1			ERVIHNQIQQAQRSPHIFNARRSS/PRPNIVELP
523	1873	A	4018	341	19	KVKEVCKTSKS/GQVIYKGVSIRLRANFLAEP
323	1075	1				KVKEVCKTSKS/GQVTTKGVSIKEIGHT EILE
	1	1	}	1	1	L*NRREWDEAIKVLKEKQ\FLSKMVYPANLSF
	1	ì	1		1	GNEGDITSFPAK
-504	1874	A	4020	1067	743	FFLRWSL/DSVAQAGVKWCNLGSLQAPPPGF
524	10/4	^	7020	1.00		TPFSCLSLPSSWDYRHPPPRLAN*LTNFLCF**
	1	1				RQGFTVLARMVLIS*PHDLPASASQSAGITGL
						SHCSWPTSSILS
	1		4021	781	351	QFRVIFFFLRSHSVAQAGMQWHDHSLLQPL
525	1875	A	4021	/61	1 32.	DDDI KOÆKHI SPPSIWDYRKVPPCLVNFSIFF
		1			Į.	VETGSCOPCLOLLGSSNPPASASQSAGLAGISH
	1		<b>\</b>			QGQPE*SFDIRFACVIAALRETFQCLCSASRVN
i	ł	ł	!	1		NIV ITATO DTHOVESSE
					341	TPSSTSRGTEEOOSSKMAWQRREEKEHLNVR
526	1876	A	4024	80	341	RSSAEDGWKADKP/VDG*TPGEDHLPTPSPFQ
						T LITHISSESOI HHSVK SPPSLSFRLM
		1				DFYLYPERKKRGQMMTAVSLTTRPQESVAFE
527	1877	A	4026	593	230	DVAVYFTTKEWAIMG\PAERALYRDVMLEN
1						YGGCGPL*CHPTSKPALVFS\LEQGKESCFSPA
}			1	1		TGSSLSRNDWRAGWIGYLELRRYTYLS
l .	Į.					GTSELLCIQRWNWGPAFPPRPGLALAPTLQLL
528	1878	A	4028	1160	242	VEMGSAKSVPVTPARPPPHNKHLARVADPRS
320	10.0					PSAGILRTPIQVESSPQPGLPAGEQLEGLKHAC
	. ]	1			1	PSAGILKI PIQVESSPQPOLI AGEQLEONIALI
	1				l	DSDPRSPTLGIARTPMKTSSGDPPSPLVKQLSE
	1		1			VFETEDSKSNLPPEPVLPPEAPLSSELDLPLGT
1	i	Y	ļ.	1		QLSVEEQMPPWNQTEFPSKQVFSKEEARQPT
ì		- 1	l .			ETPVASQSSDKPSRDPETPRSS\GSMRNRWKP
1	ļ		1		1	NSSKVL\GKSPLHPSCQDDNSPGTLTLRQGKA
1					1	AFKPLSENVSELK\EGA\ILGTGR\LLKTEGRA
1		i		1	1	WEQGQD\HDKENQHFPLVES
			4000	2	366	VDMVI IMEMOSMITMKCPOYL*E*RKIPDI I
529	1879	Α	4039	1 2	300	CW*GCGSTGILIFC/WS*PL*KTI*QPR*FKQI*1
			1			ILTITYSIM*EHTFHNAGV*LSDIYPRFMKGYV
1	1	- 1		1		LITEICT*MFIAVI.FVVVKTWKOF
				<del></del>		I EVNGNTIVTVETKAONKKNKGSRSILFKQI
530	1880	A	4057	358	3	RKYGSRINLLKSKHDKNICTENYKT*MKEIEA
1					ļ	DTDKWKDILCSWIRRIHMKDILCSWIGRTHV
1	1	1	1	1		VKISILPKVNYRFYLISIKIIMAI
1		- 1				TQGTEEIYKISSCEWVQASFSTPLITLHDFKIY
531	1881	-ta	4061	50	278	HKATVIKMVWYWHRQ*KFSKN/RIESSEIEPH
231	1001	'`		1		HKATVIKMVWYWHKŲ*AFSANIAICUIVMIIT
	1			}		IYDQFIFDKGEKIIQEKGNSFFNN/MCWKNWI
		-			1	T*KR
			4040	19	368	NDLLENFKFWE*FKE*LENINGTVTEKETGG*
532	1882	A	4069	17	1	VKET SSPKYSGTROFYGOTISNFPGKIISMVY
			1	į	1	KLFQNTE/TEGRHPISLYEFRITLITIPNKDNIY
1			-			OTWMPVSLMNIVTLKCPT
					756	PIRKFTKVAG*KSNTPK*LAFLHINNEQFENK
533	1883	A	4076	1	355	ITNIPFIIASKRIKYSGISLTKEMKDLYTETLLI
1	1					KIKEDTNKWKDI/SCFWVGR/LNIVKMPK/VI
1						

WO 01/57188

				<del></del>	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	l		914	ng to first	acid residue	Q=Giutamine, K=Arginine, 5-5a ine,
	Ì		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	•	Ì	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ì	}	peptide		/=possible nucleotide deletion, \=possible
	Į	1		sequence		nucleotide insertion
. <del></del>	<del> </del>	<del>                                     </del>	<del>                                     </del>			IFNAIPIKMPMMCMAKIEKNSS
534	1884	A	4088	3	1931	IIDSSTRRMESERSPLYRQLIDLGYLSSSHWNC
334	1004	1	1000	-		GAPGQDTKAQSMLVEQSEKLRHLSTFSHQVL
	1	1		1 .		OTRLVDAAKALNLVHCHCLDIFINQAFDMQR
		ì				DLQITPKRLEYTRKKENELYESLMNIANRKQE
	1		1	Ì		EMKDMIVETLNTMKEELLDDATNMEFKDVI
	ł	1	ı	-		VPENGEPVGTREIKCCIRQIQELIISRLNQAVA
Ì				1		NKLISSVDYLRESFYGTLERCLQSLEKSQDVS
ļ	1	}	1	1	1	VHITSNYLKQILNAAYHVEVTFHSGSSVTRM
	1	1	1			LWEQIKQIIQRITWVSPPAITLEWKRKVAQEAI
ĺ		1		1	1	ESLSASKLAKSICSQFRTRLNSSHEAFAASLRQ
	1				İ	LEAGHSGRLEKTEDLWLRVRKDHAPRLARLS
Į	1		l			LESRSLQDVLLHRKPKLGQELGRGQYGVVYL
}	1		1	ľ		CDNWGGHFPCALKSVVPPDEKHWNDLALEF
1		İ	1			HYMRSLPKHERLVDLHGSVIDYNYGGGSSIA
		ì				VLLIMERLHRDLYTGLKAGLTLETRLQIALDV
}	1	1	ł	}	}	VEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKI
	1	1	1			TDLGFCKPEAMMSGSIVGTPIHMAPELFTGK
,	1	-	1			YDNSVDVYAFGILFWYICSGSVKLPEAFERCA
						YDNSVDVYAFGILFWYICSGSVALFEAFERCA
	3.		1			SKDHLWNNVRRGARPERLPVFDEECWQLME
		1	1 .	ì		ACWDGDPLKRPLLGIVQPMLQGIMNRLCKS\
	1		1		l	NSEQPNRGLDDST
535	1885	A	4090	2	417	ALMPHEANYEEIFLKTDKDMDGFESGLEVRE
333						IFLKTR/GLPSTLLAHIWALCDSKDCGKLSKD
			1		ŀ	HFALAFHLIT\QKLIKGIDPPLVLTPEKISPSNR
ì	İ	1	1	1		ASLQKVTELTRKPVCIIFKGTILWRITDSIWMK
		1	i	1		HNRKRIWLRA
536	1886	A	4102	569	829	DHQK*KNIPCSWIGRINIVKMSILPKAIYRFSAI
330	1000	1 ^ -				PIKIPMTFFTEI*S*NVYRTTKTQE*AKAILSKK
			)		}	EQNLEESHYLDFK*YYRAV
537	1887	I A	4104	54	281	SIDCEHLIRRMLVLDPSKRLTIAQIKEHKWML
331	1007	Α	1201	1 "	1	IEVPVQRPVLYPQEQENEPSIGEFNEQVLRLM
		i		j	1	HSLGIDOOKTIE
630	1888	A	4109	141	314	IRHIPLKIRSVVSHLKCFYKFILTFFFAGCSQPL
538	1000	^	4107	1		VPRENITAWMNAIGLIITALPVS
	1000	+	4111	268	1	ASRPWGHSYP*FNOQEVDTLKRPIASSEI*MM
539	1889	A	4111	200	1'	I*KFAT\KKSPGPYRFTAEFSHTFKEDLVPILW
1	]	1	Į		1	PLFPKIYREGTLPHSFYEASITL
	1 2000		1222	198	2064	PEPGAGRAATPWGPLFWRGRGSGRCEKAAE
540	1890	Α	4142	196	2004	AALGDFLGLHRRTQQPAVDRLLSDASAQWR
				1		VRGHGGVRESGRAPQQPGRRRGRRPRKRPR
				1		GRWRREGCGAGGRGVCVAAWSQRSIAGNN
		1	1	1	1	DYRLFHKMSNSHPLRPFTAVGEIDHVHILSEH
				l		IGALLIGEEYGDVTFVVEKKRFPAHRVILAAR
						COYFRALLYGGMRESQPEAEIPLQDTTAEAFT
	į			1	1	MLLKYIYTGRATLTDEKEEVLLDFLSLAHKY
					1	GFPELEDSTSEYLCTILNIQNVCMTFDVASLY
1						SLPKLTCMCCMFMDRNAQEVLSSEGFLSLSK
	i			-		TALLNIVLRDSFAAPEKDIFLALLNWCKHNSK
				1		PUBLICATION OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRINCIPLE OF A PRIN
						ENHAEIMQAVRLPLMSLTELLNVVRPSGLLSP
		ì				DAILDAIKVRSESRDMDLNYRGMLIPEENIAT
	!		1		1	MKYGAQVVKGELKSALLDGDTQNYDLDHG
]	1					FSRHPIDDDCRSGIEIKLGQPSIINHVRILLWDR
		-		1		DSRSYSYFIEVSMDELDWVRVIDHSQYLCRS
1			}			WQKLYFPARVCRYIRIVGTHNTVNKIFHIVAF
		1				ECMFTNKTFILEKGLIVPMENVATIADCASVI
1	1			İ	1	EGVSRSRNALLNGDTKNYDWDSGYTCHQLG
1		-				SGAIVVQLAQPYMIGSIRVLLWDCDDRSY
541	1891	A	4146	282	778	GTLGYPNGARGQPQDNFFAHQ\VSHHPPISAC
		1.75	1 7140	1		

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl- eotide seq-	peptide seq- uence		in USSN 09/496	nucleotide location correspondi	location corresponding to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first amino acid	acid residue of peptide sequence	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of peptide sequence	sequence	/=possible nucleotide deletion, \=possible nucleotide insertion
						HAESENFAFWQDMKWKNKFWGKSLEIVPVG TVNVSLPRFGDHFEWNKVTSCIHNVLSGQRW IEHYGEVLIRNTQDSSCHCKITFCKAKYWSSN
					102	VHEVQGAVLSRSGRVLHRLFGKWHEGLYRG PTPGGQCIWKP SVDAYVCNDIVFSYRTTITLLEGA*LTHRYVA
542	1892	A	4147	44	433	QDPKQGQLRSLHLTCDSAPAGSQGTWSTSCR INHLIFRGGAQITFLATFDDSPKAVLGDRLLLT ANVSSENNTPRTSKTTFQLELSVKDAVYTVV SSH
543	1893	A	4153	678	11	TISYPOCLTOMYFLISFANVDTFLLPIMALDH YVAICSALO*CSITP/ELCQGLPVLA*AGSSLIS
						PVHTVIMSRLAFCSSAQISHFYRDAYLLMKIA CSHT*\NQHVFLGAVVLFLAPCALILVSYIRIA AAILRIPSPTRRRKACSICSSHLSLVTLFYGTV
					538	LGICI*PPDSFSAQDAIATIMYTVVTSMLNPFTY SLMNKEVQEAVRRLFSRGSHSSWCW LLYAQAGVQ*LNLSSLQPQPAGLKQSSHPSLP
544	1894	A	4158	3	336	SSWDYRYSTPHPANFFVEMEFHHVAQAGLEL LGSGDLPTSTSHSAGITGVSHHAPPRLISSEGS LLGHLLCLPMVFPLLCVFVLISSSLAGEEAAG
						LRVQKLWPAVVLSHLPVCWFHCSGIWSEVIE LKVGREGHVLPWQAHVVEF HPLGLGLVPSEIFSPQDKKAADGSILAPARGE
545	1895	A	4160	1	412	DLEAGLKGSFMDGRLQASVSVFRIQRVGSAM QDTASAMPCLPYYPTSHCFMAGGKSRSQGW ELELSGEPAPGWQVLAGYTYTQARYLRDASE
546	1896	A	4174	1252	1190	ANVGQPLRPVDPR  FFQVFIFLFLIFFKTEFHSCCPGAVQWHDLDSL  QPPPPRFKGFSCLSLPSSWDYRHAPAHPANFV  FLVETGFLHV\GQ\ASLELPTSGDTPAS\ASQSA
547	1897	A	4176	3029	1	GITGVSHHA*PRASGRRCW  AGPDGLAAPASCQGARGQTRVPGAFSWLAP
347	1857		1.2.5			GSHHASEGLAPGVPPAGGVSAQELTAPPQEG WGLGAPPAAPRPESDEKRAGSDAVRSFSRGA RDSLGQRRLGGTRGAGPAGKGAQRTMGPAS
						GFHSFPPRPHQEPSPRSSCWQHLLWHCPWPQ PSRLPRLTPAOLLOGPGVLAAPPGP*HVPGFL
						AQSPWPLPSGPRSP*DPLHQGALVPLPQGGSP HTAPHCLPSVLSPAIQQPLLPTAST/SSRSPPAS TMAPIPSALAVWEPAGSSPQLSSAPADSSVPLP
						ALPKVLPPWTQKPLLGCLCQSPLPLLSPPDQIV RCPPACSPAAASSFSFESQPCPSAPSKASPAPA
						ALUVGPHHPP*SQQPQSQSVHPHGPGGPQPPL AASSLFWMFCQPPPPHPQFLWHRPLPVTGKA LAS\PLCFRPAPGSLRQTPLPPQFHIPRPGLSAP/
				:		PPPASGTSDSSDSRSPSASAARVWPPA\SPPPP AARHRPHPPEYFLSPCPFSCGFPRLLGRPRRPQ
						ALQTPRAWDLPPGSSPAPLCSGPELP*APPPLP PFPRVA*LGSGHPPSAQVPGLW*RCV*GHPIP RPVGHS*SGPPHSPPL*APPQAWPLELPPSRQC
						LQPLHLRAAQPLDPCCSLSPPGPPLPVPALPS WPGRP*SPSPASSOPPYHAGLPGPQSSPLPPGL
						POLPSLRSGSQQPLLFFQCPGPGAVWGKGSPQ PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVCL TPSRSASSLPEVVLASSLPKIPQSSGSVPLGPTSP
						MP*CFHRPSPPLP/LSSPFPA\LRPQAPQFPLHLP P*PPAPSPGCPLPPLAQOHQPSPPSPHARSTLT
						PPLWPSLALLP*PLPPPPPVPSFSASLLCSLPAH

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-Americ Acid F=(ilutarnic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
aucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		]	}	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
			ì	residue of	sequence	/=possible nucleotide deletion, \=possible
		1	]	peptide		nucleotide insertion
		1		sequence		GTPASPGLGRSCLGKPQTLPWISFWPPSGRLA
	† — —			}		DCTWOPW/PVSPAPLSCLSAWDPWELPSPQPQ
			ł		1	I VCSTAFI PTSCLLSSPGP\PAFOPPREGCL*GFF
		1	Ì			GPPGLPPLQSSLSFPPPPPPPVPQPPAPPALQWG
				Ì	Ì	LITT DCCCPTK
	1	<u> </u>	1	2260	844	PRUBERDECE II KGIARLLSNPLLOTYLPNSTK
548	1898	A	4180	2369	044	I MICHIOFI I VI.FWKLCDFNKVGQPKGALQOD I
		1				GEOT PO*PGGRDSVRLRGVGQSCPSLELSPLO
			1			DSDLID*KFI FFVI KSSDVLDILVPILFFLNDAK
		1	1			ADQSRVGLMHIGVFILLLLSGECNFGVRLNKP
	Ì	1		Į	l	YSIRVPMDIPVFTGTHADLLIV\VFHKIITSGHQ
		-				RLQPLFDCLLTIVVNVSPYLKSLSMVTANKLL
				1	1	HLLEAFSTTWFLFSAAQNHHLVFFLLEVFNNI IQYQFDGNSNLVYAIIRKRSIFHQLANLPTDPP
			l	1	1	TIHKALQRRRTPEPLSRTGSQGGAPPWRAPA
			ĺ	l		PLPLQSQAPSRPVWWLLQALTS*PRSPRCQR
		ĺ		-		MAPCGPWNLSPSRAWRMAARLRGSPARHGG
		1			i	SCOPPTHSSASGOWSPTPEWVLSWKSKLPLQ
				\		TIME I OVI VPOVEKICIDKULI DESELLKILV
		1		1		LUCTI VCI LEVPHPILIRKYOANSGI AMWEKI
	- <del> </del>			l l		VMWGVIYI RNVDPPVWYDTDVKLFEIQKV
			4191	858	321	T DWODE GVI I SRGKMAVI GWLESLKIAQNI
549	1899	_ A	4191	636	1	ALL ODGRRKVHYLFPDGKEMAEE YDEKISE
		- 1		{		LLVRKWRVKSALGAMGQWQLEVGDPAPLG
	-	1	ļ			AGNLGPELIKESNANPIFMRKDTKMSFQWRIR
1			1	l l		NLPYPKDVYSVSVDQKERCIIVRTTNKKYYK
			Ì	1	<u> </u>	KFSIPDLDRHQLPLDDALLSFA\TPTAP IRHTGSDIAGVCGWLLLSGPCGVGLDLDSRLL
550	1900	A	4192	1	1980	GASAMRRSEVLAEESIVCLQKALNHLREIWE
330	1,,,,,		Ì	\ \		LIGIPEDORLORTEVVKKHIKELLDMMIAEEE
				1		of VEDI IKSISVCOKELNI LUSELH VEPPQEEG
				1	1	PETER OF EXIST RECOVER MICHAELAL
Ì	}	1	1			I DEODOELC'EILCMPHYDIDSASVPSLEELING
1	l			1		FROUNTTI RETKASRREEF/VSSICRUILLCIVIL
İ	Ì					EI DUTPOTSFERDVVCEDEDAFCLSLENIATUL
1		- [	1	Į.		OVI I POVI FMOKSONEAVCEG/LRTQI/KELW
1	]		ł			DDI ODEFERFAVATIMSGSKAKVKKVALQUE
		- 1		l l		VDRLEELEKCKTMKKVIEAIRVELVQYWDQC
						FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR FYSQEQRQAFAPFCAEDYTESLLQLHDAEIVR
İ						LKNYYEVHKELFEGVQKWEETWRLFLEFER KASDPNRFTNRGGNLLKEEKQRAKLQKMLP
1		1	-			KLEEELKARIEL WEQEHSKAFMVNGQKFME
		ļ				YVAEQWEMHRLEKERAKQERQLKNKKQTET
1				. [		EMLYGSAPRTPSKRRGLAPNTPGKARKLNTT
		Ì		. [		TMSNATANSSIRPIFGGTVYHSPVSRLPPSGSK
	İ			ļ		DVAASTCSGKKTPRTGRHGANKENLELNGSI
1	İ			Ì		I SGGVPGSAPLORNFSINSVASTYSEFADPSLS
		1			ļ	Deety GLORELSKASKSDATSGILNSTNIQS
		L_			1008	A WILLEGI VSSPAIGAYLSASYGDSLVVLVAIV
551	1901	Α	4194	3	1000	VALI DICEIL VAVPESLPEKMRPVSWGAQISW
1		[				LOADPEASI KKVGKDSTVLLUCII VCLSYLPE
1	ł	-				A CLOVSSEE/I YI R\OVIGEG\TVKIAAFIAMVG
		- 1				T CIVACTAFI SII MRSI GNKNI VLLGLGFUMI
						OLAWVCECSOAWMMWAAGIVAAMSSIIFP
1	1		1	1		A 10 A 1 USBNAFSDOOGVAOGII I GIRGLUNGL
1						CDAI VGFTFYMFHVELTELGPKLNSNN VPLQ
						CAVIPOPPELEGACIVLMSFLVALFIPEYSKAS
	1	ı	ı	i	1	The second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th
	1	- 1				GVQKHSNSSSGSLTNTPERGSDEDIEPLLQDS SIWELSSFEEPGNQCTEL

			T-650	N 3 44	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	(	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		ſ	914	ng to first	acid residue	Q=Glutamine, K=Argillile, 3-3crille,
domes	1	Ì		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
-	1	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ	ł	Ì		peptide		/=possible nucleotide deletion, \=possible
		ì	1	sequence		nucleotide insertion
	1000	<del>                                     </del>	4197	2	14302	ARPPPAPGSRQQKQKAAPGAAAAAELRGAR
552	1902	A	4197	2		FPAPARRRGTMADGGEGEDEIQFLRTDDEVV
	Į.	1	1			LQCTATIHKEQQKLCLAAEGFGNRLCFLESTS
j						NSKNVPPDLSICTFVLEQSLSVRALQEMLANT
]		ļ	1			VEKSEGQVDVEKWKFMMKTAQGGGHRTLL
		1	1			YGHAILLRHSYSGMYLCCLSTSRSSTDKLAFD
	1	l		}	1	VGLQEDTTGEACWWTIHPASKQRSEGEKVR
1	1	1				VGDDLILVSVSSERYLHLSYGNGSLHVDAAF
Į.		j	į	1	}	OCT WOLLDISCOSE A OCYLIGODY RITH
1		1			1	QQTLWSVAPISSGSEAAQGYLIGGDVLRLLH
1	1	1	Ì			GHMDECLTVPSGEHGEEQRRTVHYEGGAVS
	1	1	1		}	VHARSLWRLETLRVAWSGSHIRWGQPFRLR
			1			HVTTGKYLSLMEDKNLLLMDKEKADVKSTA
1		1	4			FTFRSSKEKLDVGVRKEVDGMGTSEIKYGDS
i	l	1	1			VCYIQHVDTGLWLTYQSVDVKSVRMGSIQR
}	ł	1	1			KAIMHHEGHMDDGISLSRSQHEESRTARVIRS
1	ļ	}				TVFLFNRFIRGLDALSKKAKASTVDLPIESVSL
<b>\</b>			ļ	1		SLQDLIGYFHPPDEHLEHEDKQNRLRALKNR
}	1	}	J		Ì	ONLFOEEGMINLVLECIDRLHVYSSAAHFAD
ì			1			VAGREAGESWKSILNSLYELLAALIRGNRKN
}	{		ı	i .	· ·	CAOFSGSLDWLISRLERLEASSGILEVLHCVL
1		-	l l			VESPEALNIIKEGHIKSIISLLDKHGRNHKVLD
1		1	i	1		VLCSLCVCHGVAVRSNQHLICDNLLPGRDLL
}	1		1			LQTRLVNHVSSMRPNIFLGVSEGSAQYKKWY
ļ	i		1			YELMVDHTEPFVTAEATHLRVGWASTEGYSP
	1		1			YPGGGEEWGGNGVGDDLFSYGFDGLHLWSG
'			1		}	CIARTVSSPNQHLLRTDDVISCCLDLSAPSISF
1	1	1				RINGQPVQGMFENFNIDGLFFPVVSFSAGIKV
1	1			İ		RFLLGGRHGEFKFLPPPGYAPCYEAVLPKEKL
1		1	1	1	Į.	KVEHSREYKQERTYTRDLLGPTVSLTQAAFT
1		Ì	1	{		PIPVDTSQIVLPPHLERIREKLAENIHELWVMN
1	1	i	· I	1	]	KIELGWQYGPVRDDNKRQHPCLVEFSKLPEQ
- (	- 1	- [	- [	İ		ERNYNLQMSLETLKTLLALGCHVGISDEHAE
				1		EKN I NE QMSEETER TEEAEGETT GIODEILE
	1		1	ŀ	]	DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT
}	- 1		1			PSQEAMVDKLAENAHNVWARDRIRQGWTY
į.	- }	1	1			GIQQDVKNRRNPRLVPYTPLDDRTKKSNKDS
-	1	-	1			LREAVRTLLGYGYNLEAPDQDHAARAEVCS
	-		1	1	1	GTGERFRIFRAEKTYAVKAGRWYFEFETVTA
		1	1	1	1	GDMRVGWSRPGCQPDQELGSDERAFAFDGF
			1		1	KAQRWHQGNEHYGRSWQAGDVVGCMVDM
	]	}	}	1		NEHTMMFTLNGEILLDDSGSELAFKDFDVGD
		1			1	GFIPVCSLGVAQVGRMNFGKDVSTLKYFTIC
1		1	1		1	GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV
						PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN
1		- [		Ì	1	SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG
1	}	1		}	1	LEGPKNDLEDYDADSDFEVLMKTAHGHLVP
	l	- 1	1	ł		DRVDKDKEATKPEFNNHKDYAQEKPSRLKQ
		1		Į.		RELIERTKPDYSTSHSARLTEDVLADDRDDY
			1			DELMOTSTYYYSVRIFPGOEPANVWVGWITS
		1	1	1		DEHOYDTGFDLDRVRTVTVTLGDEKGKVHE
		Į		1		STKRSNCYMVCAGESMSPGQGRNNNGLEIGC
			1			VVDAASGLLTFIANGKELSTYYQVEPSTKLFP
			1		1	AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS
						EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL
}	l	1	1	1	1	KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN
-	1					KADA2KI2KKO AFA KENALLI DI ASTALLEDIA
	i i					RSVDILELTEQEELLKFHYHTLRLYSAVCALG
	1	}		1		NHRVAHALCSHVDEPQLLYAIENKYMPGLLR
		.				AGYYDLLIDIHLSSYATARLMMNNEYIVPMT
1		1			<b>\</b>	EETKSITLFPDENKKHGLPGIGLSTSLRPRMQF
		1			1	SSPSFVSISNECYQYSPEFPLDILKSKTIQMLTE
1						AVKEGSLHARDPVGGTTEFLFVPLIKLFYTLLI
L						

		17/-	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ł		ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ		peptide	Sequence	/=possible nucleotide deletion, \=possible
}	ł			sequence		nucleotide insertion
				Sequence		MGIFHNEDLKHILOLIEPSVFKEAATPEEESDT
1		1	1			LEKELSVDDAKLOGAGEEEAKGGKRPKEGLL
	1	1	1			OMKLPEPVKLOMCLLLQYLCDCQVRHRIEAI
	1		1			VAFSDDFVAKLODNQRFRYNEVMQALNMSA
	l	1 .	1	1	ļ	ALTARKTKEFRSPPOEQINMLLNFKDDKSECP
1	1			1		CPEEIRDOLLDFHEDLMTHCGIELDEDGSLDG
	1	1		1		NSDLTIRGRLLSLVEKVTYLKKKQAEKPVES
ļ	1	1	ł			DSKKSSTLOOLISETMVRWAQESVIEDPELVR
		1	1		1	AMFVLLHROYDGIGGLVRALPKTYTINGVSV
ł	1	1	1			EDTINLLASLGOIRSLLSVRMGKEEEKLMIRG
				ļ		LGDIMNNKVFYOHPNLMRALGMHETVMEV
	ŀ	1				MVNVLGGGESKEITFPKMVANCCRFLCYFCR
	ŀ					ISRONOKAMEDHLSYLLENSSVGLASPAMRG
	1	1				STPLDVAAASVMDNNELALALREPDLEKVVR
ì	1	-	Í	1		YLAGCGLQSCQMLVSKGYPDIGWNPVEGER
			١.	1	1	VI.DELREAVECNGESVEENANVVVRLLIKKPE
			1		ļ	CFGPALRGEGGNGLLAAMEEAIKIAEDPSRD
			1			GPSPNSGSSKTLDTEEEEDDTIHMGNAIMTFY
	1					SALIDLLGRCAPEMHLIHAGKGEAIRIRSILRS
		1				LIPLGDLVGVISIAFQMPTIAKDGNVVEPDMS
1	1	ł		Ì		AGFCPDHKAAMVLFLDRVYGIEVQDFLLHLL
		Į.		j		EVGFLPDLRAAASLDTAALSATDMALALNRY
1	1		\			LCTAVLPLLTRCAPLFAGTEHHASLIDSLLHT
1	1					VYRLSKGCSLTKAQRDSIEVCLLSICGQLRPS
						MMQHLLRRLVFDVPLLNEHAKMPLKLLTNH
		V	1			YERCWKYYCLPGGWGNFGAASEEELHLSRK
					}	LFWGIFDALSQKKYEQELFKLALPCLSAVAG ALPPDYMESNYVSMMEKQSSMDSEGNFNPQ
	]	Ì				PVDTSNITIPEKLEYFINKYAEHSHDKWSMDK
		l		İ	}	LANGWIYGEIYSDSSKVQPLMKPYKLLSEKE
				ì		KEIYRWPIKESLKTMLARTMRTERTREGDSM
1	1	- 1	ſ	-		ALYNRTRRISQTSQVSVDAAHGYSPRAIDMS
1			1	ļ		NVTLSRDLHAMAEMMAENYHNIWAKKKKM
			1			ELESKGGGNHPLLVPYDTLTAKEKAKDREKA
l l	ì		1			QDILKFLQINGYAVSRGFKDLELDTPSIEKRFA
ļ				Ì		YSFLQQLIRYVDEAHQYILEFDGGSRGKGEHF
ľ		-		1		PYEQEIKFFAKVVLPLIDQYFKNHRLYFLSAA
		1		- }		SDDI CSGGHASNKEKEMVTSLFCKLGVLVRH
1			1	- [		PIST FGNDATSIVNCLHILGOTLDARTVMKTG
						LESVKSALRAFLDNAAEDLEKTMENLKQGQF
						THTRNOPKGVTOIINYTTVALLPMLSSLFEHI
1		İ				COHOFGEDI JI EDVOVSCYRILTSLYALGTSK
1						STYVERORSALGECLAAFAGAFPVAFLETHLD
1				1		KHNIYSIYNTKSSRERAALSLPTNVEDVCPNIP
		- 1	1			SLEKT MEETVELAESGIRYTOMPHVMEVILPM
İ						I CSYMSR WWEHGPENNPERAEMCCTALNSE
1						HANTI LONILKIIYNNLGIDEGAWMKRLAVF
{		i				SOPIINKVKPOLLKTHFLPLMEKLKKKAATVV
		1			1	SEEDHLKAEARGDMSEAELLILDEFTTLARDL
		1				VAFYPLLIRFVDYNRAKWLKEPNPEAEELFR
-		1	ŀ		1	MVAEVFIYWSKSHNFKREEQNFVVQNEINN
-					i	MSELETDTKSKMSKAAVSDOERKKMKRKGD
				1		PYSMOTSLIVAALKRLLPIGLNICAPGDQELIA
1		ì		}		I AKNRESLKDTEDEVRDIRSNIHLQGKLEDP
	1					AIRWOMALYKDLPNRTDDTSDPEKTVERVL
						DIANVLEHLEOKSKRVGRRHYCLVEHPQRSK
1		}				V AVWHKLI SKORKRAVVACFRMAPLYNLPR
						HRAVNLFLQGYEKSWIETEEHYFEDKLIEDLA
						KPGAEPPEEDEGTKRVDPLHQLILLFSRTALT
						EKCKLEEDFLYMAYADIMAKSCHDEEDDDG

SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	(	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		}	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	]		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
1			ł	peptide		nucleotide insertion
			<u> </u>	sequence		FFFVKSFEEKEMEKOKLLYOOARLHDRGAA
		1			ļ	EMVLOTISASKGETGPMVAATLKLGIAILNGG
			1	1		NSTVOOKMLDYLKEKKDVGFFQSLAGLMQS
		1				CSVLDLNAFERONKAEGLGMVTEEGSGEKV
	1		1			LODDEFTCDLFRFLOLLCEGHNSDFQNYLRT
	1	}	1	}	ł	OTGNNTTVNIIISTVDYLLRVOESISDFYWYY
	,	1	1	1		SCKDVIDEOGORNFSKAJOVAKOVFNTLTEYI
}	1		1	1	1	QGPCTGNQQSLAHSRLWDAVVGFLHVFAHM
1	1			1		QMKLSQDSSQIELLKELMDLQKDMVVMLLS
1				1		MLEGNVVNGTIGKQMVDMLVESSNNVEMIL
	}	ł	1	{	1	KFFDMFLKLKDLTSSDTFKEYDPDGKGVISK
1		1			1	RDFHKAMESHKHYTQSETEFLLSCAETDENE TLDYEEFVKRFHEPAKDIGFNVAVLLTNLSEH
						MPNDTRLQTFLELAESVLNYFQPFLGRIEIMG
1		ł	Ì		1	SAKRIERVYFEISESSRTQWEKPQVKESKRQFI
1		1			1	FDVVNEGGEKEKMELFVNFCEDTIFEMQLAA
	į.	1	1			QISESDLNERSANKEESEKERPEEQGPRMAFF
-				1		SILTVRSALFALRYNILTLMRMLSLKSLKKQM
1				)		KKVKKMTVKDMVTAFFSSYWSIFMTLLHFV
1		1	1			ASVERGEERIICSLLLGGSLVEGAKKIKVAELL
		1		1	Ì	ANMPOPTODEVRGDGEEGERKPLEAALPSED
	İ	1		1		LTDLKELTEESDLLSDIFGLDLKREGGQYKLIP
1		1				HNPNAGLSDLMSNPVPMPEVQEKFQEQKAK
}		1	}	1		EEEKEEKEETKSEPEKAEGEDGEKEEKAKED
	İ					KGKQKLRQLHTHRYGEPEVPESAFWKKIIAY
1		1	ł	1		QQKLLNYFARNFYNMRMLALFVAFAINFILL FYKVSTSSVVEGKELPTRSSSENAKVTSLDSS
		}	ì			SHRIIAVHYVLEESSGYMEPTVRILPILHTVISF
					ĺ	FCIGYYCLKVPLVIFKREKEVARKLEFDGLYI
- {		1				TEQPSEDDIKGQWDRLVINTQSFPNNYWDKF
					-	VKRKVMDKYGEFYGRDRISELLGMDKAALD
				1 .	1	FSDAREKKKPKKDSSLSAVLNSIDVKYQMW
				1		KLGVVFTDNSFLYLAWYMT
			4100	31	767	I PEL NGRGAGLRRAEPSERGGGAERTQQVAA
553	1903	A	4199	31	1.07	LPLSHGHSHGGGGCRCAAER/VGAARGSAAC
	1	1			1	AYGLYLRIDKGRLOCLNESREGSGRGVFKPW
		]	}			FRAD\DRSKFVESDADEELLFNIPFTG\HVKLK
						GIIIMGEDDDSHPSEMRLYKNIPQMSFDDTER
				Į.		EPDQTFSLNRDLTGELEYATKISRFSNVYHLSI
				1	1	HISKNFGADTTKVFYIGLRGEWTELRRHEVTI
		- 1		-		CNYEASANPADHRVHQVTPQTHFIS
554	1904	A	4200	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSL EICIKACKNLAYGEEKKKKCNPYVKTYLLPD
337	1.50.			}		RSSQGKRKTGVQRNTVDPTFQETLKYQVAPA
ĺ		[			1	QLVTRQLQVSVWHLGTLARRVFLGEVIIPLAT
Ì	}	1				WDFEDSTTQSFRWHPLRAKADKYEDSVPQS
		1	1			NGELTVRAKLVLPSRTRKLQEAQEGTDQPSL
		ļ	-			HGQLCLVVLGAKNLPVRPDGTLNSFVKGCLT
	1		}			1 PDOOKLRI KSPVLRKOACPOWKHSFVFSGV
				1		TPAOLROSSLELTVWDOALFGMNDRLLGGT\
	1		}			RLGSKGDTAVGGDACSQSKLQWQKVLSSPN
[	1	}				I WTDMTLVLH
		_		221	2419	KENKKARNLRMNOSRSRSDGGSEETLPQDH
555	1905	A	4211	331	2417	NHHENERRWOOERLHREEAYYQFINELNDE
		ĺ				DVRIMRDHNLLGTPGEITSEELQQRLDGVKE
		1		- (		OLASOPDLRDGTNYRDSEVPRESSHEDSLLE
j		-		i	}	WINTERRIGNATRSGONGNOTWRAVSRINP
		- 1		- [		NNGEFRESLEIHVNHENRGFEIHGEDYTDIPLS
1	i	Ì	1		1	DSNRDHTANRQQRST\SPVARRTRSQTSVNFN
		1	}			GSSSNIPRTRLASRGQNPAEGSFSTLGRLRNGI
1		_ 1				

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	Soquence	/=possible nucleotide deletion, \=possible
	Ì		-	sequence		nucleotide insertion
	<del> </del>	<del> </del>	<del> </del>	sequence		GGAAGIPRANASRTNFSSHTNQSGGSELRQRE
	}		1	į		GQRFGAAHVWENGARSNVTVRNTNQRLEPI
				ì		RLRSTSNSRSRSPIQRQSGTVYHNSQRESRPV
				}		QQTTRRSVRRRGRTRVFLEQDRERERRGTAY
		1	1			TPFSNSRLVSRITVEEGEESSRSSTAVRRHPTIT
			}	1		LDLQVR\RIRPGENRDRDSIANRTRSRVGLAE NTVTIESNSGGFRRTISRLERSGIRTYVSTITVP
	1		1	1		LRRISENELVEPSSVALRSILRQIMTGFGELSSL
	1	}	ŀ	1		MEADSESELQRNGQHLPDMHSELSNLGTDN
		İ	1			NRSQHREGSSQDRQAQGDSTEMHGENETTQP
		ł				HTRNSDSRGGRQLRNPNNLVETGTLPILRLAH
	1		}			FELL NESDDDDRIRGLTKEQIDNLSTRHYEHN
	1	1				SIDSELGKICSVCISDYVTGNKLRQLPCMHEF
		1		İ		HIHCIDRWLSENCTCPICROPVLGSNIANNG
	1	<del> </del>	1-1010	3	462	LOROROHPAAAPAVPVRCFTFCFTDIVIMPKR
556	1906	A	4212	3	402	KSPENTEGKDGSKVTKOEPTRRSARLSAKPA
						PPKPEPKPRKTSAKKEPGAKISRGAKGKKEEK
						QEAGKEGTAPSENGETKAEEIHISRSTVNVST
	-	Ì	Î			SRGTPPSTLSVKGQIETVRVKGTEN
557	1907	A	4213	774	507	ARRESCLTLQTSWGHRH\GPPRP\ANFVFLVET
331	1307	1 ~	1 .2.5			GFLHIGQAGHKLPTSGDPPASASQSARITGMS
		- 1				HRTWFLASFLIDSCKNFIVYKIMYTL TYRHAEREHPETSSATKVSYDYRHKRPKLLD
558	1908	A	4225	3	1253	GDQDFSDGRTQKYCKEEDRKYSFQKGPLNRI
220	1700					LDCFNTGRGRETQDGQVKEPFKPSKKDSIAC
			j	1		TYSNKNDVDLRSSNDKWKEKKKKEGDCRKE
	1	1	ļ			SNSSSNQLDKSQKLPDVKPSPINLRKKSLTVK
		1	- }	1	1	VDVKKTVDTFRVASSYSTERQMSHDLVAVG
						PKSENEHPVEEHLDSTONTENKPTGEFAQEIL
ļ		1				THOUK ANYFPSPGITLHERFS\KMADIHKAD\
		i				NEIPL NSDPEIHRRIDMSLAELQSKQAVIYESE
				ł		OT IKIIDPNDLRHDIERRRKERLQNEDEHIFH
ĺ				Į.		ASAAERDDQNSSFSKNYTTQRKDIITHKPFEV
						EGNHRNTRVRPFKSNFRGGRCQPNYKSGLVC
		-	}			KSLYIQAKYQRLRFTGPRGFITHKFRERLMRI
I	Ī	1		İ		KKVP PARTY AND LECADARS VHCNI GI
559	1909	A	4235	1	323	KFSIPFFLRWSFTLV\PRLEGNDMISVHCNLGI LGLSHSPASASQVGGITGTQHHTGLIFGFLIET
333	- 1		1			EFHHVGQAGLELLTSGDPPALAFQSAGITGV
Ì		]		}		HHAWLQVLNS
[					1550	TLSLLERVLMKDIVTPVPQEEVKTVIRKCLEC
560	1910	A	4246	2	1569	A AT VNIVSRI SEY AKTEGKKREMYELPVFCLA
		ļ		1	1	SOVMDLTIONOKDAENVGRLITPAKKLEDII
		- 1				I AFI VIEVLOONEEHHAEAFAWWSDLMVER
1		1				AETEL SI FAVDMDAALEVOPPDTWDSFPLFC
	1			ì		1 I NOTE REGULICGNGK/FHKHLODLFAPLV
		1	1	Į		PAMWOLDGSSPIAOSIHRGLLSRESWEPVNI
İ						GSGTSEDI FWKLDALOTFIRDLHWPEEEFGA
					}	HI FOR LKI MASDMIESCVKRTR\LAFEVKLQI
1					1	TSSIOOIFRVPOFNMAPCFNVMGLMAKGSIQ
		1	ļ			KINCSMEMGOEFAKMWHOYHSKIDELIEETY
1				1		KEMITLLVAKEVTILEGVLAKLSRYDEGTLE
						SELSETVK A A SKYVD VPKPGMD V ADAY V TE
		1				VRHSODVLRDKVNEEMYIERLFDQWYNSSN
		- 1				NVICTWLTDRMDLOLHIYQLKTLIRMVKKI
						RDFRLOGVLDSTLNSKTYETIRNRLTVEEAT
		- 1		1		SVSEGGGLOGISMKDSDEEDEEDD
561	1911	-	4257	1300	654	SELVQFLLIKDQKKIPIKRADILKHVIGDYKD FPDLFKRAAERLQYVFGYKLVELEPKSNTYI

				To diseased	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A enartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	Islandencine, K=Lvsine, L=Leucine,
cotide	seq-		USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ		ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	<u> </u>	1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			İ	peptide	Sequence	/=possible nucleotide deletion, \-possible
		1	i	sequence		nucleotide insertion
			ļ	sequence		INTI EPVEEDAEMRGDOGTPTTGLLMIVLGLI
_ 	ļ		1		Ì	FMKGNTIKETEAWDFLLAL\GVYPTKKHLIFG
	1	1	1		<b>†</b>	DPKKLITEDFVRORYLEYRRIPHTDPVDYEFQ
		}	1	Į	ļ	WGPRTNLETSKMKVLKFVAKVHNQDPKDW
			1	1	ļ	PAOYCEALADEENRARPQPSGPAPSS
		ļ	10.60	ļ.——	1498	NOVIWI YREI PISNMAAKLRSLLPPDLRLQF
562	1912	A	4260	1	1490	WLHARLQKCFLSRGCGSYCAGAKASPLPGK
·	•		1			MAMGLMCGRRELLRLLOSGRRVHSVAGPSQ
	1	1	1	}	}	WI GKPLTTRILEPAAPCCCRPHYLFLAASGPR
		1				SLSTSAISFAEVQVQAPPVVAATPSPTAVPEV
	l l	1	1			ASGETADVVQTAAEQSFAELGLGSYTPVGLI
	1	Į.				ONI LEEMHVDLGLPWWGAIAACTVFARCLIF
						PLIVTGOREAARIHNHLPEIQKFSSRIREAKLA
	1	1				GDHIEYYKASSEMALYOKKHGIKLYKPLILPV
	1	1			ł	TOAPIFISFFIALREMANLPVPSLQTGGLWWF
	-	1	1	Į.		ODLTVSDPIYILPLAVTATMWAVLELGAETG
1	l.	1	ł	1	1	VOSSDLOWMRNVIRMMPLITLPITMHFPTAV
	1	1	1			FMYWLSSNLFSLVOVSCLRIPAVRTVLKIPQK
	Ì	1				VVHDI DKI PPREGFLESFKKGWKNAEMIKQ
	}	1				I REREORMRNOLELAARGPLRQTFTHNPLLQ
1	1					PCKDNPPNIPSS\SSSSSKPKSKYPWHDILG
1					116	MGGLAPTOTLEPT/REYONTQLSVSYLLPEQN
563	1913	Α	4265	623	116	THGTRRTLSSGPSNNLPLPLSSSATMPSMQCK
1	ĺ	1				HRSPNGGLFRQSPVK/TPPIPMSFQPVPGGV\L
i		1			İ	PROSONPPHOTSILTAPPALLPHPPTHPTQQSF
		- }	1		}	LIQENNNTNHTHSHTHTYTETLSFFLYICVNN
-			1			DRMEWGKSVF
					368	TI KRKI SSI NSEVSTIONTRMLAFKATAQLFIL
564	1914	A	4270	3	368	GCTWCLGLLOVGPAAOVMAYLFTIINSLQGF
	İ					FIFLVYCLLS\QQVQKQYQKWFREIVKSKSES
}	}	ì			(	ETYTLSSKMGPDSKPSEGDVFPRTSE
					100	RNSRPLWCSPPASQPRQAPVSQSCCCPLPSSSS
565	1915	A	4288	83	406	PPSALLAPTKPRALGTLRLYECSPELCTTMLP
	Į	- 1				PAWLLMLCQAPRPQDPDPRLTQPEKSLQEAP
1		l				GQTGASRTPRT
		<u> </u>				LNSSQKLACLIGVEGGHSLDSSLSVLRSFYVL
566	1916	A	4298	1041	229	GVRYLTLTFTCSTPWAESSTKFRHHMYTNVS
						GLTSEGEK VVEELNRIGMMIDLSYASDTLIRK
		1				VI EVSOAPVIESHSAARAVCDNLLNYPDDILQ
		1		1	1	TI KKNGGIVMVTLSMGVLOCNLLANVSI VA
		1				DHFDHIRAVIGSEFIGIGGNYDGTGRFPQGL\E
		-				DVSTYPVLIEELLSRSWSEEELQGVLRGNLLR
1		j				VFRQVEKVREESRAQSPVEAEFPYGQLSTSCH
1		1			1	FHLGASEWTPRLLIWR
1	1	1				GATPLGSVGGRTGKMDAATLTYDTLRFAEFE
567	1917	A	4299	1	1106	DFPETSEPVWILGRKYSIFTEKDEILSDVASRL
1 20,	1,7,1	1		1		WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ
		1				WELLYKWILL CEDMENTOPADOLOGAE
		1				MIFAQALVCRHLGRDWRWTQRKRQPDSYFS
			1			VLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQ
ļ		i				WYGPNTVAQVLKKLAVFDTWSSLAVHIAMD
	:	1		1		NTVVMEEIRRLCRTSVPCAGATAFPADSDRH
- {		1				CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD
			İ			INEAYVETLKHCFMMPQSLGVIGGKPNSAHY
	1					FIGYVGEELIYLDPHTTOPAVEPIDGCFIPDES
			1			FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF
						GAECCLGMTRKTFGFLRFFFSMLG
		$\rightarrow$	4300	2012	1843	SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS
568	1918	A	4300	2012	10.5	I MSVLIPKLPOLHGVRIFGINKY
			1200	104	531	WTFCLFL/WWVPESARWLLTQGHVKEAHRY
569	1919	T A	4302	186	1 221	

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-Aspartic Acid F=Glutamic Acid,
NO: of	NO: of	bod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in	location	corresponding	I=Icoleucine K=Lysine, L=Leucine,
cotide	seq-		USSN 09/496	correspondi	to last amino	M=Methionine N=Asparagine, P=Proline,
seq-	uenœ	<b>\</b>	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	l	-		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	}	peptide	554	/=possible nucleotide deletion, \=possible
	l	1	1	sequence		nucleotide insertion
		<del> </del>	<del> </del>	Soqueine		LLHCARLNGRPVCEDSFSQEVRVNVCVSMHI
	ł	}				CVWWGVGCVKCLPPRAHHIWQEKPLGPHRT
				ł		VTESKLEAEGKTKEKAREKERKKKS
	1920	A	4308	3	869	RSGQGKVYGLIGRRRFQQMDVLEGLNLLITIS
570	1920	Ι Λ	4500	1		GKRNKLRVYYLSWLRNKILHNDPEVEKKQG
	}	1	1			WTTVGDMEGCGHYRVVKYERIKFLVIALKSS
	1	1				VEVYAWAPKPYHKFMAFKSFADLPHRPLLV
	1	1				DLTVEEGQRLKVIYGSSAGFHAVDVDSGNSY
				1	1	DIYIPVHIQSQITPHAIIFLPNTDGMEMLLCYE
		1		1		DEGVYVNTYGRIIKDVVLQWGEMPTSVAYIC
	İ	1				SNQIMGWGEKAIEIRSVETGHLDGVFMHKRA
	-	ł				QRLKFLCERNDKVFFASVRSGGSSQVYFMTL
		1				NRNCIMNW
571	1921	A	4309	9	524	ASREMDVTKVCGEMRYQLNKTNMEKDEAE
5/1	1921	1 **	,,,,,,	1		KEHREFRAKTNRDLEIKDQEIEKLRIELDESK
	1			1	1	QHLEQEQQKAALAREECLRLTELLGESEHQL HLTRQEKDSIQQSFSKEAKAQALQAQQREQE
			1			LTQKIQQMEAQHDKTENEQYLLLTSQNTFLT
	İ	1	į.			LTOKIQQMEAQHDKTENEQTEDETSQTTTE
		1				KLKEECCTLAKKLEQISQ GATPLGSVGGRTGKMDAATLTYDTLRFAEFE
572	1922	A	4318	1	1119	DFPETSEPVWILGRKYSIFTEKDEILSDVASRL
312	1722	1		ļ		WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ
		ļ	1			MIFAQALVCRHLGRDWRWTQRKRQPDSYFS
			1	1		VLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQ
[		- (				WYGPNTVAQVLKKLAVFDTWSSLAVHLAMD
		-			}	NTVVMEEIRRLCRTSVPCAGATAFPADSDRH
	ł				\	CNGFPAGAEVTNRPSPWRPLVLLIPLRLGL\T
	1			1	}	DINEAYVETL\KHCFHGWPQFPG/VVHREGK
l		- (				DNIS A HVEIGVUGEEL TYLDPHT TOPAVEPT DO
1		ł	ĺ		1	CFIPDESFHCQHPPCRMSIAELDPSIAVVRGGH
ļ .		1	ļ			I STOAFGAECCLGMTRKTFGFLRFFFSMLG
1				262	1066	GGVPVGLASKPFOILYGHTNEVLSVGISTELD
573	1923	A	4333	363	1000	MAVSGSRDGTVIIHTIOKGOYMRTLRPPCESS
		1				I FI TIPNI AISWEGHIVVYSSTEEKI ILKERM
ļ						HVICESINGKYLGSOILKEOVSDICHGEHIVIG
l		- }		į		SIGGEL SIRDLHSLNLSINPLAMRLPIHCVCVI
		)	. ]	ļ	}	KEYSHILVGLEDGKLIVVGVGKPAEVKPSISN
1						FISHAVGDYFGSPSFQLIEKSPLGINKLKAKFD
1		1				ECKUCK
			4346	359	1234	MDTLEEVTWANGSTALPPPLAPNISVPHRCLL
574	1924	Α	4346	339	123.	LIVEDIGTERVRYWDLLLLIPNVLFLIFLLWK
1						I DO AD AKIRITSSPIFITFYILVFVVALVGIAKA
1		ł				LVVSMTVSTSNAATVADKILWEITRFFLLAIEL
1		- 1				SVIII GLAFGHLESKSSIKRVLAITTVLSLAYSV
1			1		İ	TOGTI FIL YPDAHLSAEDFNIYGHGGRQFWL
1		1				VSSCFFFLVYSLVVILPKTPLKERISLPSRRSFY
		ļ	l l	1		VYAGILALLNLLQGLGSVLLCFDIIEGLCCVD
1			1			ATTELYESFFAPLTYVAFLRGFFGSEPKILF
		<del></del>	4260	2038	1512	GCWWRHPWLASORDCLDCRIQLAEKFVKAV
575	1925	A	4360	2036	1 .5.2	SKPSRPDMNPIRVKEVYRLEEMEKIFVRLEM
	1	ĺ		ļ		VIIK GSSGTPKL SYTGRDDRHFVPMGLYIVRI
	1	1			Ì	VNIEPWTMGFSKSFKKKFFYNKKTKDSTFDLF
	1	1				ADSIAPFHICYYGRLFWEWGDGIRVHDSQKP
		1		1		ODODKI SKEDVI SFIOMHRA
			- 1025		500	OVEGROGREVKRTAWRISPVWRPARCRRRS
576	1926	A	4365	69	1 300	POP/PE/PGAOOOERHROGEAPMQALDPKAEP
		1			1	CPOAOSHAACOPEPEPPRVLLDPI AARGGVQ
		1				GRP/GLSRHPGLAPHPQTHTPWPQSGRLPCAS
		1	1			EPLPLGGIRPTPGLEPKGRDLM
			1	1	ı	S. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
ucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-	1	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	derice	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience	]	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ		peptide	·	/=possible nucleotide deletion, \=possible
		(		sequence		nucleotide insertion
	1000	<del>                                     </del>	4366	785	502	SAPPKKKNGVLFLSPRLKSSGAIWVHSTPTLW
577	1927	Α	4300	783	""	ASSNSRASTPKVAGITGARPHARIIFVFLIEMG
	}	1		}	•	FHNVGOAGL/DTLTLVICPPQPPKLLGLQM
		<b></b> _	12.5	<u> </u>	221	FFFFI KKSRCVTOAGVOG\PISLHPPPPGFKRF
578	1928	Α	4367	1	221	SRLSLLSSWDYRHP/HAANFCIFSRDG\VSPYW
						SGWSRTPDLR
		J			224	FETESHSVTQAGMQWHNLGSLQPMP/PGLKR
579	1929	A	4383	1	224	FSCLRLQSSWDHRHAPPHLAHFCIFSRDGVSP
	1	ł		1		CWPGWSSTPDLK
				1		SRLKPYSTNVTAKKLPATNIPNLDCFTAKLYQ
580	1930	Α	4397	410	94	\VFKKGNIHILHELFQNKEEGAFPNS/FYEASFT
						LRPKSDRDIAKEESYSTISLLSTDTKILMSKYK
						CL ACCDI
	1		1			QLKSSDL VLVHRQCGGILRLRRKEAVSVLDSADIEVTDS
581	1931	A	4414	670	3	VLVHRQCGGILKLKKKEAVSVLDSADIEVID
361	1,22,	1		1		RLPHATIVDHRPQHRWLETCNAPPQLIQGKA
	ļ				<b>\</b>	RSAPKPSQASGHFSVELVRGYAGFGLTLGGG
	ł					RDVAGDTPLAVRGLLKDGP\AQRCGRLEVGD
	1	l	1			LVLHINGESTQGLT\HAQAVERIRAGGPQLHL
	1	1	ļ			VIRRPLETHPGKPRGVGEPRKGVVPSWPDRSI
	1				1	DPGGPEVTGSRSSSTSLVQHPPSRTTLKKTRG
	1					SPE
500	1932	- A	4424	194	449	VLYIRKKKRLEKLRHQLMPMYNFDPTEEQDE
582	1932	I A	4424	124		LEQELLEHGRDAASVQAATSVQAMQGKTTL
	1	-				PS\QGPLQRPSRLVFT\DVANAIHV
			4435	1	166	APGPPVPPPGSPPEOMPGPCPASMPP/DPPPGS
583	1933	Α	4433	1	100	PPEQMPGPCPVSAPP/GPPPGSPPEQMPGPCPV
			1	1		SAPPALLODTSV
			-1-1450-	+1	628	SATPQQPSAPQHQGTLNQPPVPGMDESMSYC
584	1934	A	4439	1	020	APPOOLPSAOPPOPSNPPHGAHTLNSGPQPG1
		1	1		Ì	APATOHSOAGPATGOAYGPHTYTEPAKPKK
		i i		1	1	GOOLWNRMKPAPGT\EVSSSTSRSDPLLLPPR
						ALAPTORASTVVLAPSPT/SEKVONHSGSSAR
		ì	- }	]	1	GNLSGKPDDWP/LGHERVCGALLHRL*VGGC
			1	l .		QGPHGKAAQGGAAGAAAGRLGLYH
		- {				HKPVTNSRDTQEVPLEKAKQVLKIIATFKHT
585	1935	A	4463	10	144	SIFDDFAHYEKRQ
						LNAESYVSFTTKLDIPTAAKYEYGVPLQTSDS
586	1936	A	4464	1309	103	LNAEST VSF I I KLDIT TAAK I ET VNA VK CTRE
130					1	FLRFPSSLTSSLCTDNNPAAFLVNQAVKCTRE
}				1	1	INLEQCEEIEALSMAFYSSPEILRVPDSRKKVI
		l			1	TVQSIVIQSLNKTLTRREDTDVLQPTLVNAGI
		1			1	FSLCVNVVLEVKYSLTYTDAGEVTKADLSFV
	.	-		1		LGTVSSVVVPLQQKFEIHFLQENTQPVPLSGN
	1	- 1		1	}	PGYVVGLPLAAGFQPHKGSGUQTTNRYGQL
[	i	- 1	1	Ţ		ILHSTTEQDCLALEGVRTPVLFGYTMQSGCK
<u> </u>	1	-	.			LRITGALPCOLVAOKVKSLLWGQGFPDYVA
		1			1	PEGNSOGP/ADMLDWVPIHFITQSFNRKDSCO
1						I PGALVIEVK WTKYGSLLNPOAKIVNVTANI
i		1	[		1	SSSFPEANSGNERTILISTAVTFVDVSAPAEAG
1		- 1				FRAPPAINARLPFNFFFPFV
				<del></del>	207	LLGRASAC/LQLQSSW/D/HRPMLPYLANFVF
587	1937	A	4471	614	387	CKDR/SFTWLPRLVLNSWLQVILLPWPPTGC
1	1				J	NKHEPPCPATKRRHSGSI
1	1		!	_l	_	HDLGSLQPPPPGFKRFSCLSLPSSWDYRLMP
588	1938	-	4480	1720	1458	HDLGSLQPPPPUTACTSCLSLFSS WD FALME
1 200	1,750	1.				CPANFCIII/DFLVETGFHHVGQASHELLTSG
1			Ì			PPTSASQSAGITGMSYHTWFGES
500	1020	<del> -</del> -	4487	922	332	APVTTSPRVGQPW/RTALALRSLYRARPSLR
589	1939	Α	1440/	1	1 332	PPVELPWAPRRGHRLSPADDELYQRTRISLL
		1	1	i i	1	REAAQAMYIDSYNSRGFMINGNRVLGPCAL
	1	- 1	ļ	1	1	KEAAQAM I IDS I NSKOP MINORK I EOI OF ID
						PHSVVQWNVGSHQDITEDSFSLFWLLEPRIE

Sept						Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
No. of No. 18 in musicoide code of Seq. unner corresponding sequence where the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding of the corresponding	SEQ ID	SEQ ID	Met	SEQ	Predicted	1	D=A spartic Acid E=Glutamic Acid,
Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision   Decision	NO: of	NO: of	hod				F=Phenylalanine, G=Glycine, H=Histidine,
conce contents of the corresponding to the contents of the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding	nucl-	peptide	į				I=Isolencine K=I vsine, L=Leucine,
1940   1940   A   1941   A   1941   A   1942   A   1945   A   1944   A   1945   A   1945   A   1945   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   1946   A   19	eotide	seq-					M=Methionine N=Asparagine, P=Proline,
1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940   1940	seq-	uence			correspondi		O-Clutamine R=Arginine S=Serine.
	_		Į	914	ng to first	1	T-Theoning V-Voline W=Tryptophan.
		1	1	<b>!</b>		of peptide	V-Tomosine V-Unknown *=Ston codon.
			{	[		sequence	Y=1 yrosine, A=Oikhown, -blop coden,
			ļ	1	peptide		/=possible nucleotide deteriori, /-possible
DTPNACATFNFLCHEGRYTGAALIPPFOGTS   SIGOQAAQ			ļ	}			nucleotide insertion
TSL.QQAAQ		<del></del>	<del> </del>	<del> </del>			VVVGTGDRTERLQSQVLQAIVIRQRGIAVEVQ
1940   A   4492   1   472		i	1	i		1	
PFS.CL.SLPSSWDYRRPPLRPANFFVPLLUS			1		1	1	TSLGQAAQ
PFSCLSLYSWDYNKPLRATHTYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATETYLAGATE		1040	<del>                                     </del>	4492	1	472	FFFFETESRSVAQAGVQWRDLGSLQAPPPGFT
ARPKRIGEPRRKCGNAVVWPSTLGDHRV1	390	1940	^	4472	1 1		PFSCLSLPSSWDYRRPPLRPANFFVFLVETGFP
1941   A   4495   1444   1116	1	]	)	)			RFSRDGLDLLT/S/GDPPTSASQSAGITGVSHR
1941   A   4495   1444   1116		i	1	1	1		ARPKRIGEPRRKCGNAVVWPSTSLGDHRVTS
1941	1		1	1	1		VPHOGGLPGPIRVAPSSAGQREASQGPPGR
1941   A		L		<del> </del>	1144	1116	TAARFTLAKTWNOLKRP\TMIDSIKKTR\YIYT
LKDNWYEDTIP/QGAVPCTATZEGMKRLLF/SPWDSSCFPIPSSGV	591	1941	Α	4495	1444	1110	MEVY A DTERNEIMSF\AGTWVELEAIILSKLM
S92	į	1	1			1	LEDNWVEDTIPOGAVPCTATAEGMKRLLFAL
1942   A	i .	1		i	1	1	EDWDSSCEPHPSSGV
1942   A	1	1	ł				PTDDL ESCRETPRYCTMSDERRLPGSAVGWL
VCGGISLAMA WILSY OXDURE	592	1942	Α	4496	2	919	WOOGLST ANAWGII SVOAKOKKWKPLEEL
EWNEGLCK VPVSIFYTILLTGESVTISLY   MWMCWPVNYRISNAKQAGHTVMGIW   GSFILSALPAVGWHDTSERFYTHGGREFIVAR   GLGFGVCFLLUGGSVAMGVICTAIALFOT   AVQVGRQADHRAFTVPTITVEDAQGKRRS   DGSEPAKTSLQTTGLVTITVIPDCLMGFFV   GFFSLADTHLSDLPYTWGDRDSGGACVM   FFFEAESCSVPQAGVQRPDLGWLHAPPPOG   HFPASASQVAGTTHARHHTQLIPAFLVENK   C			{		1		TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION OF THE TOTAL ATTIMITATION
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GSFILSALPAVGWHDTSERFYTHGCRFIVAL GLGFGVCFLLLVGGSVAMGVICTAIALPGT AVQVGRQADHRAFTVPTIVVEDAQGKRRS DGSEPAKTSLQTTGLVTTIVFIYDCLMGFPV GPFSLADTHLSDLPYTWGDRDSGGACVM FFFEAESCSVPQAGVQRPDLGWLHAPPPQG HFFASASQVAGTTHARHHTQLIFAFLVENC C  594 1944 A 4507 1327 647 EKMAGGVRPLRGLRALCRVLLFLSQFCILSG ESTEIPPYVMKCPSNGLCSRLPADCIDCTIN CTYGKPVTFDCAVKPSVTCVDQDFKSQKN NMTCRFCWQLPFIDYBCTNSTSCMTVSCPI RYPANCTVRDHVHCLGNRTFPKMLYCNW GGYKWVYGLWLLRHHPRWGLGADRRYL VAGTASGKLFSFGGLGSRLPADCIDCTIN TYGQDGLDLLNLMHPPRSFKVLGLQA  595 1945 A 4512 533 264 FFFKMESYSVARLECSGAISAPCNLHLLGSI SPASASRV/AGNIGARHHTQQIFVLLVQMR YVGQDGLDLL/NLMIHPPRSFKVLGLQA HASDHLYPNFLVNELILKQKQRFEEKFRIL HSVSSTNGHRWQIFGDDWLGLADA NLMELLVQKKCQLEAESHAAQLQILMEF VARRNKREQLEQIQKELSVLEEDIKRVEEM GLYSPYSEDSTVPQFEAPSPSRSIIDSTEYS GEFGRSGSTKKQPWYNSTLASRRKRLTAH DLEQCYFSTRMSRIDDSRTASQLDEFOEC KFITRYNSVRPLATLSYASDLYNGSQYKSI FEFDRDCDYFALAGVTKKKVYEYDTVIQE VDIHYPENEMTCNSKISCISWSSYHKJLAA DYEGTVILWDGFTGQRSKVYQEHERCW DFNLMDPKLLASGSDDAKVKLWSTNLDN ASIEAKANVCCVKFSPSSRYHLAFGCADH HYYDLRNTKQPIMVFKGHRKAVSYAKFV EEIVSASTDSQLKLWNVGKPYCLRSFKGG EKNFVGLASRGQYIACGSENNSLYLYYKG KTLLTFKFDTVKSVLLDKORKEDDTNEFVS CWRALPDGESNVLAANSQGTIKKVLELV STORM STORM A 4518 536 824 RSLALSFGLECSGMISAHCNLHLLGSSDPP ASQVAEITSVRHHTWLICTLLCQMGFHHV OAGLEILTSWRHTWLICTLLCQMGFHHV	1	i	1	1	1		EWNEGLCKYFYSTF TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF THE TELEMICIETY OF TH
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HYYDLRNTKQPIMVFKGHRKAVSYAKFV: EEIVSASTDSQLKLWNVGKP\YCLRSFKGH EKNFV\GLASNGDYIACGSENNSLYLYYKO KTLLTFKFDTVKSVLDKDRKEDDTNEFVS CWRALPDGESNVLIAANS\QGTI\KVLELV CWRALPDGESNVLIAANS\QGTI\KVLELV ASQVAEITSVRHHTWLIFCILGQMGFHHV OAGLELLTSWDPAILPSQSAGIIGMSPHAW	1	İ		[	1		A SIE AK ANVCCVKESPSSRYHLAFGCADHCV
EEIVSASTDSQLKLWNVGKP\YCLRSFKGH EKNFV\GLASNGDYIACGSENNSLYLYYKO KTLLTFKFDTVKSVLDKDRKEDDTNEFVS CWRALPDGESNVLIAANS\QGTIKVLELV CWRALPDGESNVLIAANS\QGTIKVLELV ASQVAEITSVRHHTWLIFCILGQMGFHHV OAGLELLTSWDPAILPSQSAGIIGMSPHAW		1					TOVOL BUTY OPIMVEK GHRKAVSYAKEVSG
EKNFV:GLASNGDYIACGSENNSLYLYYKO KTLLTFKFDTVKSVLDKDRKEDDTNEFVS CWRALPDGESNVLIAANS\QGTIKVLELV CWRALPDGESNVLIAANS\QGTIKVLELV RSLALSPGLECSGMISAHCNLHLLGSSDPP ASQVAEITSVRHHTWLIFCILGQMGFHHV OAGLELLTSWDPAILPSQSAGIIGMSPHAW					-		TELUCACTOCOL KI WANGKPAVCI RSEKGHIN
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CWRALPDGESNVLIAANS\QGTIKVLELV  S97 1947 A 4518 536 824 RSLALSPGLECSGMISAHCNLHLLGSSDPP ASQVAEITSVRHHTWLIFCILGQMGFHHV OAGLELLTSWDPAILPSQSAGIIGMSPHAW		1					EKNFY/GLASNGD LIACOSENIASE LET TROPS
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ASQVAEITSVRHHTWLIFCILGQMGFHHV  OAGLELLTSWDPAILPSQSAGIIGMSPHAW		1042	<del></del>	1519	536	824	RSLALSPGLECSGMISAHCNLHLLGSSDPPTS
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FDTEFVNIGGDFDAAAGVFR\CRLPGAYF						384	FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF
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				<del></del>	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ì	Ì		peptide		/=possible nucleotide deletion, \-possible
	1	}		sequence		nucleotide insertion
	<del> </del>	<b>├</b> ──		Sequente	·	RREMQSQSVMLALRRGDAVWLLSHDHDG
		1				YGAYSNHGKYITFSGFLVYPDLAPAAPPGLG
	1		1			ASELL
500	1949	A	4526	366	776	MGQPAPYAEGPIQGGDAGELCKCDFLVFTSP
599	1343	^	1520			NPEAVCEAGTPAMFQTAWRQMESCSI/AQAG
						VQWRDPGSLHPPPLGFKRFSCLSLPSSWDYK
	1				}	HAPPHPANFCIFSRDQVSPCWPGWSRSLDLVI
	1	1			_	PPPWLPKVLGLQA
700	1950	A	4529	776	334	FFFETESCYVAQAGVQWCDLCSLQAPPPG\SS
600	1930	Α	132	1		DPPASASRVAGTTGARHHTQLIFVFLVETGFH
	1	i				MLARDGLKLLTSSDPPASASQSSWDYRREPP
	}				l	RLANFFVFLVETGSRYVAQAGVQWLFTGAIP
	}	1				LLISTGVLTCSVSDLGRFTPP
601	1951	A	4533	1460	403	HEVQESIHFLESEFSRGISDNYTLALITYALSS
901	1951	1 ''	.555			VGSPKAKEALNMLTWRAEQEGGMQFWVSSI
	· ·	1				SKLSDSWQPRSLDIEVAAYALLSHFLQFQTSE
	ł	1		1		GIPIMRWLSRQRNSLGGFASTQDTTVALKAL
	<b>\</b>	1			ļ	EFAALMNTERTNIQVTVTGPSSPSPVKFLIDT
		1				HNRLLLQTAELADGTANGSV/SISANGFGFAI
		.,			1	CQLNVVYNVKASGSSRRRRSIQNQEAFDLDV
	1	1		1		AVKENKDDLNHVDLNVCTSFSGPGRSGMAL
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	Ì	-		İ		LNLYLDSVNETQFCVNIPAVRNFKVSNTQDA SVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSI
	İ	- 1				SASIADA JELKKAVA AKS INSPAKTEROESTER
	-					VQRLPSL MRAPGRPALRPLPLPPLLLLLLSSPWGRAVPC
602	1952	A	4540	1963	295	VSGGLPKPANITFLSINMKNVLQWTPPEGLQ
002	1700				l l	VKVTYTVQYFIYGQKKWLNKSECRNINRTY
	1	1				DLSAETSDYEHQYYAKVKAIWGTKCSKWAI
	1	1				SGRFYPFLETQIGPPEVALTTDEKSISVVLTAI
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1	1	ļ			1	NIS/DDSKISHQDMSLLGKSSDVSSLNDPQPS
		- 1			1	NLRPPQEEEEVKHLGYASHLMEIFCDSEENT
		· [				FGTSFTOOESLSRTIPPDKTVIEYEYDVKI'ID
ļ		- }	ł	1	Ì	CACPEROFI SI OFFVSTOGTLLESUAALAVI
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	1	1			Į	EDOTTE VIDWIDPOTGRI CIPSLSSFDQDSEGCI
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1				1	1	IMOFMEEWGLYVOMEN
1		_l				YSAVEFVEQASGISDWWNPALRKRMLSDSC
603	1953	A	4543	3	600	CMIAPYYEDSDLKDLSHSRVLOSPVSSEDHA
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ļ		- 1	ĺ	]		I LIV A AFTONGEIVKYILDHGPSELLDMADS
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1			}	}		VKVIGHEDLETAV
1	(					QDNKVQNGSLHQKDTVHDNDFEPYLTGQA
604	1954	A	4548	3	938	QSNSYPSMSDPYLSSYYPPSIGFPYSLNEAPY
		Ì				STAGDPPIPYLTTYGQLSNGDHHFMHDAVF
1						QPGGLGNNIYQHRFNFFPENPAFSAWGTSG
1		1			1	QGQQTQSSAYGSSYTYPPSSLGGTVVDGQP
		- 1		- {		FHSDTLSKAPGMNSLEQGMVGLKIGDVSSS
1					]	VKTVGSVVSSVALTGVLSGNGGTNVNMPV
1		1	(			KPTSWAALASKPAKPQPKMKTKSGPVMGG
		- 1	1	1	1	I E PLAW ARIABNEANE OF AMILE TOOL THEOO.
		Į.	1	1		LPPPPIKHNMDIGTWDNKGPVPKAPVPQQA

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
iucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence	{	1	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		amino acid residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	Sequence	/=possible nucleotide deletion, \-possible
		ì		sequence	1	nucleotide insertion
	<b> </b>		<del></del>	sequence		SPQAAPQPQQVAQPLPAQPPALAQPQYQSPQ
				j		OPPO
	1955	A	4553	2	2304	ILLQEKRNCLLMQLEEATRLTSYLQSQLKSLC
505	1933	Δ.	4333	-		ASTLTVSSGSSRGSLASSRGSLASSRGSLSSVS
		1	1			FTDIYGLPQYEKPDAEGSQLLRFDLIPFDSLGR
		1			1	DAPFSEPPGPSGFHKQRRSLDTPQSLASLSSRS
	1					SLSSLSPPSSPLDTPFLPASRDSPLAQLADSCE
	1	1			}	GPGLGALDRLRAHASAMGDEDLPGMAALQP
	1	1				HGVPGDGEGPHERGPPPASAPVGGTVTLRED
		1				SAKRLERRARRISACLSDYSLASDSGVFEPLT KRNEDAEEPAYGDTASNGDPQIHVGLLRDSG
	1	1	ŀ			SECLLVHVLQLKNPAGLAVKEDCKVHIRVYL
	1	1				PPLDSGTPNTYCSKALEFQVPLVFNEVFRIPV
		1	1		l	HSSALTLKSLQLYVCSVTPQLQEELLGIAQIN
			İ		[	LADYDSLSEMQLRWHSVQVFTS\LNHQGRGR
	ļ			ļ		I GVOER APPOTLHTPSPSPA/STDAVTVLLAR
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	Ì	ļ			PEPCCMGIDSILGHPFAAQAGPYSPEKFQPSPL	
			İ			KVDKETNTEDLFLEEAASLVKERPSRRAKGSI
		1			}	FVRSGTIVRSQTFSPGARSQYVCRLYRSDSDS
		1	1			STLPRKSPFVRNTLERRTLRYKQSCRSSLAEL
					MARTSLDLELDLQASRTRQRQLNEELCALRE	
					LRORLEDAQLRGQTDLPPWVLRDERLRGLLR	
	-				EAERQTRQTKLDYRHEQAAEKMLKKASKEI YQLRGQSHKEPIQVQTFREKIAFFTRPRINIPPI	
	}	ł				PADDV PGSGPGPAPFLAPVAAPVGGISFHLQIGLSREP
606	1956	A	4555	3429	776	VLLLQDSSGDYSLAHVREMACSIVDQKFPEC
					}	GFYGMYDKILLFRHDPTSENILQLVKAASDIQ
				1		FGDI JEVVI SASATFEDFOIRPHALFVHSYKA
				1		PAECDHCGEMI.WGLV\RQGLKCEGCGLNYH
		1				KRCAFKIPNNCSGVRRRRLSNVSLTGVSTIKT
					]	SSAFLSTSAPDEPLLOKSPSESFIGREKRSNSQ
		1				SVIGRPIHLDKILMSKVKVPHTFVIHSYTRPTV
		-				OVCKKI I KGI FROGLOCKDCRFNCHKRCA
	j	}				PKVPNNCLGEVTINGDLLSPGAESDVVMEEG
i				1		SDDNDSERNSGLMDDMEEAMVQDAEMAMA
		l	-			ECQNDSGEMQDPDPDHEDANRTISPSTSNNIF
		1	1	i		LMRVVQSVKHTKRKSSTVMKEGWMVHYTS
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Į						IPLSEILSLEPVKTSALIPNGANPHCFEITTANV VYYVGENVVNPSSPSPNNSVLTSGVGADVAI
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l		ĺ			ļ	SISVSNCQIQENVDISTVYQIFPDEVLGSGQFC
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1		1	1			EKLHGDMLEMILSSEKGRLPEHITKFLITQILV
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1		-		1		KLCDFGFARIIGEKSFRRSVVGTPAYLAPEVL
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1		1				LLQVKMRKRYSVDKTLSHPWLQDYQTWLD
						RELECKIGERYITHESDDLRWEKYAGEQGLQ
		1			- (	VPTHI INPSASHSDTPETEETEMKALGERVSI
	1				1400	SRPWWLRASERPSAPSAMAKRSRGPGRRCL
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607						TVRCMHLLLEAVPAVAPQTSILDLRFNRIRE. QPGAFRRLRNLNTLLLNNNQIKRIPSGAFEDI ENLKYLYLYKNEIQSIDRQAFKGLASLEQLY

			CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	_	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	]	USSN	location		M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	ĺ	1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1			amino acid	of peptide	1=Inreonine, v=valine, w=1typiopian,
	1	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	l		1	peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<del>}</del>	<del> </del>	<del> </del>	3042333		HFNQIETLDPDSFQHLPKLERLFLHNNRITHL
	1					VPGTFNHLESMKRLRLDSNTLHCDCEILWLA
		ļ	1			DLLKTYAESGNAQAAAICEYPRRIQGRSVATI
		ļ				TPEELNCERPRITSEPQDADVTSGNTVYFTCR
			ì			AEGNPKPEIIWLRNNNELSMKTDSRLNLLDD
	1		1			GTLMIQNTQETDQGIYQCMAKNVAGEVKTQ
	ľ	1		1	}	EVTLRYFGSPARPTFVIQPQNTEVLVGESVTL
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l	l					ECSATGHPPPRISWTRGDRTPLPVDPRVNITPS
į	1	į	1			GGLYIQNVVQGDSGEYACSATNNIDSVHATA
1		1				FIIVQALPQFTVTPQDRVVIEGQTVDFQCEAK
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	1		1		1	SGVALHDOGOYECQAVNIIGSQKVVAHLTVQ
	1					PRVTPVFASIPSDTTVEVGANVQLPCSSQGEP
					[	EPAITWNKDGVQVTESGKFHISPEGFLTINDV
		1				GPADAGRYECVARNTIGSASVSMVLSVNVPD
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į.	1.		<b>\</b>			RTHDGTCNNLQHPMWGASLTAFERLLKSVY
		1	}			ENGFNTPRGINPHRLYNGHALPMPRLVSTTLI
}	1	İ			1	GTETVTPDEQFTHMLMQWGQFLDHDLDSTV
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1	- 1		1		1	I RVWODCCEDCRTRGOFNAFSYHFRGRRSLE
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1		1	1		1	TQIKKLESR\LSTTECVDAGGESHANNTKWK
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1 000	1,730	1 **		1	1	IIVAVQCGCDGTFLLTQSGKVLACGLNEFNKL
	1				1	GLNQCMSGIINHEAYHEVPYTTSFTLAKQLSF
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1						LGVGNYKKRLGINLLGGPLGGKQVIRVSCGD
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						HRFSRDGLDLLT/S/GDPPASASQSAGITGVSH
		1	Ì	Į.	į	RARPRINLRNVIYSFAVTYCLNYISLAMSSTL
			1			KLSFHVLSGS
			<del>   </del>	- 607	467	ECRGVISAH\CCTLCLPSSSDSASAF\RVARTT
610	1960	Α	4570	697	407	GTCDYAQLIFAFLVEMGFHHVGQDGLHLLN
}	1	İ	1			LVIRPPRPPKVLGLQA
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			1.000	No. of the d	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		Ì	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1			sequence	/=possible nucleotide deletion, \=possible
		ļ	į.	peptide		nucleotide insertion
		<u> </u>		sequence	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRT
611	1961	A	4571	25	1390	WNPNVPESPRIPAPRLPKRMSGAPTAGAALM
			1			LCAATAVLLSAQGGPVQSKSPRFASWDEMN
·	1	1	1	-		VLAHGLLQLGQG\CANT\GAHPQSAERAGA\R
	ļ		1			LSACGSACQGTEGSTDLPLAPESRVDPEVLHS
		Ì	1	ì	Į.	LQTQLKAQNSRIQQLFHKVAQQQRHLEKQHL
		]	ļ	1		RIQHLQSQFGLLDHKHLDHEVAKPARRKRLP
ĺ	1	1				EMAQPVDPAHNVSRLHRLPRDCQELFQVGER
	1	1	1		1	QSGLFEIQPQGSPPFLVNCKMTSDGGWTVIQR
ļ			1	1		RHDGSVDFNRPWEAYKAGFGDPHGEFWLGL
	ļ	1	}			EKVHSITGDRNSRLAVQLRDWDGNAELLQFS
}		j	1	1	l	VHLGGEDTAYSLQLTAPVAGQLGATTVPPSG
		1	1		1	LSVPFSTWDQDHDLRRDKNCAKSLSGGWWF
		1	l l		1	GTCSHSNLNGQYFRSIPQQRQKLKKGIFWKT
	1		į.			WRGRYYPLQATTMLIQPMAAEAAS
					<u> </u>	FFFETESRSVAQAGVQWRDLSSLQPPPPG\SR
612	1962	A	4575	162	3	GSPASASPVAGITGTRHHRTRG
					<del> </del>	PLAQRRPFLWYTVKTNGHIWGSSTYPHFWGS
613	1963	·A	4584	687	321	SNS/PASASQVAGIPNARHQARIIFVFLVEPRF
Ì	1	1			<b>j</b>	HHVGRAGLGFL/NLAICLPQHPKVLGLQACN
İ	İ	1	1		.]	LNIKPHPAHKYISMIQFNVHFMCMSVHIYI
					100	PGSAQSAQRGRGRRARAGSATQITMYSFMG
614	1964	A	4589	727	299	GGLFCAWVGTILLVVAMATDHWMQYRLSGS
		1	ł			FAHQGLWRYCLGNKCYLQTDSIAYWNATRA
1	1	1	1		1	FMILSALCAISGIIMGIMAF/GWVAVLMTFFA
					ł	GIFYMCAYRVHECRRLSTPR
					414	TILPEKIQAWAQKQCPQSGEEAVALVVHLEK
615	1965	Α	4590	2	414	ETGRLRQQVSSPVHREKHSPLGAAWEVADFQ
		-			1	PEQVETQPRAVSREEPGSLHSGHQEQLNRKR
			1			ERRPLPKNARPSPWVPALADEWNTLHQEVTT
		1				TRLPAGSQEPVKD
			1.500	772	488	DFALVAQAGVQWHNLGSPQPLPPGFKRFSCL
616	1966	A	4592	773	400	SLPSSWEYRCVPP/RLANFVFLVEMGFLHVGQ
						AGLELPTSGDPPALASQSAGITGVTTVPSGPG
			1202		478	XRHGLREPLLERRCAAASSFQHSSSLGRELPY
617	1967	В	4595	84	470	DPVDTEGFGEGGDMQERFLFPEYILDPEPQPT
1		1	ļ	1		REKQLQELQQQEEEERQRQQRREERRQQNL
	1		ĺ			RARSREHPVVGHPDPALPPSGVNCSGCGAEL
			ļ	1		HCQDAR*
			1.506	12045	1188	ARSRNSARGVYGMCVDTLFLCFLEDLERNDG
618	1968	A	4596	2945	1100	SAERPYFMCSTLKKPLARRCFPAIHAYKGVL
		1				MVGNETTYEDGHGSRKNITDLVEGAKKANG
1		1	J	J		VLEARQLAMRIFEDYTVSWYWIIIGLVIAMA
				1		MSLLSIILLHLLAGIMGWVMIIMENSELGYRIF
	ļ	Ì				HCYMEYSRLRGEAGSDVSLVDLGFQTDFRV
		-	1			YLHLRQTWLAFMILSILEVIIILLLIFLRKRILI
			1			AIALIKEASRAVGYVMCSLLYPLVTFFLLCLCI
	]			1		AYWASTAVFLSTSNEAVYKIFDDSPCPFTAKT
	1					CNPETFPSSNESRQCPNARCQFAFYGGESGYH
1				1	İ	RALLGLQIFNAFMFFWLANFVLALGQVTLAG
		-		1	1	AFASYYWALRKPDDLPAFPLFSAFGRALRYH
1	1	1	1			TGSLAFGALILAIVQIIRVILEYLDQRLKAAEN
		-				KFAKCLMTCLKCCFWCLEKFIKFLNRNAYIM
					1	IAIYGTNFCTSARNAFFLLMRNIIRVAVLDKV
1	1					TDFLFLLGKLLIVGSVGILAFFFFTHRIRIVQDT
		1				APPLNYYWVPILTVIVGSYLIAHGFFSVYGMC
		1	J	1	I	ALLINA A MALITI ALA OPITIVIDALIPA I OMIC
1		ĺ				ADLI EI CEI EDI EDVIDGEYEDDAENGGLI KKI
						VDTLFLCFLEDLERNDGSAERPYFMSSTLKKL
			4601	2	357	VDTLFLCFLEDLERNDGSAERPYFMSSTLKKL LNKTNKKAAES RTSVEPYILGEF/RKLSNNTKVVKTEYKATEY

555 FD	CCO ID	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	поа	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1		ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	<b>\</b>	1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	}	1			Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	1		residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ	1	1	peptide		nucleotide insertion
	{	1	1	sequence	ļ	GLAYGHFSYEFSNHRDVVVDLQGWVTGNGK
					•	GLAYGHFSYEFSNIKDVVVDLQGWVTGKGK
	}	1	Ì	1		GLIYLTDPQIHSVDQKVFTTNFGKRGIFYFFN
	1		i			NOHVECNEICHRLSLTRPSMEKPCKS
620	1970	A	4606	1	2415	MERLWGLFQRAQQLSPRSSQTVYQRVEGPR
020	1970	1	1 1000	1	1	KGHLEEEEEDGEEGAETLAHFCPMELRGPEP
		1	1	1	ļ.	LGSRPRQPNLIPWAAAGRRAAPYLVLTALLIF
	1		i	1	[	TGAFLLGYVAFRGSCQACGDSVLVVSEDVN
	1	1	1	1		YEPDLDFHQGRLYWSDLQAMFLQFLGEGRL
	)	1	1		1	EDTIRQTSLRERVAGSAGMAALTQDIRAALS
	1	1		i	1	ROKLDHVWTDTHYVGLQFPDPAHPNTLHWV
	}	1	1			RONLDHY WIDITITY OLGIT DITHETTERS
	1	1			Į.	DEAGKVGEQLPLEDPDVYCPYSAIGNVTGEL VYAHYGRPEDLQDLRARGVDPVGRLLLVRV
	1	1			1	VYAHYUKPEDLUULKAKUVDPVUKLLLVKV
	}	ł		1		GVISFAQKVTNAQDFGAQGVLIYPEPADFSQ
	1			l		DPPKPSLSSQQAVYGHVHLGTGDPYTPGFPSF
		1	1	1	1	NQTQFPPVASSGLPSIPAQPISADIASRLLRKL
		1	1			KGPVAPQEWQGSLLGSPYHLGPGPRLRLVVN
					,	NHRTSTPINNIFGCIEGRSEPDHYVVIGAQRDA
			1		1	WGPGAAKSAVGTAILLELVRTFSSMVSNGFR
		1		1		PRRSLLFISWDGGDFGSVGSTEWLEGYLSVL
	}	1	1		Ì	HLKAVVYVSLDNAVLGDDKFHAKTSPLLTSL
	- N		ł			IESVLKQVDSPNHSGQTLYEQVVFTN\PSWD\
			Ì			AEVIRPLPM\DSSAY\SFTAFVGVPAVEFSFME\
	į		1			DDQ\AYPFLHTKEDTYENLHKVLQGRLPAVA
ļ	1	1	}	1	1	QAVAQLAGQLLIRLSHDRLLPLDFGRYGDVV
	1		i	ţ		LRHIGNLNEFSGDLKARGLTLQWVYSARGDY
ì	1	i	i		1	IRAAEKLRQEIYSSEERDERLTRMYNVRIMRV
1		1	1	1		IRAAEKLKUEI I SSEEKDERLI KAITIT TAMIT
	-	ļ		1	}	EFYFLSQYVSPADSPFRHIFMGRGDHTLGALL
		l	ļ	1	1	DHLRLLRSNSSGTPGATSSTGFQ\ESRFRRQL\
	1	ĺ				ALL\TWDACKGAANALSGDVWNIDNNF
621	1971	A	4610	793	334	ISRVDDFVGSGIANVIIAVAIFSIPAFARLVRG\
021	19/1	1	1 4010	1		NTLVLKQQTFIESARSIGASDMTVLLRHILPGT
	1					GSSIVVFFTMRIGTSIISAASLSFLGLGAQPPTP
	ļ	1	1	İ		EWGAMLNEARADMVIAPHVAVFPALAIFLTV
	ļ	1		ļ	}	LAFNLLGDGLRDALDPKIKG
						LVYVMIAIFCIASAMSLYNCLAALIHKIPYGQ
622	1972	A	4614	2	820	CTIACRGKNMEVRLIFLSGLCIAVAVVWAVF
						RNEDRWAWILQDILGIAFCLNLIKTLKLPNFK
1		1		1	{	COURT OF LIT VIOLENCE TELEVIORE IN A COURT OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL O
į .						SCVILLGLLLYDVFFVFITFFITKNGESIMVEL
1						AAGPFGNNEKNDGNLVEATGQPSAPHEKLPV
			1			VIRVPKLIYFSVMSVCLMPVSILGFGDIIVPGL
		1				LIAYCRRFDVQTGSSYIYYVSVTVAYAIGMIL
}				l		TFVVLG\LMKKGQPALLYLVPCTLITA/CQFV
[						AWETVREMKKFWERVTS
				+17	691	TLVSVVEFVRRADLTREDLAPSSVDSGQAGF
623	1973	A	4619	17	1051	GGCCESGLPNTMPSAFSVSSFPVSIPAVLTQT
		- 1		1		DWTEPWLMGLATFHALCVLLTCLSSRSYRLQ
		}	1	1		IGHFLCLVILVYCAEYINEAAAMNWRLFSKY
	]	}	1	1	1	OYFDSRGMFISIVFSAPLLVNAMIIVVMWVW
					-	CALDSKOWLISIALSWAPPTANWAMIA AMAMA
						KTLNVMTDLKNAQERRKEKKRRKED*GAA
1		ĺ	1			AAWSLRPSRPPSAAPSAAVCVAWASFQLTHG
						LKNRCFI
1		+	4622	164	668	VSCYTALQSIMNQPESANDPEPLCAVCGQAH
624	1974	A	4022	104	000	SLEENHFYSYPEEVDDDLICHICLQALLDPLD
		1		}	1	TPCGHTYCTLCLTNFLVEKDFCPMDRKPLVL
						QHCKKSSILVNKLLNKLLVTCPFREHCTQVL
i						QRCDLEHHFQTSQAWGTHL*SQLLGRLRQED
	1			1	1	CLSPGVHHCSEV
1	ľ			1	1	L CT COGVERE SEV
		i				CLOI O VIII COLV
625	1975	A	4625	474	473	CFLSPSPLLPPLLLSSSSSPSFPLPPPPTLLPSTLP PPLLIPSS*LSP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nuclcotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide			09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience	ļ	1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Į.	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	l	1			Sequence	/=possible nucleotide deletion, \=possible
	1	Ì	1	peptide	l	nucleotide insertion
		i		sequence		KLKGNECFCYHCNVCIFLMIKK*GLFLC*IYFI
626 1976	A	4629	249	3	LFFET*SHSFTRLECSGTISAHCSLQLQGSSNSP	
	1	1	1			LFFE1*SHSF1RLECSG115AHCSEQEQGG116A
	[	[				ASASQVAGIAGTHH
627	1977	A	4635	1	301	FFFFTKPFFAPQAGGQGPSRGSLNPLPTGLK
021	1977	Α	1033	1		QFSGLTLSRSGNNGPRPPPRVNFGILRGNGVP
			1			PGGAG*PRPPDLRGPPGLAPPQGGNNGGDPP
					1	ARAYI.
			1.10	12.67	782	KI ESSORI EGPHIOAINPSFLLLSFFPS*LLAMR
628	1978	A	4648	1357	/62	TUGNINAFIL VELVYRIVLLLF*HV*PAYFQPSK
	1	1	l .		1	NKTAKINCN*RPFLFLVCYLL*AELHIGIFIANF
	ļ	1	i			YDCIPNKLNEHLWPKLLQSLIFHVDFCGFLHK
			1			VFYICFTEFLLFLYFL*LFIIKVSCSII*CSTICVF
	1	1	1		1	VFYICE TEPLETETE TEPEEEEE
		}	}			SYKSFAVIIFFVDNTRFFSFGF
629	1979	A	4660	18	999	HHELHTLELLQNPKEVLTRSEIQDVNYSLEAV
629	1979	\ ^	1000	1.0		KVKTVCQIPLMKEMLKRFQVAVNLAEDTAH
		1			1	PKLVFSQEGRYVKNTASASSWPVFSSAWNYF
				İ		AGWRNPOKTAFVERFOHLSCVLGKNVF1SG
		1	1			KHYWEVESRDSLEVAVGVCREDVMGITDRS
	Ì	1	ł	(		KMSPDVGIWAIYWSAAGYWPLIGFPGTPTQQ
			1	1		FPAT HRVGVYLDRGTGNVSFYSAVDGVHLH
	1					TFSCSSVSRLRPFFWLSPLASLVIPPVTDRK*G
	}	1			ļ	FSSPDQNSFPVVQLRDTHPWALFCPSCLYPG
	1	1	1		l	WSIFWVSLTVPFGICPLCASQEAVPWEVGLA
		1	1		1	W2ILM A2FI ALLOICI POUPORILI
		ì			<u> </u>	NGDGTGNFPRRFWEIFL FFFFFETESHSVAQAGMQWRNLGSLPAPPPGF
630	1980	A	4669	2	358	FFFFFETESHSVAQAOMQWANEGOEITH IT OF
050	1300	1		1		TPFFCLSLLNGWDYRRPPPHLANFFVLLVETC
ì			ļ			FHDVGQDGLDLLTS*STPSASQSAEITGVSHC
	ł		ı			TRLKKIRFAKGHVEFFFESHVE
	1981	A	4674	953	614	TPIRGTDDEHEECTVQEYSAGKNTCLRPGAV
631	1961	A .	14074	755		AHTCNPCTLGGRGRWIT*GSGVQDQPGPTWC
	-		1			NPVFLERRPRALHSSPGLTTQRILWAQGLWV
			1			GAGSTGCSRGPRGEGVFREG
					314	PSTHASGMISPSFGFMGHLLRLEFEILPSTPNP
632	1982	Α	4678	34	314	*LPSYQGEAAGSSLISHLQTFSPDLKGVYCTFI
	1				ASGLAPVPTHWTVSELSRSPVATATFC	
i	1					RTLGMEGERRASQAPSSGLPAGGANGESPGG
633	1983	A	4696	1	1365	KILUMEUEKKASQAFSSULI AUGANGESI OC
333	1 -7 -7			1	}	GAPFPGSSGSSALLQAEVLDLDEDEDDLEVFS
	}	]	1		1	KDASLMDMNSFSPMMPTSPLSMINQIKFEDE
1	1				}	DLKDLFITVDEPESHVTTIETFITYRIITKTSRG
		-		1		EFDSSEFEVRRRYQDFLWLKGKLEEAHPTLII
i		1				PPI PEKFIVKGMVERFNDDFIETRRKALHKFL
[		ı		1		NRIADHPTLTFNEDFKIFLTAQAWELSSHKKQ
		1		-		GPGLLSRMGOTVRAVASSMRGVKNRPEEFM
1		-	1	1	1	FMNNFIELFSOKINLIDKISORIYKEEREYFDE
1		- 1		- }	ì	MKEYGPIHILWSASEEDLVDTLKDVASCIDRO
		1				CKATEKRMSGLSEALLPVVHEYVLYSEMLM
l			Ì	1		GVMKRRDQIQAELDSKVEVLTYKKADTDLL
		1		1	ľ	GAWKKENGIATERNA VEALLI LYANIEDIANOVITA
1				1		PEEIGKLEDKVECANNALKADWERWKQNM
	İ	1				QNDIKLAFTDMAEENIHYYEQCLATWESFLT
	1					SOTNI.HI.EEASEDKP
<u></u>			4708	421	158	SYWVGEDYTYKFFEVILIDPFHKAIRRNPDTC
634	1984	Α	4 /08	421		WISKAVYKHREMCGLTSTGRKSHGLEKDRM
					1	FPHAIGGSCRAA*RRKTLQFPCYH
						YTKQPDAKERRTVHWKKETESEASEITIPPS
1	1985	A	4709	42	341	TIKUTUAKERKKI YII WAKETESEASEITUTS
635	1 .,,,,	1				PGVPQAPGHWEDYGRGDNFYLPH*DPGGIVI
635	- 1		1	1	1	WNIFNRMPIARKNITDGEHHEYLIEVPRLFHT
635		- 1			i	
635						sen.
635	1986	A	4721	2	351	

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	l	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	ļ	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
			l .	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ì	1		residue of	sequence	/=possible nucleotide deletion, \=possible
		1	1	peptide	}	nucleotide insertion
	1			sequence	ļ	ISPNFNSMDQPLDFQRTLGLRSPCYNRVPAQK
						MYFTTPSNHNAYQVDSVQST
	1		J			NTGLTCSIQRKCGETQLYRREENRLILLLQDH
637	1987	A	4726	664	253	LKSESFQVLTLSPRLEFSGLISAHCNLRLPGSS
			1	ł		DSSASSSRAAGITGVHHHAWLIFFFLVETGFL
	1	1	1	1	Ì	HAG*AGLELLTSGDPPASASRSAGITGVSHHA
	ł	1	}	}	ì	DDDCTDFI
	.\			\	592	GGMDSRVSGTTSNGETKPVYPVMEKKEEDG
638	1988	A	4734	24	392	TI FRGHWNNKMEFVLSVAGEIIGLGNVWRFP
		}			1	VI CYKNGGGAFFIPYLVFLFTCGIPVFLLETAL
		}		1		COVISOGGVTAWRKICPIFEGIGYASQMIVIL
		ì				I NIVYVIIVI AWALFYLFSSFTIDLPWGGCYHE
	Ì			1		WNTEHCMEFOKTNGSLNGTSENATSPYLEFW
			4545	1040	699	OGL TUL PRIMECSATITAHCSLELPGSIDLPTSA
639	1989	A	4743	1040	099	S*VARTTGTHHHPWLILVLLL*TWGSYYVAQ
			· I			AGLELLGSSNLPAAMVSQSAQIIGHDHCAWA
	-	}		1		TONIHVI YTOEGLRRGKEG
			4771	527	2	CRIDOPHPATVI AOPIFIDACSVLGAYQGAQN
640	640 1990	A	4//1	321	1	WIRERPCT PSGCLKMNREIGPLOHSLCCPGWS
		1	1			OTPGIKAILLROPPK*LGLOMESHSCPPAWSA
			1		ł	MARSRITATSASOVOAILLPOPPGTTDSCSPS
	[		i			PDHEOOPLSWVLPPPQKDMNPREQQVALGP
	1		1	1		QAAALPWAVWRNDCFPR
	1001	+	4780	16	473	RPSSQCGGIPTGWKKGLAPELSSELSSPPLPAR
641 1991	1991	A	4780	1.0		LQLAASPYFSPSWAECPQPVPAGTHATWCLA
	1	- {	ì	1	ĺ	RVWARMTPPGPAGIPSHPLPPPPPERSVPIPSP
		-	1	ľ	1	FPARDSGSRQGHSTDRYKHTDAPRDAHRRVP
		1	- 1	1		QRDTDTGVHTGSGTHTHAHTPPEK
642	1992	A	4798	1	487	GYSFRCDIVDYSRSPTALRMARTCWLYYFSK
642	1992	1	1,,,,			FIELLDTIFFVLRKKNSQVTFLHVFHHTIMPW
		1			1	TWWFGVKFAAGGLGTFHALLNTAVHVVMY
	}	1		İ		SYYGLSALGPAYQKYLWWKKYLTSLQLVQF
l				}	1	VIVAIHISQFFFMEDCKYQFPVFACIIMSYSFM
ĺ		- 1				FLLLFLH LMAFIEMHISGSLVYLKIKTKIYSYFSMLNFLI
643	1993	A	4799	2	391	QEIPLSEILRISSPRDFTNISQGSNPHCFEIITDT
073	1,7,5			1		MYYFVGENNGDSSHNPVLAATGVGLDVAQS
			- 1	l,		WEKAIRQALMPVTPQASVCTSPGQGKDHSK
1		-	1	1		Q*ASVCTSPGQGKDHSKQ
	ł					AYPLFAVHPVHTECVAGVVGRAYLLCALFFI
644	1994	A	4800	488	101	LSFLGYCKAFRESNKEGAHSSTFWVLLSIFLG
011						AVAMLCKEQGITVLVRAATWLGPAFSVCPFI
1						SYKDIWGWPCLCGVLHAYIPLLV
1		1				LLWTTVLCQTPARPQSTMIHLGHILFLLLLPV
645	1995	A	4805	458	126	AAAQTTPGERSSLPAFYPGTSGSCSGCGSLSL
""						PLLAGLVAADAVASLLIVGAVFLCARPRRSP
1	i	Ì	Í	1		AQEDGKVYINMPGRG
1						LQGDTWHLSFLSHFSRLHGGVPGRGLLEGNI
646	1996	A	4817	47	1033	LQPQAPGHDMTSIPFPGDRLLQVDGVILCGL
- ' -				- {	i	HKQAVQCLKGPGQVARLVLERRVPRSTQQC
	- 1	- 1		1		PSANDSMGDERTAVSLVTALPGRPSSCVSVT
1				1		DGPKF*SSN*KRIANGLGFSFVQMEKESCSHI
	1					KSDLVRIKRLFPGHPAEENGAIAAGDIILGRE
		1				WEGPRKASSSRCRGSWAMQLSVQAGPSFAS
1				1		YYPAAVEVLHLLRGAPQEVTLLLCRPPPGAL
}		ł	1			PELEQEWQTPELSADKEFTRATCTDSCTSPIL
		1		1		GSRGQLGGTVPPQMQGKAWGLRPESSQKAI
		-			Į į	EGTMGAKTERDLGPVP
						PRVRGDWPLEKKKSNSNHPIFSWCGSTDSK
					335	

					The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A enartic Acid E=Glutamic Acid,
O: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
:q-	uence		09/496	correspondi	acid residue	Glutamine R=Arginine, S=Serine,
ence	1		914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	ì		]	amino acid	of peptide	V=Tyrosine, X=Unknown, *=Stop codon,
	]			residue of	sequence	/=possible nucleotide deletion, \=possible
	1		1	peptide		nucleotide insertion
	1		1	sequence	<u> </u>	IVMPTYDLTDSVLETMGRVSLDMMSVQANT
					1	GPPWESKNSTAVWRGRDSRKERLELVKLSRK
	1	l	ł	Ì	(	HPELIDAAFTNFFFFKHDENLYGPIVKHISFFD
	İ	1	ì		-	FFKHKYQINIDGTVAAYRLPYLLVGDSVVLK
	1	ļ	1			QDSIYYEHFYNELQPWKHYIPVKSNLSDLLEK
		ĺ	1	1		LKWAKDHDEEAKKIAKAGQEFARNNLMGD
		1	1	)		LKWAKDHDEEAAAIAAAOQLI MUTABA
	1	l	Į.			DIFCYYFQTFPRNMPIYK
48	1998	A	4867	2030	837	AGMLPAVGSADEEEDPAEEDCPELVPMETTQ
40	1776	1	1		}	SEEEKSGLGAKIPYTIITGYLGAGKTTLLNYI
	1		1		ļ	LTEQHSKRVAVILNEFGEGSALEKSLAVSQG
		1	1	ļ	ļ	GELYEEWLELRNGCLCCSVKDNGLRAIENLM
		1	1		(	QKKGKFDYILLETTGLADPGAVASMFWVDA
			İ			ELGSDIYLDGIITIVDSKYGLKHLAEEKPDGLI
	1		}		ţ	NEATRQVALADAILINKTDLVPEEDVKKLRT
	1		ł	Ì		TIRSINGLGQILETQRSRVDLSNVLDLHAFDSI
	1			1		SGISLQKKLQHVPGTQPHLDQSIVTITFDVPG
	ļ	į	1	1		NAKEEHLNMFIQNLLWEKNVRNKDNHCME
	1					IRLKGLVSIKDKSQQVIVQGVHELYDLEETPV
		1		1		SWKDDTERTNRLVLLGRNLDKDILKQLFIAT
	1	1	l l	}	)	VTETEKQWTTHFKEDQVCT
	1999	A	4873	226	189	DGVSLLLPKLGVQWAQYWAHWQPPLPGFKH
649	1999	1 ^	4073	1 220		FSCLSLRSSWD+KCAPPHPAFVFLVEMGFHR
	į	1	- 1	Į.	Ì	GQAGLELRTSGDPPASASQSAGITGVSHLA*P
İ	1	1	1		TSMPLLPFQRLCVYI	
		A	4874	12	437	FFFLRRSFAFVAQAGVQWCDLGSPQPLPPGF
650	2000	A	4074	1		K*FSCLSLPSSWDYRHAPPPCPS*FLYF**RQG
			l	1		ETMLARI VI NS*PHDLPTSPSQSAEIKGVSHK
		İ	1	ì	İ	CPASFYLFLKYYLEAKFCA*GECAPSAGVGA
		i	1			GYKRGHKSCLLINCVVQI
			4898	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATI
651	2001	A	4070	1701	, · · ·	PHMEPKASCPAAAPLMERKFHVLVGVTGSV
	- 1		1	ļ		A AT KLPLLVSKLLDIPGLEVAVVTTERAKHI
		-	1		1	SPODIPVTLYSDADEWEMWKSRSDPVLHIDL
	·			i	1	RRWADLLLVAPLDANTLGKVASGICDNLL
	ł		i i			VMR A WDR SKPLLFCPAMNTAMWEHPITAQ
	ŀ			1		VDOLKAFGYVEIPCVAKKLVCGDEGLGAMA
	Į.	- 1		Ì		FVGTIVDKVKEVLFOHSGFQQS*PGISVMGV
			1			I VSEWVOAKSVKMDVGKIGGYPHLLNGGPA
	1	ļ	ì			1 ST PRODACSRI NWTEGPGLSFFOPGEAAA
		4-	4005	<del>-  </del>	611	EDGROTSRPARGESPWRPPGTMOEPSSGECP.
652	2002	A	4927	1	011	SD*I PCASNRLAFGGLIFPCAPLVPYPAPFSPL
			1	1		PARSCAPRPRAHTHSRTHPSAPLVPKPSSRAF
			- 1	1		GOSPIPSRASSPSCSWAOVPGVALARCAGVC
	1	j		}		KPGDSWRVAACISGRCCSRGRRRGSGPRNPI
	- {	1		[		QSFRGAWGPSFWGSWKSQRELSAGGAQAW
		1	1	l		LLGSAGSGLRGEA
		1				FFFFI*DGVSLCHPGWNAVARSWLTATSASR
653	2003	A	4965	2	283	VOAVSCERLPSSWDYRHATMPG*FF*YF**R
_						WGFTHAILVLNS*PQVICPPWPPKVLTLQA
	)	)				RPGIPGRRFRRSWFCQLP*EPEPGLESLATPG
654	2004	A	4968	3 .	437	IPAVGLGALGVIPPVRVPQRPPTQRSQGRGW
			ļ			DPERDPGCRVQVSRGPRFGEQKTPGLQGCL
1		1				PPCLTHLAAASCVVVWCGRWKRDSAECQC
1		1	}		1	PPCLIHLAAASUV V WUUKWKUSAECQC
		1			l	HSCSAVSQQEDRCRSSSCS
		-	4983	201	397	MNNTTCIQPSMISSMALPHYILLCIVGVFG
220	7711114	1 1	1 1703	1		TLSQWIFLTKIGKKTSTHIYLSHLVTANLLVC
655	2005	i		l l		
			4088	332	159	LVHKDMYREFFEEEAQASNKHVTRCLTSLV
655	2005	A	4988	332	159	LVHKDMYREFFEEEAQASNKHVTRCLTSLV REVHIKTMR*HFLPIRLEKNKNNIKD MAGMKTASGDYIDSSWELRVFVGEEDPEAI

000 m	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
nucl-	peptide	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	<b>!</b>	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	!	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	denec	ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ì	1	1.	peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
		<del>                                     </del>	<u> </u>			VTLRVTGESHIGGVLLKIVEQINRKQDWSDH
	i	Į.				AIWWEQKRQWLLQTHWTLDKYGILADARLF
		(				FGPQHRPVILRLPNRRALRLX*
658	2008	A	5017	1	292	FFFFKETESHSVTQAGVQWHDLGSLQPPPPGF KRFSCLSLLSSWDYRCAPPHPANFVFLVETGF
050						HHVAQAGLKLLTL*SANLGLSTSLPIPLFILLS
						HHVAQAGLKLLIL-SANCOLSISLII LI LELES
659	2009	A	5018	17	338	RGHGGKSLTGGTPGNWGDGLLVSEDWSHLIF T*NSLVSPVLGKWSPCLQGPGLSAVHTWPWL
000		İ			1	T*NSLVSPVLGKWSPCLQGFGLSAVIII WI WE
		1		1		MAACWAVHVKTHMRPGLAVLPRLVLNSWS
	}	1	1	•		*AITLLWPPKALGLQA
660	2010	A	5028	2	310	SRVDDFVGERRGGCDECLCGHRGLRAVPLG
000	2010			1		HPGHLCLQPPGGPA*FLDYCRGCCPHPVPGST
	ĺ	j		1	1	AGSCPRQKKTTPGPTVLCVCSFWIYQRGEPH
	1	1		1		HRTGARWNH
661	2011	A	5050	752	431	ROSCSSTOAKVOWFHYGPLQSQPPGLKQSSQ
001	2011	1				LSLPNSRDHRHVPPRLAIFSFAETGSPYFAQAS
	1	ļ		1		LELLGSSHPPTSASQSARITGVSHRAWPLK*F
		1				NLNQYQTLTMN
662	2012	A	5054	48	103	ELNNGPFQMPLCNGGNLAVTGSWADRSPLH
002	2012	1				EAASQGRLLALRTLLSQGYNVNAVTLDHVTP
	1	l			1	LHEACLGDHVACARTLLEAGANVNAITIDGV
	l	ì		İ	1	TPLFNACSQGSPSCAELLLEYGAQAQLESCLP
	į	1		}		SPTHEGASKGHHECLDILISWGIDVDQEIPHSG
				1		TPLYVACMAQQFHCIWNLIYAGAGVRKGKY WDTPLPGAGHQSTQKLE*LFAMVEIWQ
	Ì		j			VRNS*SFAHCASVYKHHYMDGQTPCLFVSSK
663	2013	A	5066	951	580	ADLPEGVAVSGPSPAEFCRKHRLPAPVPFSCA
"		- }				GPAEPSTTIFTQLATMAAFPHLVHAELHPSSF
	1	L	1			WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ
1	1	Ì	1			LSFIEVLSMEQVNKTVVREFVVLGFSSLARLQ
664	2014	A	5071	550	1	OLLFVIFLLLYLFTLGTNAIIISTIVLDRALHTP
						MYFFLAILSCSEICYTFVIVPKMLVDLLSQKK
				]		TISFLGCAIQMFSFLFFGSSHSFLLAAMGYDR
ĺ	İ				Į.	YMAICNPLRYSVLMGHGVCMGLMAAAWAC
1	-			ļ		GFTVSLVTTSLVFHLPFHSSNQHE
ł	1	1				QQYHNTGSAGHHAHCQVGHSPHVHYPSGCG
665	2015	A	5074	496	692	PL*IQRGLPSFNSLEGHSLKDSGHEESVQLDSE
	]	- 1			ł	HDVQRSLYCDTAVNDVLNTSVTSMGSQMPD
İ	1	ļ				HDQNEGFHCREECRILGHSDRCWMPRNPMPI
1	i	}		1	1	RSKSPEHVRNILALSIEATAADVEAYDDCGPT
Į.	ì	1	1			KRTFATFGKDVSDHPAEERPTLKGKRTVDVT
	1	1	ł			ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL
		1				PTKPSVSYEIVDPGITARRC
				J		IMLLSTSS*VYFQSSTKDSHFFLFDFQKTGPPL
666	2016	A	5080	408	248	IMPROJECT OF ODC! AKBB
1		[				VGPKAQLSGLQLQPCLYKRR DLTNSHFFLFDFQKTGPPLGGPKAQFSSLQLQ
667	2017	A	5081	129	247	
		1				PCVY*RR NIKSNDRWVQIKTAYKYFF*KNGDNYNWVF
668	2018	A	5086	852	233	NIKSNUKW VQIKTATATITTANGUNTINW VI
""		"				RALPTIFADIENLKYLLFTRDASQPFYLGHTV
			1	İ		IFGDLEYVTVEGGIVLSRELMKRLNRLLDNSE
1				1		TCADQSVIWKLSEDKQLAICLKYAGVHAENA
1		1				EDYEGRDVFNTKPIAQLIEEALSNNPQQVVEG
						CCSDMAITFNGLTPQKMEVMMYGLYRLRAF
1						GHYFNDTLVFLPPVGSEND
669	2019	A	5101	1	329	PGRPTRPPLLTLLAHVSPEPAGPSCDSLAQPG
009	2019	1	7.0.	1		ASGV*VQHDSHPPLLCGSQCLSEPVPGSHGPP
						RGCQHEAAPCPRGPGSDGLHHASAACASLPP
l				1	į	SPILPVLLPELGPL
100	2020		5102	3	547	DAWGNRCAVGAAPRLIHLHLCCTPADPSRKP
670	2020	Α	3102			

			CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	Ì	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1	Ì		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		Ì	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide	)	nucleotide insertion
	1	Í		sequence		DEL*NMNGRVDYLVTEEEINLTRGPSGLGFNI
				1		VGGTDQQYVSNDSGIYVSRIKENGAAALDGR
	ļ			1		LQEGDKILSVNGQDLKNLLHQDAVDLFRNA
			1	1		GYAVSLRVQHRLQVQNGPIGHRGEGDPSGIPI
	į	1				FMVLVPVFALTMVAAWAFMRYRQQL
		İ				RDGREELCLQCEPTLPSRICSSAPLLYFLFICPF
671	2021	A	5105	672	400	RDGREELCLQGEFILFSRICSSAI LETTERICIT
***		1	1		i	VLLLLLISLLCLYWKARKLSTLRSNTRKEKA
		1				LWVDLKEAGGVTTNRMED*EEDECN
672	2022	A	5148	72	314	IIYFSYNIFLKITELLNDVERLKQALNGLSQLT
072	2022	1	1		}	YTSGNPTKRQSQLIDTLQHQVKSLEQQLAVS
}	ļ	1	1			NQAHGALQEYVLAPCS
673	2023	A	5152	210	335	REILCSRIGRLNIV*MSLFPNLTCRLNAIPIKIPA
0/3	1 2023	^	3132		Ì	NHFVEVT
	2024	I <sub>A</sub>	5153	3	2953	LTEDQPFDILQKSLQEANITEQTLAEEAYLDA
674	2024	A	3133	١		SIGSSQQFAQAQLHPSSSASFTQASNVSNYSG
	i	1	1	1		OTLOPIGVTHVPVGASFASNTVGVQHGFMQH
}	ì	1	1			VGISVPSOHLSNSSOISGSGQIQLIGSFGNHPS
}		1	1	}		MMTINNLDGSOIILKGSGQQAPSNVSGGLLV
		1				HROTPNGNSLFGNSSSSPVAOPVTVPFNSTNF
ì		1				OTSLPVHNIIIORGLAPNSNKVPINIQPKPIQM
		1	1 -		i	GOONTYNVNNLGIQQHHVQQGISFASASSPQ
1		i i	ļ			GSVVGPHMSVNIVNQQNTRKPVTSQAVSSTG
1	1	1		1		GSIVTHSPMGOPHAPOSQFLIPTSLSVSSNSVH
ŀ	ı	ļ	i			HVOTINGOLLOTOPSOLISGOVASEHVMLNR
1	1		1			NSSNMLRTNOPYTGPMLNNQNTAVHLVSGQ
	1	1	l l	ì		TEAASGSPVIANHASPOLVGGQMPLQQASPT
	i i		1			VLHLSPGOSSVSOGRPGFATMPSVTSMSGPSR
]			1			FPAVSSASTAHPSLGSAVQSGSSGSNFTGDQL
1	1.	1		}	1	TOPNRTPVPVSVSHRLPVSSSKSTSTFSNTPGT
	1		1	}		GTQQQFFCQAQKKCLNQTSPISAPKTTDGLR
	ļ	- 1	ŀ			QAQIPGLLSTTLPGQDSGSKVISASLGTAQPQ
			1			QEKVVGSSPGHPAVQVESHSGGQKRPAAKQ
			į.			LTKGAFILQQLQRDQAHTVTPDKSHFRSLSD
1	- 1					AVQRLLSYHVCQGSMPTEEDLRKVDNEFETV
1	1		1	1		ATQLLKRTQAMLNKYRCLLLEDAMRINPPAE
1	ļ	i	1		Ì	MVMIDRMFNQEERASLSRDKRLALVDPEGFQ
	1	}	1			ADFCCSFKLDKAAHETQFGRSDQHGSKASSS
	1	ļ		l		LOPPAKAQGRDRAKTGVTEPMNHDQFHLVP
					1	NHIVVSAEGNISKKTECLGRALKFDKVGLVQ
	}		j	}		YQSTSEEKASRREPLKASQCSPGPEGHRKTSS
		1				RSDHGTESKLSSILADSHLEMTCNNSFQDKSL
1	1					RNSPKNEVLHTDIMKGSGEPQPDLQLTKSLET
	[					TFKNILELKKAGRQPQSDPTVSGSVELDFPNF
}				1		SPMASQENCLEKFIPDHSEGVVETDSILEAAV
	ŀ			ſ	1	
	1	1	1			NSILEC
675	2025		5154	599	1880	LKKMEPFSCDTFVALPPATVDNRIIFGKNSDR
0/3	2023	1^	7.57	1		LYDEVQEVVYFPAVVHDNLGERLKCTYIEID
		1		1		QVPETYAVVLSRPAWLWGAEMGANEHGVCI
1						GNEAVWGREEVCDEEALLGMDLVRLGLERA
		1 .				DTAEKALNVIVDLLEKYGQGGNCTEGRMVF
						SYHNSFLIADRNEAWILETAGKYWAAEKVQE
j	1					GVRNISNOLSITTKLAREHPDMRNYAKRKGW
						WDGKKEFDFAAAYSYLDTAKMMTSSGRYCE
				1		GYKLLNKHKGNITFETMMEILRDKPSGINME
						GEFLTTASMVFILPQDSSLPCIHFFTGTPDPER
	-					SVFKPFIFVPHISQLLDTSSPTFELEDLVKKKS
	1		{	1		HFKPDRRHPLYQKHQQALEVVNNNEEKAKI
	1	1	i			In VI DIGGIT P I AND I AND A LITTLE BEIGHT
ì	1	j		1	L	I NAT DVINADAI EAEL EBENYEZII UNK HITIALEK IA
						MLDNMRKLEKELFREMESILQNKHLDVEKIV NLFPQCTKDEIQIYQSNLSVKVSS

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	De Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ı	in		corresponding	1=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		l	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1	l	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	residue of	sequence	/=possible nucleotide deletion, \=possible
			ì	peptide	}	nucleotide insertion
				sequence		FFFLRRSLALSPRPDCGLQWRNLGSLQAPPPG
676	2026	A	5155	2	306	FTPFSCLSLPSSWDYRRPPPRPANFLYF**RRG
070	2020	1	i			FTPFSCLSLPSS WDYRRFFRY ANTETT INCO
		1	]		Ì	FTLLARMVSIS*PHDPPASASQSAGITGVSHRA
		1	1	J		RPT
-	2027	A	5167	97	740	FFHSVDLLALEQSKTFYKPDWFDIVESEVKCC
677	2027	1	310,	1 "		KEAVCVIDMSSFTEFEITSTGDQALEVLQYLF
	1	1	i	ì	1	SNDLDVPVGHIVHTGMLNEGGGYENDCSIAR
		1	1	1		LNKRSFFMISPTDQQVHCWAWLKKHMPKDS
	1	1				NILLEDVTWKYTALNLIGPRAVDVLSELSYA
	1		Ĭ	<b>\</b>		PMTPDHFPSLFCKEMSVGYANGIRVMSMTHT
				1	ļ	GEPGEMI YIPIEYRWGFTMLSTLVSNS
				1010	2018	PALCELEDDMTVCVADFGLSKKIYSGDYYRQ
678	2028	A	5183	1919	2010	GRIAKMPVKWIAIESLADRVYTSKSDVWAFG
				Į.	1	VTMWEIATRGMTPYPGVQNHEMYDYLLHG
	1	-		1		HRLKQPEDCLDELCKI**SPQSP
	1		1		100	RESQVKHFKMRKIDLCLSSEGSEVILATSSDE
679	2029	Α	5190	39	499	KHPPENIIDGNPETFWTTTGMFPQEFIICFHKH
		1	l,	ŀ	1	VRIERLVIQSYFVQTLKIEKSTSKEPVDFEQWI
	- [	-	ì			EKDLVHTEGQLQNEEIVAHDGSATYLRFIIVS
	}	-	1	ļ		AFDHFASVHSVSAEGTVVSNLSS
	i	}	j			EILAVLKLACGDISLNALALMVATAVLTLAPL
680	2030	A	5204	541	92	LLICLSYLFILSAILRVPSAAGRCKAFSTCSAH
000	2030		1	1	1	LLICLSYLFILSAILKVPSAAGKCKAI STOOIGI
<b>.</b>	1	-	- 1	1		RTVVVVFYGTISFMYFKPKAKDPNVDKTVAL
ļ		-	Į.	\ \	Ì	FYGVVTPSLNPIIYSLRNAEVKAAVLTLLRGG
			1			LLSRKASHCYCCPLPLSAGIG
(0)	2031	A	5207	10	247	VPDNGDVTKLPVCSTLVEETSLTVSEAMEQSI
681	2031	^	3207	1.5		KNESPLPGTLAHTCNTSTLGGRGRWIT*GREF
1		1	1			DTSMANMVKPCLYRK
		$ +$ $\overline{A}$	5210	12	231	FFFETESYSITQAGVQWPNLSSLKTLPPGFK*F
682	2032	I A	3210	-		SCLSLPSSWDYRCLPPCPANFCIFSRNGVLPC
1		- {	l	1		WPGWSRTPDLS
			6310	85	402	CPSVSGLIKSDLRRHNINIGITNVDVKAVSNIF
683	2033	A	5218	1 92	102	MILLESMYRINVKPYFFI*LFFSRVNC*SVIIG
		1			1	YARCYTFLIF*LFL*IPADSPTDQEPKTVMLSK
1	\ \		ļ			OSESAL
	l			<del></del>	194	NI MKEMONLNSENHKTWEEYKDTK*IMSYF
684	2034	A	5220	1	124	YG*ALNVIKMAVLPKLMYRFSATLVKIPQHL
		1			1	TDS
						LHSQDGNSDPRKPQGEMSAHAFPVQTCGEEL
685	2035	A	5228	260	440	OVYTROVPINFTELSKCS*S*KIMSGERE
1						GGEAAARAKLSSPRPHRVGRRERGVGGMS
686	2036	A	5239	79	508	AFSEAALEKKLSELSNSQQSVQTLSLWLIHHI
550	1 3323	1	1	[		KHSRPIVTVWERELRKAKPNRKLTFLYLAND
1		1	[	1		KHOKPIVI V WEKELKAAATIKAETI DI DAND
1		-		}		VIQNSKRKGPEFTKDFAPVIVEAFKHVSSETD
				ļ		ESCKKHLGRVLSIWEERS
(07	2037	A	5244	1	428	MAAVVAATALKGRGARNARVLRGILAGATA
687	203/	^	3277	1 -		NKASHNRTRALQSHSSPEGKEEPEPLSPELEY
	1	1		1		PRERGKNPMKAVGLAWAIGFPCGILLFILIK
1		-		1		EVDKDRVKQMKARQNMRLSNTGEYESQRFI
			}			ASSOSAPSPDVGSGVOT
				<del></del>	1407	LOOTEDKSLLNOGSSSEEVAGSSQKMGQPGF
688	2038	A	5249	1	1407	SCOSDI ATALHRISLRRONYLSEKOFFALEW
		1	1			ORKIOVI ADOKEGVSGCVTPTESLASLCTTQ
		- 1				EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY
			ĺ			HWQQLAQPNLGTILDPRPGVITKGFTQLPGD
			1			AIYHISDLEEDEEEGITFQVQQPLEVEEKLSTS
				}		KPVTGIFLPPITSAGGPVTVATANPGKCLSCT
1			1			KPV I GIFT LL THE DIT ON THE CEDET COCCE
1	1	1	1	1	1	NSTFTFTTCRILHPSDITQVTPSSGFPSLSCGSS
	1	1	j.		1	GSSSSNTAVNSPALAYRLSIGESITNRRDSTT

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, 1 =1 toine,
uence	1	Ì	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	l		ĺ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	l	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	1	/=possible nucleotide deletion, \=possible
		ĺ	1	sequence		nucleotide insertion
	<del> </del>	<del> </del>	<del> </del>	-		FSSTMSLAKLLQERGISAKVYHSPISENPLQPL
	į.	1				PKSLAIPSTPPNSPSHSPCPSPLPFEPRVHLSEN
		1	1			FLASRPAETFLQEMYGLRPSRNPPDVGQLKM
		ì				NLVDRLKRLGIARVVKNPGAQENGRCQEAEI
	[	1	}	]		GPQKPDSAVYLNSGSSLLGGLRRNQSLPVIM
	1				Ì	GSFAAPVCTSSPKMGVLKED
			1	L	<del> </del>	LSLFGSRALGRSGARAMAKAKKVGARRKAS
689	2039	A	5254	2	2621	LSLFGSKALGKSUAKAMAKAKA VOAKKAS
	1		1	\		GAPAGARGGPAKANSNPFEVKVNRQKFQILG
ł	1	1		1		RKTRHDVGLPGVSRARALRKRTQTLLKEYKE
	1	1	1			RDKSNVFRDKRFGEYNSNMSPEEKMMKRFA
1	1	ļ	1		1	LEQQRHHEKKSIYNLNEDEELTHYGQSLADIE
	1	ł	(			KHNDIVDSDSDAEDRGTLSGELTAAHFGGGG
1		ì		1		GLLHKKTOOEGEEREKPKSRKELIEELIAKSK
		1	1			QEKRERQAQREDALELTEKLDQDWKEIQTLL
}	ì	ļ	1	{	İ	SHKTPKSENRDKKEKPKPDAYDMMVRELGF
ŀ	i		1	}		EMKAQPSNRMKTEAELAKEEQEHLRKLEAE
1	1		1			RLRRMLGKDEDENVKKPKHMSADDLNDGFV
l	-	{	Í			LDKDDRRLLSYKDGKMNVEEDVQEEQSKEA
]	}	1	1		Ì	SDPESNEEEGDSSGGEDTEESDSPDSHLDLES
	Ì		1			NVESEEENEKPAKEQRQTPGKGLISGKERAG
}	ł	ı	.			NVESEEENERPAREQROTTOROLISORETORO
ì	)	1	}		ì	KATRDELPYTFAAPESYEELRSLLLGRSMEEQ
	ì	1	1	İ		LLVVERIQKCNHPSLAEGNKAKLEKLFGFLLE
Į.		1				YVGDLATDDPPDLTVIDKLVVHLYHLCQMFP
1		1	}	i	1	ESASDAIKFVLRDAMHEMEEMIETKGRAALP
1			1	Ì	ļ	GLDVLIYLKITGLLFPTSDFWHPVVTPALVCL
1		1		1		SQLLTKCPILSLQDVVKGLFVCCLFLEYVALS
	]	1			İ	QRFIPELINFLLGILYIATPNKASQGSTLVHPFR
1	i	1			1	ALGKNSELLVVSAREDVATWQQSSLSLRWA
1		1	1		1	SRLRAPTSTEANHIRLSCLAVGLALLKRCVLM
1	Ì	1	Ì	ĺ		YGSLPSFHAIMGPLRALLTDHLADCSHPQELQ
	ì		1	)	}	ELCQSTLTEMESQKQLCRPLTCEKSKPVPLKL
			1	}	ì	FTPRLVKVLEFGRKQGSSKEEQERKRLIHKHK
	İ			1	1	REFKGAVREIRKDNQFLARMQLSEIMERDAE
1	1		]			RKRKVKQLFNSLATQEGEWKALKRKKFKK
	{	1				RARK V ROLLING COLOR WALLES IN THE COUNTY
690	2040	A	5261	1	304	FFFFVFLVETGFHHVGQAGLELLTSGDPPTW
""		1	1			ASQSAGITGVSHCSWPVIYVLSTLLHAVRNVL
İ	1	1	-	,		FKRTFPLKSSSFLSYDKEIFPILIVLKFYLVTLT
	i i	1	1	Ĭ	1	SFVK
(01	2041	<del>                                     </del>	5270	3	158	NCHTTHCTANWVHLPGTPPGWKIDGPAAAL
691	2041	Α	32/0	1	1 3	EVLSSFFFFFLKFSYKPONIV
	10000	<del></del>	6202	56	1268	GMEPVGCCGECRGSSVDPRSTFVLSNLAEVV
692	2042	Α	5282	30	1200	ERVLTFLPAKALLRVACVCRLWRECVRRVLR
1			1	1	1	THRSVTWISAGLAEAGHLEGHCLVRVVAEEL
1	1		1		1	ENVRILPHTVLYMADSETFISLEECRGHKRAR
}	}		1	1		KRTSMETALALEKLFPKQCQVLGIVTPGIVVT
1			1	1	1	PMGSGSNRPQEIEIGESGFALLFPQIEGIKIQPF
1		1	1	ļ	1	PMOSOSNKPQEIEIGESGFALLFPQIEGIAIQFF
1	1	1		1	1	HFIKDPKNLTLERHQLTEVGLLDNPELRVVLV
1		1	1		1	FGYNCCKVGASNYLQQVVSTFSDMNIILAGG
1	1	1	(		1	QVDNLSSLTSEKNPLDIDASGVVGLSFSGHRI
1	[				Į.	QSATVLLNEDVSDEKTAEAAMQRLKAANIPE
				1	J	HNTIGEMEACVGRGFQYYRAKGNVEADAFR
1	1			1	1	KFFPSVPLFGFFGNGEJGCDRIVTGNFILRKCN
1					1	EVKDDDLFHSYTTIMALIHLGSSK
				<del></del>	+	EEIKERFGPGLVIYWYGFIQELDCNRERGILLK
693	2043	A	5301	362	507	EEINEKTUTULVII W I OFIQEEDCINEKOIEEN
J					1	ACFPTNIVTLCHSIA
694	2044	T <sub>A</sub>	5310	1	204	RVLTAINHTLKENLRKFYKGKKDKPLDLRPK
1 374	257	1				KTRAMRRRLNMHEENLKTKKQHRKERLYPL
	}		ì	1		RKYAAKA
695	2045	<del> </del>	5315	125	1596	ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP
1 500	2045	Α	כוכנ	120		

				D. Card	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspertic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	l=Isoleucine, K=Lysine, L-Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	defice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	Ì		314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	<b>\</b>		1		sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	<b>\</b>		1	residue of	sequence	/=possible nucleotide deletion, \=possible
		l	1	peptide		/=possible flucteonide defending ( possible
ļ	l	ĺ		sequence		nucleotide insertion
	<del> </del>	<del></del>	+			TGSGKEEGPAPCKQMKLEAAGGPSALNFDSP
	ļ		1			SSLFESLISPIKTETFFKEFWEQKPLLIQRDDPA
	l	Į	1	ĺ		LATYYGSLFKLTDLKSLCSRGMYYGRDVNV
				İ		CRCVNGKKKVLNKDGKAHFLQLRKDFDQKR
	Ì		1	1		ATIQFHQPQRFKDELWRIQEKLECYFGSLVGS
	1	ŀ	1	ļ		A HOPHOPORTADEL WRIGHTED OF ECENH
	Į.		1		1	NVYITPAGSQGLPPHYDDVEVFILQLEGEKH
	1	1				WRLYHPTVPLAREYSVEAEERIGRPVHEFML
	}	i	i	{	1	KPGDLLYFPRGTIHQADTPAGLAHSTHVTIST
	1	}	]			VONNSWGDFLLDTISGLVFDTAKEDVELRTG
	ì		1	1	}	IPRQLLLQVESTTVATRRLSGFLRTLADRLEG
		l	į	1	1	TKELLSSDMKKDFIMHRLPPYSAGDGAELSTP
	ì	ĺ		1		TRELLSSOMENDI INTIME TO PRODUCE
	1		1	l	1	GGKLPRLDSVVRLQFKDHIVLTVLPDQDQSD
	]	1	1	1		ETQEKMVYIYHSLKNSRETHMMGNEEETEFH
	1	1	1	1		GLRFPLSHLDALKQIWNSPAISVKDLKLTIDE
		1			<b>\</b>	FKESLVI.SLWTECLIOVV
	Į		L			LMKXYLEAAELGEISDIHTKLLRLSSSQGTIET
696	2046	A	5318	1476	742	SLQDIDSRLSPGGSLADAWAHQEGTHPKDRN
0,70		1	1			SEQUIDSKESFOGSEADAWAIIQEGTIII AVN
	ì		į	1		VEKLQVLLNCMTEIYYQFKKDKAERRLAYN
r	1	1			1	EEQIHKFDKQKLYYHATKAMTHFTDECVKK
İ	ł	1	1			VEAFT NKSEEWIRKMLHLRKOLLSLINQCIDI
			1			FEEVSKYOEYTNELQETLPQKMFTASSGIKHI
		1	ŀ		1	MTPIYPSSNTLVEMTLGMKKLKEEMEGVVKE
	1	Į	1			LAENNHILESGGSLTMDGGLRNVDCL
1						LAENNAILESCOSETVIDOGEICVE DEL
697	2047	A	5320	244	478	LDYNFFLFEMTFGLVSQAGVQWHDLGSLQPP
097	2047	1.,				PPGFKQFSCLSLPSSWDYRHLPPHLANFSREG
	ļ	1	1		1	VSPSWPGWSRTPDFR
			5324	266	714	LPIRKSLRSVRSGFPTSQSPITRNLDGTASGSC
698	2048	Α	3324	200	1'''	LAKTVTGSLFRINVGLRGLVAGGIIGALLGTP
	1	1			1	VGGLLMAFOKYSGETVOERKQKDRKALHEL
1	1	1	1	İ		KLEEWKGRLQVTEHLPEKIESSLQEDEPENDA
1	1				1	KKIEALLNLPRNPSVIDKQDKD
ŀ	ĺ	1				KKIEALLNEPRINI SVIDRODICE ADVCASKEAA
699	2049	A	5334	699	277	RPHGHLVCISSSAGLSGVNGLADYCASKFAA
699	2049	Α.	333.	***	}	FGFAESVFVETFVQKQKGIKTTIVCPFFIKTGM
	)	i i	i	ì		FEGCTTGCPSLLPILEPKYAVEKIVEAILQEKM
1	ì		1		İ	YLYMPKLLYFMMFLKSFLPLKTGLLIADYLGI
l	}	1	- 1			LHAMDGFADQKK
	1					PTAEEMSSLTPESSPELAKRSWFGNFISLDKEE
700	2050	A	5344	3	614	PIACEMODLIFEODRELANG WI ON TOLDINE
1 '00	2030	1.,		1		QIFLVLKDKPLSSIKADIVHAFLSIPSLSHSVLS
1	1		1	Į		QTSFRAEYKASGGPSVFQKPVRFQVDISSSEG
1	l l	ĺ	1			PEPSPRRDGSGGGGIYSVTFTLISGPSRRFKRV
	1	ļ			1	VETICACILISTHDOPSVOALADEKNGAQTRP
	- 1	1				AGAPPRSLQPPPGRPDPELSSSPRRGPPKDKK
1	- [			Į	}	
1			i	1 .	1	LLATNGTPL
	1000	<del>-   -   -   -   -   -   -   -   -   -  </del>	5346	3	1383	HASVLFCRVMAASKTQGAVARMQEDRDGSC
701	2051	A	7340	٦		STYGGYGYGDSKDCILEPLSLPESPGGTTTLE
1	1	ĺ	1	1	1	GSPSVPCIFCEEHFPVAEQDKLLKHMIIEHKIV
1		1	1		1	LADVKLVADFQRYILYWRKRFTEQPITDFCSV
1	1		l l	1	1	IRINSTAPFEEQENYFLLCDVLPEDRILREELQ
1	1	1	1		1	IKINSTAPPEDQENTFLECTVE EDICITION OF THE PER
1	l l		l	1	1	KQRLREILEQQQQERNDTNFHGVCMFCNEEF
1	1	1	1	1	1	LGNRSVILNHMAREHAFNIGLPDNIVNCNEFL
1	ł	-	1	[	1	CTLOKKLDNLOCLYCEKTFRDKNTLKDHMR
1	- 1	1				KKOHRKINPKNREYDRFYVINYLELGKSWEE
1	1	1	1	[		VQLEDDRELLDHQEDDWSDWEEHPASAVCL
1			1			ACTED VETERI AND CED Y REED! I KIK CE! U
	- L		,	1		FCEKQAETIEKLYVHMEDAHEFDLLKIKSELG
		- 1			,	
				}		INFYOOVKLVNFIRROVHOCRCYGCHVKFKS
						LNFYQQVKLVNFIRRQVHQCRCYGCHVKFKS KADI RTHMEETKHTSLLPDRKTWDQLEYYFF
						LNFYQQVKLVNFIRRQVHQCRCYGCHVKFKS KADI RTHMEETKHTSLLPDRKTWDQLEYYFF
						LNFYQQVKLVNFIRRQVHQCRCYGCHVKFKS KADLRTHMEETKHTSLLPDRKTWDQLEYYFF TYENDTLLWTLSDSESDLTAQEQNENVPIISE
					1540	LNFYQQVKLVNFIRRQVHQCRCYGCHVKFKS KADI RTHMEETKHTSLLPDRKTWDQLEYYFF

		N/A	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=A spartic Acid E=Glutarnic Acid,
IO: of	NO: of	noa	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
otide	seq- uence		09/496	сопеspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
		ļ		sequence		nucleotide insertion
	<del> </del>		1			LASLRCTLGAFCECDFRPDLPGLECDLAQHL
	}				İ	AGQHLAKALVVKALKAFVRDPAPTKPLVLSL
	1	1		ļ		HGWTGTGKSYVSSLLAHYLFQGGLRSPRVH HFSPVLHFPHPSHIERYKKDLKSWVQGNLTA
	1	İ	1	Ì		CGRSLFLFDEMDKMPPGLMEVLRPFLGSSWV
		ļ	1	\ .		VYGTNYRKAIFIFISNTGGEQINQVALEAWRS
		}	}		1	RRDREEILLQELEPVISRAVLDNPHHGFSNSGI
		}	1			MEERLLDAVVPFLPLQRHHVRHCVLNELAQL
		1	1	,		GLEPRDEVVQAVLDSTIFFPEDEQLFSSNGCK
				ł		TVASRIAFFL
	1	1	1		<u> </u>	LELOVI PMKTEFEARTHTETEMFLRKEOOKL
703	2053	A	5380	278	657	FEDI FEWMEK YDKDTEMKONELNALKA I KA
		1		1		SDI AHLODI AKMIREYEQVIIEDKIEKERSKA
		1			}	KVKQDLLELKSVIKLQAWWRGTMIRREIGGF
						KM
					1003	FRORAVKMAAVVEVEVGGGAAGERELDEV
704	2054	Α	5381	1	1003	DMSDI SPEFOWRVEHARMHAKHRGHEAMH
		1	1	1		A EMVI ILIATI. VVAOLLL VOWK QRHPKSYN
		1	1	1		MUTI FOMWVVPLYFTVKLHWWRFLVIWILF
		.	}			SAVTAFVTFRATRKPLVQTTPRLVYKWFLLIY
		1	1			KISYATGIVGYMAVMFTLFGLNLLFKIKPEDA
		į.				MDFGISLLFYGLYYGVLERDFAEMCADYMA MDFGISLLFYGLYYGVLERDFAEMCADYMA
		1		Ļ		STIGFYSESGMPTKHLSDSVCAVCGQQIFVDV
						SEEGIIENTYRLSCNHVFHEFCIRGWCIVGKK QTCPYCKEKVDLKRMFSNPWERPHVMYGQL
						LDWLRYLVAWQPVIIGVVQGINYILGLE
	ĺ					IYDRDPLQLATRAGQPLDINMAGEPKPYRPKP
705	2055	A	5396	3	675	GNKRPLSALYRLESKEPFLSVGGYVFDYDYY
						PDDEVNRLEDYHGRVPPPPRAVIPLKRPRVA
						VTTTRRGKGVFSMKGGSRSTASGSTGSKLKS
		İ				DELOTIKKEL TOIKTKIDSVLGRLDKIEKQQK
		Ì				AFAFAOKKLLEESLVLIOEECVSEIADHSTEEP
		ļ				AEGGPDADGEEMTDGIEEAFDEDGGHELFLQ
			İ			IK
	2056	+	5410	12	98	GRVGLNLEGRGCSEPKWRHCTPTWATEQDSI
706	2056	/ A	0,10	17		S
707	2057	A	5415	6	287	PFKLTPSFLSHAFSSGQERKVFIELNHIKKCNT
707	2037	1^	1 3413	1		VRGVFVLEEFGNYTILLLGLDSHGSNSNLGAP
		i	j	1		EEGLGAGRKRTSVEKSGGAGVTRKKRDP
708	2058	A	5423	3	291	SSSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPTLRAITLTVRVCGFIPEVSKTTNPLGRTNNS
1 ,08	2000	1				GCTIFKTVTLTARSTASLLKSVRPRTHQKE
1		- 1				RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG
709	2059	A	5424	679	347	SEFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ
1			ì	1	{	VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK
		1	1			GKWFCPRCVQEKRKKK
	1	1	<u> </u>			QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS
	1		5442	1073	559	GSLTPPVTPPITPSSSFRSSTPTGSEYDEEEVDY
710	2060	A	1442			
710	2060	A	3442		ļ	EESDSDESWTTESAISSEAILSSMCMNGGEEK
710	2060	A	3442			EESDSDESWTTESAISSEAILSSMCMNGGEEK
710	2060	A	)442			EESDSDESWTTESAISSEAILSSMCMNGGEEK
710	2060	A	3442			EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQ RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV
710	2060	A			210	EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSI CVPQYNKYREERVILFLKMASGHAFQP
710	2060	A	5449	3	319	EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP DI VKRIRDAIRMGLSARHVPSLILETKGIPYTI
				1	319	EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQ: RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQF DI VKRIRDAIRMGLSARHVPSLILETKGIPYTI
				1	319	EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQ: RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQF DLVKRIRDAIRMGLSARHVPSLILETKGIPYTI NGKKVEVAVKQIIAGKAVEQGGAFSNPETLL
	2061	A	5449			EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQ! RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPSLILETKGIPYTI NGKKVEVAVKQIIAGKAVEQGGAFSNPETLE LYRDIPELQGF  BPTFGHGDFWMOPLTKDAGMSLSSVTLASAI
				91	319	EESDSDESWTTESAISSEAILSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQ! RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ GDSLCVPQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPSLILETKGIPYTI NGKKVEVAVKQIIAGKAVEQGGAFSNPETLL

			1000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	in ID NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience	,		714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			Ì	peptide	1	/=possible nucleotide deletion, \=possible
			1	sequence		nucleotide insertion
			<del> </del>	Sequent		KAPELLQGQSEDEQPDASQMHVYSLGMTLY
		Ì	1	Ì	1	WSAGFHVPPHQPLQLCEPLHSILLTMCEDQPH
	1		1			RRCTLQSVLEACRVHEKEVSVYPAPAGLHIR
		1		1		RLVGLVLGTISEVSREPCFSSSSCWSCVAIKI
713	2063	A	5506	22	478	VEELILVSRLDPHLHTPMYFFLAHLSFLDLSFT
/13	2005	1.	1	1		TSSIPQLLYNLNGCDKTISYMGCAIQLFLFLGL
	1					GGVECLLLAVMAYDRCVAICKPLHYMVIMN
	1		-	1	1	PRLCRGLVSVTWGCGVANSLAMSPVTLRLPR
	1		1	l .		CGHHEVDHFLCEMPALIRMACISTV
714	2064	A	5514	25	220	AIRPYWCENNIIGIGKLSTADGKAFADPEVLR
/ 14	2004	1				RLTSSVSCALDEAAAALTRMRAESTANAGQS
	1	İ		1		DK DK
715	2065	A	5526	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAM GRTALFHHSGGSSGYESLRRDSEATGSASSAP
		1				DSMSESGAASPGARTRSLKSPKKRATGLQRR
			1	}	}	RLIPAPLPDTTALGRKPSLPGQWVDLPPPLAG
						SLKEPFEIKVYEIDDVERLQRPRPTPREAPTQG
		1		1		LACVSTRLRLAERRQQRLREVQAKHKHLCEE
				İ		LAETQGRLMLEPGRWLEQFEVDPELEPESAE
				1	<u> </u>	YLAALERATAALEQCVNLCKAHVMMVTCFD
	1	{		-	Ì	ISVAASAAIPGPOEVDV
				1.50	790	SPGYGENKETVTSXNIAVPLCEMNKIYSYYSL
716	2066	Α	5529	458	190	**COSERTMOLVLEMCNTNSIHWCGISGRQLG
			1		1	KLHPSSSLCLALTLLSSVQGLQSISGLRLTDTF
	1	ì	1		ł	IKRTYEYDDIAOVCV
		A	5531	13	460	NSEDLLKYFNPESWQEDLDNMYLDTPRYRG
717	2067	A	3331	'	1.55	RSYHDRKSKVDLDRLNDDAKRYSCTPRNYS
		1			]	VNIREELKLANVVFFPRCLLVQRCGGNCGCG
			ļ	i		TVNWRSCTCNSGKTVKKYHEVLQFEPGHIKE
	1		l	1		RGRAKTMALVDIQLDHHERCDCICSSRPPR
718	2068	A	5586	311	88	AVLKNMAPMTALGLLDLHILNLILFLSAGED
/10	2008	1				TSVVSEIMMYILLVFLTLWLLIEMIYCYRKVS
1						KAEEAAQENA
719	2069	A	5598	1	330	KNCANEAVVQKILDRVLSRYDVRLRPNFGSN LATNSTRGLNEDELMAHGQEKDSSSESEDSC
/13	2007	1				PPSPGCSFTEGFSFDLLNPDYVPKVDKWSRFI
						PPSPGCSFTEGFSFDLLRFDT VI KVDR WORLD
	1	1				FPLAFGLFNIVAAERC LPPAQIPEAWLLLANVVVVLILVPLKDRLIDP
720	2070	A	5628	798	148	LLLRCKLLPSALQKMALGMFFGFTSVIVAGV
		ł	1			LEMERLHYIHHNETVSQQIGEVLYNAAPLSIV
		[		1		WQIPQYLLIGISEIFASIPGLEFAYSEAPRSMQ
1	}		.			AIMGIFFCLSGVGSLLGSSLVALLSLPGGWLF
<b>\</b>		Ì	1			CPKDFGNINNCRMDLYFFLLAGIQAVTALLF
	}					VWIAGRYERASQGPASHSRFSRDRG
					626	MSALIVRKLRSAELTLFSELPTVLGANVNAA
721	2071	A	5632	146	536	KLHETALHHAAKVKNVDLIEMLIEFGGNIYA
1				1		PONRGKKPSDYTWSSSAPAKCFEYYEKTPL
		1	Į.			LSQLCRVNLRKATGVRGLEKIAKLNIPPRLII
1	1	i			ļ	YLSYN
-		1			2006	CPSLDIRSEVAELRQLENCSVVEGHLQILLM
722	2072	A	5638	3	3806	TATGEDERGLSFPRLTOVTDYLLLFRVYGLE
	l			1		I RDL FPNLAVIRGTRLFLGYALVIFEMPHLRI
		1				VALPAL GAVERGAVRVEKNOELCHLSTIDW
				1		GLLQPAPGANHIVGNKLGEECADVCPGVLG
			1	1	1	
						AGEPCAKTTESGHTDYRCWTSSHCQRVCPC
						AGEPCAKTTFSGHTDYRCWTSSHCQRVCPC
						AGEPCAKTTFSGHTDYRCWTSSHCQRVCPC HGMACTARGECCHTECLGGCSQPEDPRACV
						AGEPCAKTTFSGHTDYRCWTSSHCQRVCPC HGMACTARGECCHTECLGGCSQPEDPRACV ACRHLYFQGACLWACPPGTYQYESWRCVT ERCASI HSVPGRASTFGIHOGSCLAQCPSGF
						AGEPCAKTTFSGHTDYRCWTSSHCQRVCPC

Seq III wince cutder sequence where the control of the control of the cutder sequence where the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the							
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nucice ceticle sequence  USN 19496   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948   1948					beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
denote wence wence where the service of the service of the service of the service of peptide sequence wence wence where the sequence wence of peptide sequence wence of peptide sequence wence of peptide sequence wence of peptide sequence wence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of				in			F=Phenylalanine, 0=Olychic, 1=Tristicale,
sequence    Sequence   914    0			ł	USSN		corresponding	1=1soleucine, K-Lysine, E Bedeine,
uence residue of peptide residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence pept		ł -		09/496			M=Methonine, N=Asping S=Serine.
residue of peptide sequence   Sequence   Y=Tyrosine, X=Usknown, "Stop codon, y-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, t-possible nucleotide deletion, text to text the			1	914			T-Threonine V=Valine, W=Tryptophan,
Popsible miclotide deletion, 'Popsible miclotide insertion included insertion of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property		ļ			•		V=Tyrosine X=Unknown, *=Stop codon,
nucleotide insertion  Sequence  QDLVGCTHVEGSILINLRQGYNLEPG GLVETTIGFLKIKHSFALVSLGFFKNL AMVDGNYTLYVLDNONLOGLGSW PVGKIYFAFNPRLCLEHIYRLEEVTGI KAENPRTNGDRAACQTRILREVSNN LILRWERYEPLEARDLLSFIVYYKESP HIVGPDAGGTGSWNLDVELPLSRIVG ASLKPWTQVAVFVRAITLITEEDSPH PIVYLRTLPAAPTVPQOVISTSNSSSH KPPTQRNGNLTYYLLVURALAEDGI YCHGLILPTSNNDPRFDGEDGDPE CCPCQHPPPGQVLPPLEAQEASTQKK NATIPISPWKVTSINKSPQRDSGRIRR RLGGNSSDFEIGEDEKVPRERAVLSGI RICHARAHTVGGSAATFVFAR ADGPGKVAWFASSNNSVLJRULEF ILKYEIKVRRLGEBATVLCVSRLRVA HLALLPPGNYSARVRATSLAGNGSW YULGPEEDAGGLHVLLTATPVGLT LGFFYGKKRNRTLYASVNPEYFSAS EWEVPREQSIBRELGQGSFGMVVEG AGESSTVALKTVNELASPRECIEFL KAFKCHHVVRLLGVVSQGCPTLVIR GDLKSHLRSLRPEAENNFGLGPAAL AGEIADGMAYLAANKFVRDLAAR DPTVKIGDFGMTRDVVETDYYYKKG VRWAMPESLKOGIFTHISDVWSFGY TLAEQPYGGLSNEGVUKPVMDGGV PLQLQELMSKCWQNPRELRPSTHIL RPSFRLLSFYYSPECRGARGSLPTTD TPRDCSPONGGPGH LAWDDNILPEKEKETDKKRRKKK EEPQPPPPSVIKIPMESVQSDPQNGI SSSWSYSIS.  722 2073 A 5672 1 216 LAWDDNILPEKEKETDKKRRKKK EEPQPPPPSVIKIPMESVQSDPQNGI SSSWSYSIS.  7724 2074 A 5704 4235 940 ARGRESRFVWAASWGGRGRPAARI ARGRELDREDGDVDPDLCCALCH LTTTCGHVFCAGCVLPWVVQEGGC LSAKELNIVLPLRKLILKDIKCAY VVKLQQLPEHLERCDFAPARCHAA RRDVEAHMBACADARFVGCCGG GEGRAGGHCCARALRAHNGALQAA ALKKEALRAGKRESLUVAQLAAAC ALRYQKFTEYSARLDSLSRCVAA ETKSLTLVLHIRDGSGLGFNIGGRS SSSGGIFVSKIVDSGPAAKEGGLOH KMSSTSPVLDPYLLPEHPSAHEY GDHGEMDREGELELEEVDLYRINN VCYRTDDEDDIGIYISEIDPNSIAAK DRIQNIGGEVQNREEAVALLTSEEN ARELQLDEGWMDDRNDFLDDL EQHHQAMMOFTASVLQQKKHDEDG ILSNOHENDSGVGRTDESTRNDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS DDATASSNPLAGGRKLTSCONTLG NOSESTENDESS			İ			sequence	/=possible nucleotide deletion, \=possible
QDLVGCTHVEGSLILNLRQCYNLERG GLVETTIGFLKIKRSTAUVSLGFFKNL AMVDGNYTLYVLDNONLQQLGSWY PVGKIYFAFRPTLCLEHIYRLEEVTGI KAEINPRTLCEHIYRLEEVTGI KAEINPRTLCEHIYRLEEVTGI KAEINPRTLCEHIYRLYTKESPH HVGPDAGGTQSWNLLDVELPLSRTQI ASI,KPWTQYAVFVARILLTTEEDSPH PIVYLRTLPAAPTVPQDVISTSNSSHH KPPTQRNGNLTYYLUWQRLAEDGI YCHRGILHITSNNDPRFDEGDGPFE CCPCQHPPPGQVLPPLEAQEASTQIKK NAITHISPWKVTSINKSPQRDSGRIRR RLGGNSSDEEJQEDKVYBERAVLSGI RIDIHACNHAAHTIVCCSAATIVFAR ADGIPGKVAWEASSKNSVLLRVLLER ILKYEKYRRLGEEATVLCVSRLRYA HLALLPPGNYSARVRATSLAGNGSW YULGPEEDAGGHAVLLTAPVGLIT LGFFYGKKRNRTLYASVNPEYFSAS EWEYPREQSIBIRELQGGSFGMYYEG AGESTPVALKTYNELASPRECIEFL KAFKCHHVVRLLGVVSGQOPTLVIN GDLKSHLRSLRPEAENNFGLEPQFAL AGEIADGMAYLAANKFVHRDLAAR DFITVKIGDFGMTEDVVETDYYRKG VRWMAFESLKDGIFTHSDVWSFGI TLAEQPYQGLSJNEQVUKFVMDGGY PLQLQELMSRCWQPNFRLRPSFTHIR RPSFRLLSFYYSPECRAGRSSLPTTD TFRDCSRQNGGFGH  723 2073 A 5672 1 216 LAWIDNILPEKEKETDKKRKKKG EEPQFPPPSVKIPMESVQSDPQNGEI SSSWSYSL 724 2074 A 5704 4235 940 ARGRESRFVWAASWGGRGFAAR ARGREDAFDARDACHARAR RRDYGAHMBACADARFVGCQGG GFGRAGGHCCARALRAHNGALQAA ALKYGKKFFYSALDSLSRCVAA ARGRESRFVWAASWGGRGFAAR RRDYGAHMBACADARFVGCQGG GFGRAGGHCCARALRAHNGALQAA ALKYGKFFYSSALDSLSRCVAA ALKYBLKFETSSALDTIDTIFT KMSSPSPVLDPYLLFELHLILDIKCAY VVKLQQLPHLERCDFAPARCRAG RRDYSATMDQAVEAFKTAKEPIV PRIKMFTIPSSGLVDTGTQTIDTIFT KMSSPSPVLDPYLLFELHLILDIKCAY VVKLQQLPHLERCDFAPARCRAG RRDYSATMDQAVEAFKTAKEPIV PRIKMFTPSSGLVDTGTQTIDTIFT KMSSPSPVLDPYLLFELHLILDIKCAY VVKLQQLPHLERCDFAPARCRAG RRDYSATMDQAVEAFKTAKEPIV PRIKMFTPSSGLVDTGTQTIDTIFT KMSSPSPVLDPYLLFELHLILDIKCAY VVKLQQLPHLERCDFAPARCRAG RRDYSATMDQAVEAFKTAKEPIV PRIKMFTPSSGLVDTGTQTIDTIFT KMSSPSPVLDPYLLFELHLIKULVALTSEEN ARGLQLDEGWMDDRNDTLIDDL EQHHQAMOFTASVLQQKKHDEDG LISNQHEADSGVGRTDESTRNDESS DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC DDATASSNPLAGORGLUTSCOPTIC			ł				muslestide insertion
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KSDKDSSSAYNTGESCRSTPLTLEIS		1					KSDKDSSSAYNTGESCRSTPLTLEISPDNSLRI
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ì	in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	Į	09/496	correspondi	acid residue	GeGlutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	1		amino acid	sequence	V=Tyrosine X=Unknown, *=Stop codon,
	ļ	ì	1	residue of	sequence	/=possible nucleotide deletion, \=possible
		1		peptide sequence	<b>!</b>	avalentide insertion
		<u> </u>	ļ	sequence		AAEGISCPSSEGAVGTTEAYGPASKNLLSITE
						DDEVGTPTYSPSLKELDPNOPLESKERRASDG
	1	ł		1		SRSPTPSOKLGSAYLPSYHHSPYKHAHIPAHA
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	1	1				NKKIFDNWMTIQELLTHGTKSPDGTRVYNSF
		1				VTTV
	1	<del> </del>	5707	13	1770	OVETEVER A DV A NDK PKTI. VVK VOKKAADLP
725	2075	Α	3/0/	3	1 ****	DPDTWKGRFDFLMSCVGYAIGLGNVWKFP1
		1				I CCKNGGGAFLIPYFLTLIFAGVPLFLLEUSLU
		]		1		OVTSIGGI GVWKLAPMFKGVGLAAAVLSFW
	1	1				T ATTOVIVIEW ATTYLYNSFTTTLPWKQCDNP
	1			1		WNTDRCFSNYSMVNTTNMTSAVVEFWERN
				1		MHQMTDGLDKPGQIRWPLAITLAIAWILVYF
						CIWKGVGWTGKVVYFSATYPYIMLIILFFRGV
		i				TLPGAKEGILFYITPNFRKLSDSEVWLDAATQ
		İ				IFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVC
	1	1			-	CINSCTSMFAGFVIFSIVGFMAHVTKRSIADV
	1	1				AASGPGLAFLAYPEAVTQLPISPLWAILFFSM
		- 1				LLMLGIDSQFCTVEGFITALVDEYPRLLRNRR
		-				ELFIAAVCIISYLIGLSNITQGGIYVFKLFDYYS
		ļ				ASGMSLLFLVFFECVSISWFYGVNRFYDNIQE MVGSRPCIWWKLCWSFFTPIIVAGVFIFSAVQ
						MVGSRPCIWWKLCWSFFFFFWAGVITISMVQ MTPLTMGNYVFPKWGQGVGWLMALSSMVL
ŀ	i	1	1		İ	IPGYMAYMFLTLKGSLKQRIQVMVQPSEDIV
		1				RPENGPEQPQAGSSTSKEAYI
]		1	1			PRRDPGRTPELRGSAPRKTGANMPVRRGHVA
726	2076	A	5711	156	423	PONTFLGTIIRKFEGONKKFIIANARVONCAII
120	20.0					YCNDGFCEMTGFSRPDVMQKPCTCD
		1				HASEYFFKLCSFQVFLSFPLATIVIDVGLVVIP
727	2077	A	5716	3	274	LVKSPNVHYVYVLLLVLSGLLFYIPLIHFKIRI
121	20		1			AWFEKMTCYLQLLFNICLPDVSEE
		- [				IQASRASPYPRVKVDFALSCHEDLLAPISEPIE
728	2078	A	5737	1899	649	WKYHSPEEEISLGPACWLWDFLRRSQQAGFI
120	20.0				1	LPLSGGVDSAATACLIYSMCCQVCEAVRSGN
[	ł	i	Ĩ			EEVLADVRTIVNQISYTPQDPRDLCGRILTTC
	1	- 1				YMASKNSSQETCTRARELAQQIGSHHISLNIC
		\				PAVKAVMGIFSLVTGKSPLFAAHGGSSRENL
				Ì		ALQNVQARIRMVLAYLFAQLSLWSRGVHGC
1		-		İ		LLVLGSANVDESLLGYLTKYDCSSADINPIGO
						ISKTDLRAFVQFCIQRFQLPALQSILLAPATAE
			-	- [		LEPLADGQVSQTDEEDMGMTYAELSVYGKI
ł		1			1	RKVAKMGPYSMFCKLLGMWRHICTPRQVAL
	ł	{		1		KVKRFFSKYSMNRHKMTTLTPAYHAENYSP
1	ļ					DNRFDLRPFLYNTSWPWQFRCIENQVLQLEF
1		1		1		DUKLDEKLE IN 19 M. A GLYCTELIA LEADER
		1				AEPQSLDGVD PGCAARLSRARAPGPGAAGAGRKRLADPGP
729	2079	A	5741	1	5976	PGCAARLSKARAPUPUAAUAURARLADPUI
123	2017	1				PASRRLRAPGSRPRLAPCTRRAAQPAHARM. PRAAGGAPLSARAAAASPPPFQTPPRCPVPLI
		1				LLLLLGAARAGALEIQRRFPSPTPTNNFALDO
					ļ	AAGTVYLAAVNRLYQLSGANLSLEAEAAVO
			1			AAGTVYLAAVNKLYQLSUANLSLEAEAAAV
				1	1	PVPDSPLCHAPQLPQASCEHPRRLTDNYNKII PVPDSPLCHAPQLPQASCEHPRRLTDNYNKII
1		İ	1			QLDPGQGLVVVCGSIYQGFCQLRRRGNISAV
1	ļ	-				AVRFPPAAPPAEPVTVFPSMLNVAANHPNAS TVGLVLPPAAGAGGSRLLVGATYTGYGSSFI
1		1	1	ŀ	ı	TVGLVLPPAAGAGGSKLLVGAIIIGIGSSFI
		1			ì	PRNRSLEDHRFENTPEIAIRSLDTRGDLAKLF

CIO IN	SEO ID	N.d.a.	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
10: of	NO: of peptide	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
iucl-		1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
цепсе			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ł	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
					saquence	/=possible nucleotide deletion, \=possible
	Ì	i	1	peptide		nucleotide insertion
		<u> </u>	<del></del>	sequence		FDLNPSDDNILKIKQGAKEQHKLGFVSAFLHP
	}	}	ŀ		İ	SDPPPGAQSYAYLALNSEARAGDKESQARSL
		ļ		1		LARICLPHGAGGDAKKLTESYIQLGLQCAGG
			ļ		]	AGRGDLYSRLVSVFPARERLFAVFERPQGSPA
		1				ARAAPAALCAFRFADVRAAIRAARTACFVEP
		ļ				APDVVAVLDSVVQGTGPACERKLNIQLQPEQ
		1				LDCGAAHLQHPLSILQPLKATPVFRAPGLTSV
		1			ļ	AVASVNNYTAVFLGTVNGRLLKINLNESMQ
		1		ĺ		VVSRRVVTVAYGEPVHHVMQFDPADSGYLY
			1			LMTSHQMARVKVAACNVHSTCGDCVGAAD
						AYCGWCALETRCTLQQDCTNSSQQHFWTSA
		}		Ì	}	SEGPSRCPAMTVLPSEIDVRQEYPGMILQISGS
		1		1		LPSLSGMEMACDYGNNIRTVARVPGPAFGHQ
						LAYCNLLPRDQFPPFPPNQDHVTVEMSVRVN
						GRNIVKANFTIYDCSRTAQVYPHTACTSCLSA
	}	1			}	QWPCFWCSQQHSCVSNQSRCEASPNPTSPQD
		1				CPRTLLSPLAPVPTGGSQNILVPLANTAFFQG
						AALECSFGLEEIFEAVWVNESVVRCDQVVLH
	1	1				TTRKSQVFPLSLQLKGRPARFLDSPEPMTVM
						VYNCAMGSPDCSQCLGREDLGHLCMWSDGG
-1	1					RLRGPLQPMAGTCPAPEIRAIEPLSGPLDGGT
						LLTIRGRNLGRRLSDVAHGVWIGGVACEPLP
	İ	-	-	1	İ	DRYTVSEEIVCVTGPAPGPLSGVVTVNASKE
						GKSRDRFSYVLPLVHSLEPTMGPKAGGTRITI
		1				HGNDLHVGSELQVLVNDTDPCTELMRTDTSI
	1	Ì				ACTMPEGALPAPVPVCVRFERRGCVHGNLTF
	1				İ	WYMQNPVITAISPRRSPVSGGRTITVAGERFH
		1	- 1	ļ		MVQNVSMAVHHIGREPTLCKVLNSTLITCPSI
	1	1				GALSNASAPVDFFINGRAYADEVAVAEELLD
	1	1				PEEAQRGSRFRLDYLPNPQFSTAKREKWIKH
			1			HPGEPLTLVIHVSTKGAGKEQDSLGLQSHEY
				]		RVKIGQVSCDIQIVSDRIIHCSVNESLGAAVGC
	1		1	1		LPITIQVGNFNQTIATLQLGGSETAIIVSIVICS
		1				LLLLSVVALFVFCTKSRRAERYWQKTLLQME
		1		]		EMESQIREEIRKGFAELQTDMTDLTKELNRSC
						GIPFLEYKHFVTRTFFPKCSSLYEERYVLPSQT
		1	ľ			LNSQGSSQAQETHPLLGEWKIPESCRPNMEE
						GISLFSSLLDNKHFLIVFVHALEQQKDFAVRD
		1	1			RCSLASLLTIALHGKLEYYTSIMKELLVDLID
		1		1		ASAAKNPKLMLRRTESVVEKMLTNWMSICM
	ļ	- (	1			YSCLRETVGEPFFLLLCAIKQQINKGSIDAITG
	İ	Ì				KARYTLNEEWLLRENIEAKPRNLNVSFQGCG
	Ì	l.		1		MDSLSVRAMDTDTLTQVKEKILEAFCKNVPY
	1	}	1			SQWPRAEDVDLEWFASSTQSYILRDLDDTSV
						VEDGRKKLNTLAHYKIPEGASLAMSLIDKKD
			ļ		1	NTLGRVKDLDTEKYFHLVLPTDELAEPKKSH
		1	1	1	1	ROSHRKKVLPEIYLTRLLSTKGTLQKFLDDLF
	}	}				KAILSIREDKPPLAVKYFFDFLEEQAEKRGISI
	1				1	PDTLHIWKTNSLPLRFWVNILKNPQFVFDIDK
		1				LDTILD TO CANTO VELD TO CALCULATION OF CALCULATION
	1	-		1	}	TDHIDACLSVIAQAFIDACSISDLQLGKDSPTN
		ł				KLLYAKEIPEYRKIVQRYYKQIQDMTPLSEQE
						MNAHLAEESRKYQNEFNTNVAMAEIYKYAK
					1	RYRPQIMAALEANPTARRTQLQHKFEQVVAI
		}				MEDNIYECYSEA
730	2080	A	5744	3	292	QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ
150	2080	^	7,	1-		VANGKGNORNMGSPQPSLLAFERNLELQIMO
						LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT
						LKD
	2081	+	5747	+1	382	FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC FRVDEVNWTTWNT.VVGIINEDPGNCEGVKR
731						

	00010	1/24	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid.
O: of	NO: of	hod	1 -	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
ence	1		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
CIICO	1	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	1	residue of	sequence	Y=Tyrosine, X=Unknown,stop codors,
		\	1	peptide		/=possible nucleotide deletion, \=possible
			1	sequence	Į.	nucleotide insertion
			<del></del>	sequence	<del> </del>	LSFSLRSSRVSGRHWKNFALVPLLREASARD
		)	1	}		RQSAQPEEVYLRQFSGSLKPEDAEVFKSPAAS
	1	l	1	1	1	
	1	1	1	_	l	GEK CTP IDATED TO CTP IDATED TO THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON O
22	2082	A	5753	198	3	AQAESSTVASPEATAGPLCTRIPNVPPPTPIRP
32	2002	1 ^	1 3,755			PGKLQAQLPCPSPVRFTSARIPPASRPQTKS
		<b>↓</b>	COSA	2	2223	AAGPPGLEAEGRAPESAGPGPGGDAAETPGL
33	2083	Α	5754	2	2223	DRAUGGTI MMAFRDYTVOIANONISVSSSTAL
		1	1	<u> </u>		SVANCLGAQTVQAPAEPAAGKAEQGETSGR
		1	1		ļ	EAPEAPAVGREDASAEDSCAEAGASGAADG
	İ	1	1	1		EAPEAPAVGREDASAEDSCALAGASOFE ES
	1		j	}	1	ATAPKTEEEEEEEETAEVGRGAEAEAGDLEQ
	1	1	Į.		1	LNRTSTSTKSAKSGSEASASASKDALQAMILS
	1	1			1	I PRVHCENPASCKSPTLSTDTLRKRLYRIGLN
	1	Į.		1	1	I ENTRIPDICTION LISRGEIPDTPIGVAHFLLQKK
		ŀ	1		1	GLSRQMIGEFLGNSKKQFNRDVLDCVVDEM
	1		ł	}	1	DESSMELDEALRKEQAHIRVQGEAQKVERLIE
	1		1			AFSQRYCMCNPEVVQQFHNPDTIFILAFAIILL
	1			ţ	i	AFSQRYCMUNPEV VQQFANI DTII ILAI 74102
	l.	i	1			NTDMYSPNIKPDRKMMLEDFIRNLRGVDDG
		Į		ì		ADIPRELVVGIYERIQQKELKSNEDHVTYVTK
			1	1	ļ	VEKSIVGMKTVLSVPHRRLVCCSRLFEVTDV
	1	1			1	NKLOKOAAHOREVFLFNDLLVILKLCPKKKS
		l		1	Ì	SSTYTFCKSVGLLGMQFQLFENEYYSHGITLV
	- \	ĺ				TPLSGSEKKQVLHFCALGSDEMQKFVEDLKE
		Ì		1	· I	TPLSGSERRQVEHICAEGSDENQIA VEDELE
	1	-	i i	}	1	SIAEVTELEQIRIEWELEKQQGTKTLSFKPCGA
	1	ĺ	1		1	QGDPQSKQGSPTAKREAALRERPAESTVEVS
	1					HNRLQTSQHNSGLGAERGAPVPPPDLQPSPPI
	- 1	1	1	ļ		OOTPPI PPPPPTPPGTLVOCQQIVKVIVLDKPQ
		1	1	1		I ARMEPI I SOALSCYTSSSSDSCGSTPLGGPG
	- 1	1	- 1			SPVKVTHQPPLPPPPPPYNHPHQFCPPGSLLH
	ì	1	1			GHRYSSGSRSLV
	ĺ		l l			GHK 1 2202K2L A
70.1	2084	HA	5788	8	362	SSVMGDLVGQGLEEQIVARDENSWLIDGGT
734	2084	Α.	3700			IDDVMRVLDIDEFPQSGNYETIGGFMMFMLR
	1			İ		KIPKRTDSVKFAGYKFEVVDIDNYRIDQLLV
	1	Ì	!			PIDSKATALSPKLPDAKDKEESVA
	1	1				MVFSAVLTAFHTGTSNTTFVVYENTYMNITL
735	2085	A	5827	1	1257	PPPFQHPDLSPLLRYSFETMAPTGLSSLTVNS
133	1 2000			İ		PPPFUHPULSPLLKTSTETMALT GEOGET
	ì	- 1	- }	1		AVPTTPAAFKSLNLPLQITLSAIMIFILFVSFLO
	}	1	1	ì	i	NLVVCLMVYQKAAMRSAINILLASLAFADM
		- 1		1		I I AVI NIMPEAL VIII TTRWIFGKFFCRVSAM
	l l		- 1			EWI EVIEGVAILLISTORFLIIVORODKLNPYK
	1					AKVLIAVSWATSFCVAFPLAVGNPDLQIPSR
	1	ĺ	1			PQCVFGYTTNPGYQAYVILISLISFFIPFLVILY
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	1	ļ	1	1		SFMGILNTLRHNALRIHSYPEGICLSQASKLG
		1	1			MGLQRPFQMSIDMGFKTRAFTTILILFAVFIV
	1	1	- 1		1	WAPFTTYSLVATFSKHFYYOHNFFEISTWLL
	1		- [		1	WI CVI KSAI NPLIYYWRIKKFHDACLDMM
	1		1	1	1	KSFKFLPQLPGHTKRRIRPSAVYVCGEHRTV
		1				FTRSDELARHYRTHTGEKRFSCPLCPKQFSR
77/	2086	A	5870	3	268	FIRSUELARMIKINI GERRAGGILGI KQI BIG
736	2080	^	1 33.0	1		DHLTKHARRHPTYHPDMIEYRGRRRTPRIDF
	i	1	1	1		LTSEVESSASGSGPGPAPSFTTCL
					621	L TWPOLELETLPELLHMSRPAEDGPSPGALV
737	2087	A	5871	2	521	RSSSLGYISKAEEYFLLKSRSDLMFEKQSERI
			1	İ	İ	GLARRLTTARRPPASSEQAQQELFNELKPAV
		1	ļ			GLAKKLI I AKKITASSEVAVVELITIELKI AT
		-				DGANFIVNHMRDQNNYNEEKDSWNRVART
	1	1	}	]		VDRLCLFVVTPVMVVGTAWIFLQGVYNQPI
		- 1	1			OPERGDRYSYNVODKRFI
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		A	5881	1	1160	LANIALIMENTAL LIMING PROPERTY OF
720	ኃስያያ	1 ~	1 - 30.	1	i	LLDSSKLCDYENRFNTSKGGELPDRPAGVG
738	2088	i		I		
738	2088			- [	İ	YSAMWQLALTLILKIVITIFTFGMKIPSGLFIP
738	2088					YSAMWQLALTLILKIVITIFTFGMKIPSGLFII MAVGAIAGRLLGVGMEQLAYYHQEWTVFI

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-A coortic Acid F=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I=Isoleucine K=Lvsine, L=Leucine,
otide	seq-	1	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	neuce		09/496	correspondi	acid residue	C=Glutamine R=Arginine, S=Serine,
ience	1	1	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
		1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	l.	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	<b>\</b>	1	peptide	}	nucleotide insertion
	l	ł		sequence	<u> </u>	WCSQGADCITPGLYAMVGAAACLGGVTRMT
	1	<del>                                     </del>			1	VSLVVIMFELTGGLEYIVPLMAAAMTSKWVA
	1	1	]		ļ	DALGREGIYDAHIRLNGYPFLEAKEEFAHKTL
	]	ļ	ì		1	AMDVMKPRRNDPLLTVLTQDSMTVEDVETII
	1	[				AMDVMKPKKNDPLLIVEIQDSMITVLDVISIE
	<b>\</b>	1	1			SETTYSGFPVVVSRESQRLVGFVLRRDLIISIE
	1	1				NARKKODGVVSTSIIYFTEHSPPLPPYTPPTLK
		1	1		1	LRNILDLSPFTVTDLTPMEIVVDIFRKLGLRQC
		1	1	}		LVTHNGRLLGIITKKDVLKHIAQMANQDPDSI
		l	ì		1	LFN
			5892	2	916	TLQLAASVPFFAISLISWWLPESARWLIINGKP
739	2089	A	3692	2	1 3 1 2	DQALQELRKVARINGHKEAKNLTIEVLMSSV
		1	1			I VDEVASAKEPRSVI DI FCVPVLRWRSCAMLY
	1			1	1	VALEST I ISVVGI VEDLOSLGRDIFLLQALFGA
	1		1	1		LVDELCRATTALLI SFLGRRIIOAGSQAMAGL
	ł	1	1	1		ATT ANIMI VPODI OTLRVVFAVLGKGCFGISL
		1	\	ł	1	TOT TIVE A FI FPTPVRMTADGILH I VGRLUA
		1	İ	1	ì	AMORI II MSROALPLLPPLLYGVISIASSLVVI
	1	1	1	ļ		FFLPETQGLPLPDTIQDLESQKSTAAQGNRQE
	- 1		1			AETVESTSLLEIVALHGAL
		1	1		106	DDIVITI CIGENESVDGVHFLTOREVQNLWKE
740	2090	A	5900	2	426	NI III DTAKKHGYEVVDTFTTTMGKYKEFLQC
		-		ļ	i	KCGCHFHEVVKSKLSKEYNFIKMKRSRNHIM
	l	l	1			GRYFSNQSKLQQGTVTNFRSPYHVRGPINQV
		1	1	ł	(	CSEILLSRMCANKRTM
	}	į	ì			RMPESTLLIICENGYILEAPLPTIKQEEDDHDV
741	2091	A	5910	3	412	VSYEIKDMCIKCFHFSSVKSKILRLIEIEKRER
, 41	2051					QRELKEKIREERRNKLAAEMGEDGEKEFQEE
	1	-	1		<b>\</b>	EEEKEEEEEEPLPEIFIPSTPSPILCGFYSEPG
!			}		(	
	}					MGCRLLCCVVFCLLQAGPLDTAVSQTPKYLV
742	2092	A	5936	1	482	TOMGNDKSIKCEONLGHDTMYWYKODSKK
142	2052	1.				TOMONDKSIKCEONLOHDIMI WIRQUINI FLKIMFSYNNKELIINETVPNRFSPKSPDKAHI
Ì	[	-	i			FLKIMFSYNNKELINET VPNKF3FK3FDIGHT
Ì	1		ſ	1		NLHINSLELGDSAVYFCASSQDTALQSHCIPV
i		- 1	ł	ł		HKPPGSARKLQGSVCTCTQGSSLHSLMASDC
	İ	1		- {		VPVC
	1 0000		5938	<u>1</u>	1566	MNSFFGTPAASWCLLESDVSSAPDKEAGRER
743	2093	Α	ودور	1.	· ·	RALSVQQRGGPAWSGSLEWSRQSAGDRRRL
		- 1	[	1	l	CI CDOTAK SSWSRSR DRTCCCRRAW WILL VP.
		1		1	1	ADRARREREIMNEKWDINSSENWIPIWIYI
		ŀ	}	1		DTVILLI VSDINTTYVNYYLHOPOVAAIPIISI
				1		I IEEI CMMGNTVVCFIVMRNKHMHTVINLE
1		1			1	I TAIT AISDLI VGIFCMPITLLDNILAGWPFUNII
1		1			}	CVISCI VOGISVAASVFTLVAIAVDRFQCVV
1		1	(	{	1	DEVDUI TIKTA FVIIMIIWVI AITIMSPSAVML
1					1	UCEEV VOR VRI NSONKTSPVYWCKEDWPN
1				1		EMRKIYTTVLFANIYLAPLSLIVIMYGRIGISI
1			1			RAAVPHTGRKNQEQWHVVSRKKQKIIKMLI
1		1		1		VALLFILSWLPLWTLMMLSDYADLSPNELQ
	1			ĺ		VALLEILS WELL WILLIAM LED I ADESI NEDQ.
1		1				NIYIYPFAHWLAFGNSSVNPIIYGFFNENFRR
1		ŀ	l	1		FQEAFQLQLCQKRAKPMEAYALKAKSHVLI
1			j			TSNQLVQESTFQNPHGETLLYRKSAEKPQQE
		(	1	1		LVMEELKETTNSSEI
			- 600	149	327	CUVCVSHVAGSSGCPAGAGAGAVALGISAV
744	2094	A	5966	149	321	1 YDYOGGRLGVARGAWYMEAPDIRQGDM
					956	GAPHTDWAWAPTPMSGLGSGRGRQGILAS
745	2095	A	5970	413	856	DI SI DI LI AGVTGILATELFDOMARPAACM
		{	-			CGALMWIMLILVGLGFPFIMEALSHFLYVPF
1		,	i	1		GVCVCGAIYTGLFLPETKGKTFQEISKELHR
1	l.	1	1			
			1			NFPRRAQGPTWRSLEVIQSTEL

			1.650	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	l .	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ì	09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	Ì	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1	}	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	1		residue of	sequence	/=possible nucleotide deletion, \=possible
	Į.	1		peptide		nucleotide insertion
		·		sequence	<del> </del>	AQTARRIGLELDTEGHRLFVAFSGCIVYLPLS
746	2096	Α	5971	3	1343	RCARHGACQRSCLASQDPYCGWHSSRGCVDI
	1				1	RGSGGTDVDQAGNQESMEHGDCQDGATGSQ
	1	]	}		1	SGPGDSAYGVRRDLPPASASRSVPIPLLLASV
	1		ļ			AAAFALGASVSGLLVSCACRRAHRRRGKDIE
		1	1		,	TPGLPRPLSLRSLARLHGGGPEPPPPSKDGDA
		Į			}	VQTPQLYTTFLPPPEGVPPPELACLPTPESTPE
	1					LPVKHLRAAGDPWEWNQNRNNAKEGPGRSR
	1	1				GGHAAGGPAPRVLVRPPPPGCPGQAVEVTTL
		1				EELLRYLHGPQPPRKGAEPPAPLTSRALPPEP
	1			Ì		APALLGGPSPRPHECASPLRLDVPPEGRCASA
	1			}	1	PARPALSAPAPRLGVGGGRRLPFSGHRAPPAL
	1		i i			LTRVPSGGPSRYSGGPGKHLLYLGRPEGYRG
		1				RALKRYDVEKPQLSLKPPLVGPSSRQAVPNG
		1				
		į.				GRFNF DHASLPCSWNHRFDVETRHVFIGDHSGQVTI
747	2097	A	5998	2	754	LKLEQENCTLVTTFRGHTGGVTALCWDPVQ
' ' '	1	1			1	RVLFSGSSDHSVIMWDIGGRKGTAIELQGHN
	1	1				DRVQALSYAQHTRQLISCGGDGGIVVWNMD
	l	1	1	1		VERQETPEWLDSDSCQKCDQPFFWNFKQMW
}	1	1		1	1	DSKKIGLRQHHCRKCGKAVCGKCSSKRSSIPL
1					1	MGFEFEVRVCDSCHEAITDEERAPTATFHDSK
		1	1			HNIVHVHFDATRGWLLTSGTDKVIKLWDMT
	1	Ì			1	
ļ		1				PVVS AMVFGGVVPYVPQYRDIRRTQNADGFSTYV
748	2098	Α	6001	2	747	CLVLLVANILRILFWFGRRFESPLLWQSAIMIL
						TMLLMLKLCTEVRVANELNARRRSFTAADS
1	ł	ļ				KDEEVKVAPRRSFLDFDPHHFWQWSSFSDYV
}	ł	1				QCVLAFTGVAGYITYLSIDSALFVETLGFLAV
i	I	1	ł	·		LTEAMLGVPQLYRNHRHQSTEGMSIKMVLM
1	1	1				WTSGDAFKTAYFLLKGAPLQFSVCGLLQVLV
	j	1				DLAILGQAYAFARHPQKPAPHAVHPTGTKAL
			_			GRPDRSELVRMHILEETFAEPSLQATQMKLK
749	2099	A	6002	2	447	RARLADDLNEKIAQRPGPMELVEKNILPVDSS
1		-			1	VKEAIIGVGKEDYPHTQGDFSFDEDSSDALSP
		- 1			ł	DQPASQESQGSAASPSEPKVSESPSPVTTNTP
1		-1		İ	{	AQFASVSPTVPEFLKTPPTAD
						LLTQAMLVLPHRPQWFTPGPRLQAQGPCQEG
750	2100	A	6004	2	427	LLIQAMENEPHRIQUEDEDI NKBBNPOAKPDAV
		1		}	1	WRWELRLRNYVPEDEDLNKRRVPQAKPDAV QEKVKEQLEAAKPEPVIEEVDLAKLAPRKPD
1	1					WDLKRDVAKKLEKLLKRTQRAIAELIRERLK
						WULKEDVANALENDARTOKATABLIKEREK
						GQEDSLDSAVDAATEHKTC
751	2101	A	6007	33	1280	TDQAKVDNQPEKLVRSAEDVSTVPTQPDNPF
1 "		"			ſ	SHPDKLKRMSKSVPAFLQDESDDRETDTASE
		}		Ì		SSYQLSRHKKSPSSLTNLSSSSGMTSLSSVSGS
1	1			1	1	VMSVYSGDFGNLEVKGNIQFAIEYVESLKEL
1		1		İ		HVFVAQCKDLAAADVKKQRSDPYVKAYLLP
1			ľ	(		DKGKMGKKKTLVVKKTLNPVYNEILRYKIEK
-			1			QILKTQKLNLSIWHRDTFKRNSFLGEVELDLE
1				}		TWDWDNKQNKQLRWYPLKRKTAPVALEAE
)	}		}	1		NRGEMKLALQYVPEPVPGKKLPTTGEVHIWV
1			[	1		KECLDLPLLRGSHLNSFVKCTILPDTSRKSRQ
1						KTRAVGKTTNPIFNHTMVYDGFRPEDLMEAC
1						VELTVWDHYKLTNOFLGGLRIGFGTGKSYGT
	1					EVDWMDSTSEEVALWEKMVNSPNTWIEATL
		1	- 1	1		PLRMLLIAKISK
		}	į.	1		
			(020	100	1283	KEIESPEELISVKPLCLLLGVTCSQSMAFEELL
752	2102	A	6028	108	1283	KEIFSPFELISVKPLCLLLGVTCSQSMAFEELL SOVGGLGRFOMLHLVFILPSLMLLIPHILLENF
752	2102	A	6028	108	1283	KEIFSPFELISVKPLCLLLGVTCSQSMAFEELL SQVGGLGRFQMLHLVFILPSLMLLIPHILLENF AAAIPGHRCWVHMLDNNTGSGNETGILSEDA

			000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ		nucleotide	D=A spartic Acid. E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in		corresponding	1=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	<b>\</b>		1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	1	residue of	sequence	/=possible nucleotide deletion, \=possible
			İ	peptide	1	nucleotide insertion
	Ì	ļ	ì	sequence		LLRISIPLDSNLRPEKCRRFVHPQWQLLHLNG
	<del> </del>					TIHSTSEADTEPCVDGWVYDQSYFPSTIVTKW
		1				THSTSEADTEPCVDGWVTDQSTTTSTTVTK
	1	}	1		1	DLVCDYQSLKSVVQFLLLTGMLVGGIIGGHV
		ļ.	Į			SDRFGRRFILRWGLLQLAITDTCAAFAPTFPV
	1	Į.		1	}	YCVLRFLAGFSSMIIISNNSLPITEWIRPNSKAL
	i	Į.	Ì	į.		VVILSSGALNIGQIILGGLAYVFRDWQTLHVV
	ì	i	Ì			ASVPFFVFFLLSRWLVESARWLITTNKLDEGL
	1	1	ì		1	VALRKVARTNGIKNAEETLNIEVVRSTMQEE
	1	1	1			LDAAQTKTTVWDLFRNPSMRKRICILVFLRK
	1	ì	1			KNIKEKA
		<u> </u>			1470	DSEESIL RI IFEIHHSGEKGDIVVFLACEQDIEK
753	2103	Α	6043	1	1470	VCETVYOGSNLNPDLGELVVVPLYPKEKCSL
					1	FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN
		1				SVRFVIDVGVERRKVYNPRIRANSLVMQPISQ
		1				SQAEIRKQILGSSSSGKFFCLYTEEFASKDMTP
		1			1	LKPAEMQEANLTSMVLFMKRIDIAGLGHCDF
	Į.		1		1	MNRPAPESLMQALEDLDYLAALDNDGNLSE
	1					FGIIMSEFPLDPQLSKSILASCEFDCVDEVLTIA
	1	1	i	)	1	AMVTAPNCFSHVPHGAEEAALTCWKTFLHPE
	i	1		ļ		AMVIAPNOPHI NECCEVOVEKWORD
	i	1	i			GDHFTLISIYKAYQDTTLNSSSEYCVEKWCRD
	l					YFLNCSALRMADVIRAELLEIIKRIELPYAEPA
	-				ì	FGSKENTLNIKKALLSGYFMQIARDVDGSGN
	1				l l	YLMLTHKQVAQLHPLSGYSITKKMPEWVLF
	1	1		1		HKFSISENNYIRITSEISPELFMQLVPQYYFSNL
	1	1			1	PPSESKDILQQVVDHLSPVSTMNKEQQMCET
	}	ł			<b>{</b>	CPETEQRCTLQ
	2104	A	6055	2	394	YYALHHWPFPDLLCQTTGAIFQMNMYGSCIF
754	2104	^	0033	_		LMLINVDRYAAIVHPLRLRHLRRPRVARLLC
		1	-	i		LGVWALILVFAVPAARVHRPSRCRYRDLEVR
	Ì	1	İ	·		LCFESFSDELWKGRLLPLVLLAEALGFLLPLA
		1	1	1		AVVYSS
			6059	3	1795	LGLGSGTLLSVSEYKKKYREHVLQLHARVKE
755	2105	A	0039	1 3	.,,,	PNARSVKITKRFTKLLIAPESAAPEEALGPALE
	1	- 1		}		DEPGRARRSDTHTFNRLFRRDEEGRRPLTVVL
i			ł	l l		OCPAGIGKTMAAKKILYDWAAGKLYQGQVD
	ļ	1	ļ	i	1	FAFFMPCGELLERPGTRSLADLILDQCPDRGA
		l	ţ			DVDOMI AOPORLLFILDGADELPALGGPEAAP
l		1		1		CTDPFEAASGARVLGGLLSKALLPTALLLVII
1		- [				RAAAPGRLOGRLCSPQCAEVRGFSDKDKKK
						YFYKFFRDERRAERAYRFVKENETLFALCFV
		}			1	PFVCWIVCTVLRQQLELGRDLSRTSKTTTSVY
1	{			į		LLFITSVLSSAPVADGPRLQGDLRNLCRLARE
		- 1	1			GVLGRRAQFAEKELEQLELRGSKVQTLFLSK
	1					KELPGVLETEVTYQFIDQSFQEFLAALSYLLE
		ļ			- {	DGGVPRTAAGGVGTLLRGDAQPHSHLVLTT
	]		1		1	DGGVPKTAAGGVGTLLKGDAQFRONLVDT1
l .		i		!	1	RFLFGLLSAERMRDIERHFGCMVSERVKQEA
1		1		i		LRWVQGQGCPGVAPEVTEGAKGLEDTEE
1				İ		PEEEEGEEPNYPLELLYCLYETQEDAFVRQA
		- 1		İ		LCRFPELALQRVRFCRMDVAVLSYCVRCCPA
		ļ				GQALRLISCRLVAAQEKKKKSLGKRLQASLG
	1					GG
			7070	12	436	SCRPTRPAKPTGOGMGRFMLTLVCQGSIMMS
756	2106	A	6060	12	7.50	ARDLIMNNI TELOPGLEHHLRELEELRLSGNE
i			!		}	T SHIPGOAFSGLYSLKILMLHNNQLGGIPAQA
1	1		!		Į	LWELPSLQSLRLDANLISLVPERSFEGLSSLRH
1				İ		LWLDDNALTEIPS
		1 .	1			ITPLGLGAADMCAFPWLLLLLLQEGSQRRL
757	2107	A	6063	54	419	TIPLOCOFFICIAL OFFICE DE FIDDREVENII
757	2107	A	6063	54	419	WRWCGSEEVVAVLQESISLPLEIPPDEEVENII WSSHKSLATVVPGKEGHPATIMVTNPHYQG

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ليوا فيود فيما فيمد الباب الأساس

					S 5 4 4 2 2 2 2	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	пепсе	)	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	{	Ì	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	ļ			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
	}		į	peptide	1	/=possible nucleotide deterior, /-possible
	ì	1	}	sequence		nucleotide insertion
	+	<del> </del>	1			QILTMLLRSLQQPSASWPRDCSSSCSW
758	2108	A	6066	125	438	IGISCPATIFVPMFSHSLIGIGEEYQLPYYNMV
/38	2100	1				PSDPSYEDMREVVCVKRLRPIVSNRWNSDEC
ł		ł		1		LRAVLKLMSECWAHNPASRLTALRIKKTLAK
1	ļ					MVESQDVKI
	I	<del>  </del>	6072	3	650	PGRRFRPAALEERAMEKLREKVPFQNRGKGT
759	2109	A	6072		050	I SSIIPNNSDTRKATETTSLSSKPEYVNPDFRW
				1		SKDPSSKSGNLLETSEVGWTSNPEELDPIRLA
		1	1		]	LLGKSGLSCOVGSATSHPVSCOEPIDEDQRISP
ł	1	1	1	1	1	KDKSTAGREFSGOVSHOTTSENQCTPIPSSTV
ļ		1	,	1		HSSVADMQNMPAAVHALLTQPSLSAAPFAQ
1	1	)	1		i	RYLGTLPSTGSTTLPQCHAGNATVW
	_1		1,	<del> -</del>	730	PLRLTLMEEVLLLGLKDREGYTSFWNDCISSG
760	2110	A	6077	3	/30	LRGCMLIELPLRGRLQLEACGMRRKSLLTRK
1	1		\			VICKSDAPTGDVLLDEALKHVKETQPPETVQ
1	1	{	į	1		NWIELLSGETWNPLKLHYQLRNVRERLAKNL
	1	1		l .		VEKGVLTTEKQNFLLFDMTTHPLTNNNIKQR
		1	İ			LIKKVQEAVLDKWVNDPHRMDRRLLALIYL
		i				AHASDVLENAFAPLLDEQYDLATKRVRQLLD
1	l	1	1			LDPEVECLKANTNEVLWAVVAAFTK
}			1			IVSFHLSGFKKFVRPFSFLSVHGLQVDEYHSV
761	2111	A	6078	833	390	HQKLSADMADHSNLIRSLLVGAEDARLMRD
/ 01			1	1		HQKLSADMADHSNLIKSLLVGAEDAKLIVIKO
1	l		1	İ	1	MKTMKSRYMELYDLNRDLLNGYKIRWNNH MKTMKSRYMELYDLNRDLLNGYKIRWNNH
1	ļ	1	i			TELLGNLKAVNQAIQRAGRLRVGKPKNQVIT
	1	- 1		_		ACRDAIRSNNINTLFKIMRVGTASS
762	2112	A	6079	2	2686	KKAITCGEKEKQDLIKSLAMLKDGFRTDRGS
102		1				HSDLWSSSSSLESSSFPLPKQYLDVSSQTDISG
	İ	-			•	SFGINSNNQLAEKVRLRLRYEEAKRRIANLKI
						QLAKLDSEAWPGVLDSERDRLILINEKEELLK
		1		1	1	EMRFISPRKWTQGEVEQLEMARKRLEKDLQ
•	-		1	l		AARDTQSKALTERLKLNSKRNQLVRELEEAT
i			1			RQVATLHSQLKSLSSSMQSLSSGSSPGSLTSSR
	1		1	ļ		GSLVASSLDSSTSASFTDLYYDPFEQLDSELQ
1		1	1	1		SKVEFLLLEGATGFRPSGCITTIHEDEVAKTQ
j	]		ļ		Ì	KAEGGGRLQALRSLSGTPKSMTSLSPRSSLSS
			1			PSPPCSPLMADPLLAGDAFLNSLEFEDPELSA
			i			TLCELSLGNSAQERYRLEEPGTEGKQLGQAV
1		ļ	]		Į.	NTAGGCGLKVACVSAAVSDESVAGDSGVYE
					1	ASVORLGASEAAAFDSDESEAVGATRIQIALK
1			ł	1	{	VDEKNKOFAILIIOLSNLSALLQQQDQKVNLK
		1			1	VAVI POSESTTOLFRTRPLDASDTLVFNEVFW
1				1	}	VSMSVPALHOKTLRVDVCTTDRSHLEECLGG
		ł		{	1	A DISLA EVERSGER STRWYNLLSYKYLKKQS
1		- 1		1	1	RELKPYGYMAPASGPASTDAVSALLEQTAVE
				l .	1	LEKRQEGRSTQTLEDSWRYEETSENEAVAE
		1			1	EEFEEVEEEGEEDVFTEKASPDMDGYPALK
		1	1		1	VDKETNTETPAPSPTVVRPKDRRVGTPSQGPF
	1					A D COMMON TECRNO POR CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL AND CONTROL
	l	1	ł	}		LRGSTIIRSKTFSPGPQSQYVCRLNRSDSDSST
						LSKKPPFVRNSLERRSVRMKRPSPPPQPSSVK
						SLRSERLIRTSLDLELDLQATRTWHSQLTQEIS
			}	]	1	VLKELKEQLEQAKSHGEKELPQWLREDERFR
1				1		LLLRMLEKRMDRAEHMGELQTDKMMRAAA
ì						KDVHRLRGQSCKEPPEVQSFREKMAFFTRPR
						MNIPALSADDV
			(000	3	1558	PHPIRESKLCVSFNNOEYNQFCVIEEASKANE
763	2113	A	6082	د ا	1550	VI FNI TOGKMCLVPGKTRKLLFKFVAKTED
						VGKKIEITSVDLALGNETGRCVVLNWQGGGG
}						DAASSOEALOAARSFKRRPKLPDNEVHWGSII
	1					IQASTMIISRVPNISVHLLHEPPALTNEMYCLV
1	1	1			1	14,201,

لبلة فيها فيها فيما طبط أجست سند أأديد للبد

				-6-0-0-0	Dedicted and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	•	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uchee	,			amino acid	of peptide	T=Ihreonine, v=vaine, w=Itypiophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
Į.	ļ	Į.	1	peptide		/=possible nucleotide deletion, \=possible
ļ	ì		1	sequence		nucleotide insertion
L	<del> </del>			Soque		VTVQSHEKTQIRDVKLTAGLKPGQDANLTQK
İ		1	1			THYTLHGTELCDESYPALLTDIPVGDLHPGEQ
1			l	ļ		LEKMLYVRCGTVGSRMFLVYVSYLINTTVEE
1			1	ļ	}	KEIVCKCHKDETVTIETVFPFDVAVKFVSTKF
1	I	İ	[	1		FHI ERVYADIPFLLMTDLLSASPWALTIVSSE
1		i	1	1	1	I HI APSMITTVDOLESQVDNVILQTGESASECF
1		1	1		ĺ	CLOCPSLGNIEGGVATGHYIISWKRTSAMENI
	1		1	l .		PIITTVITLPHVIVENIPLHVNADLPSFGRVRES
1	1	ļ	}	}		LPVKYHLQNKTDLVQDVEISVEPSDAFMFSG
1	1	1	1	1	1	LKQIRLRILPGTEQEMLYNFYPLMAGYQQLPS
Į.	1	1	1	1		LNINLLRFPNFTNQLLRRFIPTSIFVKPQGRLM
	j	1	1	1		
1		1	1			DDTSIAAA AAADLANSNAGAAVGRKAGPRSPPSAPAPAP
764	2114	A	6093	1	1422	PPPAPAPPTLGNNHQESPGWRCCRPTLRERN
'"		1				ALMFNNELMADVHFVVGPPGATRTVPAHKY
				1		VLAVGSSVFYAMFYGDLAEVKSEIHIPDVEPA
1			}	}	1	VLAVGSSVFYAMFI GULAEVASEIIII DVEFA
	1		1			AFLILLKYMYSDEIDLEADTVLATLYAAKKYI VPALAKACVNFLETSLEAKNACVLLSQSRLF
i	1		ŀ	ļ		VPALAKACVNFLETSLEAKNACVLLSQSKLI
1			1	1		EEPELTQRCWEVIDAQAEMALRSEGFCEIDR
1	Ì	1	1			QTLEIIVTREALNTKEAVVFEAVLNWAEAEC
	Ì		}	1		KRQGLPITPRNKRHVLGRALYLVRIPTMTLEE
ſ	1		1			FANGAAQSDILTLEETHSIFLWYTATNKPRLD
}	1	ļ		1		FPLTKRKGLAPQRCHRFQSSAYRSNQWRYRG
		Ì	Į		İ	RCDSIQFAVDRRVFIAGLGLYGSSSGKAEYSV
- 1		1	1	ļ		KIELKRLGVVLAQNLTKFMSDGSSNTFPVWF
j ,	1		}	}	ĺ	EHPVQVEQDTFYTASAVLDGSELSYFGQEGM
1	1				1	TEVQCGKVAFQFQCSSDSTNGTGVQGGQIPE
		1				LIFYA
		<del></del>		+1	1150	SGFTHYAIYDFIVKGSCFCNVHADQCIPVHGF
765	2115	A	6099	1 '	1130	RPVK APGTFHMVHGKCMCKHNTAGSHCQH
}	1	l	1	1		CAPI VNDRPWEAADGKTGAPNECRTCKCNG
i	İ	1				HADTCHEDVNVWEASGNRSGGVCDDCQHN
1		1	-			TEGOYCORCKPGFYRDLRRPFSAPDACKPCS
}	1	ì	-	ł		CHPVGSAVLPANSVTFCDPSNGDCPCKPGVA
1						GRRCDRCMVGYWGFGDYGCRPCDCAGSCD
1			ì	1		PITGDCISSHTDIDWYHEVPDFRPVHNKSEPP
		1				WEWEDAOGESALLHSGKCECKEQTLGNAKA
	İ		1	1		FCGMKYSYVLKIKILSAHDKGTHVEVNVKIK
		1	1	1		KVLKSTKLKIFRGKRTLYPESWTDRGCTCPIL
						NPGLEYLVAGHEDIRTGKLIVNMKSFVQHWK
						PSLGRKVMDILKRECK
		-				MTAAATATVLKEGVLEKRSGGLLQLWKRKR
766	2116	A	6103	2	384	CVLTERGLQLFEAKGTGGRPKELSFARIKAVE
, 00				1		CVETERGLQLFEARGTGGRFREESTAIGHTVE
				1		CVESTGRHITT ILV I EUGUEIDFROI GTGTI
1						NAQITLGLVKFKNQQAIQTVRARQSLGTGTL
	l	1	Ì	1	1	VS
			6106	+1	542	SGSSHASDGSGFQELRICSEDQTPLIAGMCSLP
767	2117	A	1 0100	1.		LALA D VVIIK VADOKAL YTRDGOLL VGDP VAD
		1	İ	1		NCCAEKICTLPNRGLDRTKVPIFLGIQGGSRC
						1 ACVETEEGPSLOLEDVNIEELYKGGEEAIRF
		1		1		TEFOSSSGSAFRLEAAAWPGWFLCGPAEPQQ
						PVOI TKESEPSARTKEYFEOSW
					202	FIL OAVLOLSSOEARYKAFGTCVSHIGAILAF
768	2118	A	6109	3	292	YTPSVISSVMHRVARCAAPHVHILLANFYLLF
		1				PPMVNPIIYGVKTKQIRDSLGSIPEKGCVNRE
		1				RHEPSCSNGVASTKSKQNHSKYPAPSSSSSSS
769	2119	A	6110	1	711	SSSSSSPSSVNYSESNSTDSTKSQHHSSTSNQ
1,07						ETSDSEMEMEAEHYPNGVLGSMSTRIVNGAY
						EISDSEMEMEACH I PHOVE COOK OF A TE
l	ì		1	1		KHEDLQTDESSMDDRHPRRQLCGGNQAATE

				7 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Glutamine, R=Arginine, S=Serine,
uence	1		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	Sequence	/=possible nucleotide deletion, \=possible
	1	1		sequence	1	nucleotide insertion
		<del> </del> -	<del> </del>	sequence		RIILFGRELQALSEQLGREYGKNLAHTEMLQD
		1			ļ	AESLLAYSDPWSCPVGOOLDPIQREPVCAAL
		(	1			NSAILESQNLPKQPPLMLALGQASECLRLMA
		1			ì	RAGI GSCSFARVDDYLH
	12100	<del>  </del>	6125	2	570	YFGLNLHVQHLGNNVFLLQTLFGAVILLANC
770	2120	A	0123	-		VAPWALKYMNRRASOMLLMFLLAICLLAIIF
		1				VPOEMOMLREVLATLGLGASALANTLAFAH
			}			GNEVIPTIIRARAMGINATFANIAGALAPLMM
		1				ILSVYSPPLPWIIYGVFPFISGFAFLLLPETRNK
		1	1			PLFDTIQDEKNERKDPREPKQEDPRVEVTQF
		A	6126	909	353	RSFVLDTASAICNYNAHYKNHPKYWCRGYF
771	2121	A	0120	100		RDYCNIIAFSPNSTNHVALRDTGNQLIVTMSC
		1			}	LTKEDTGWYWCGIQRDFARDDMDFTELIVT
	1	-		1		DDKGTLANDFWSGKDLSGNKTRSCKAPKVV
		1				RKADRSRTSILIICILITGLGIISVISHLTKRRS
ł		1	l			QRNRRVGNTLKPFSRVLTPKEMAPTEQM
	2122	A	6148	7	810	FVLGILALSHTISPFMNKFFPASFPNRQYQLLF
772	2122	1 ^	0140	1		TOGSGENKEEINYEFDTKDLVCLGLSSIVGV
		1		}		WYLLRKHWIANNLFGLAFSLNGVELLHLNN
	1		Ì	1		VSTGCILLGGLFIYDVFWVFGTNVMVTVAKS
		1	}			FEAPIKLVFPQDLLEKGLEANNFAMLGLGDV
1		ļ				VIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF
ļ		1	1			GLGLTIFIMHIFKHAQPALLYLVPACIGFPVLV
l	1	1	1			ALAKGEVTEMFSYEESNPKDPAAVTESKEGT
		1				EASASKGLEKKEK
773	2123	A	6161	3	1088	CQPMLVTRKNHPKLLLRRTESVAEKMLTNW FTFLLYKFLKESAGEPLFMLYCAIKHQMEKG
1 '''		1		1		PIDAITGEARYSLSEDKLIRHLIDYKTLTLNCV
	ł	1		1		NPENENAPEVPVKGLDCDTGTQAKEKLLDA
1		į				AYKGVPYSQRPKAADMDLEWRQGRMARIIL
	1			}	}	QDEDVTTKIDNDWKRLNTLAHYQVTDGSSV
1	1	Į				ALVPKQTSAYNISNSSTFTKSLSRYESMLRTA
1		İ				SSPDSLRSRTPMITPDLESGTKLWHLVKNHDH
ł		1	1			LDQREGDRGSKMVSEIYLTRLLATKGTLQKF
1	1	Ì	1			VDDLFETIFSTAHRGSALPLAIKYMFDFLDEQ
1	1			İ		ADKHQIHDADVRHTWKSNCLPLRFWVNVIK
	-		}			NPOFVEDIHKNSITDACLSVV
				<del></del>	125	KTAVKKRNINPVFNETLRYSVPQAELQGRVL
774	2124	A	6163	860	125	gi gywhresi.GrniflGevevPldi wdwgse
1			1	1		PTWI PLOPR VPPSPDDLPSRGLLALSLKY VPA
		1	ļ			CSEGAGI PPSGELHFWVKEARDLLPLRAGSL
1	]	ļ	Į			DTVVOCEVLPDDSRASRORTRVVRRSLSPVF
1		ŀ				NHTMVYDGFGPADLROACAELSLWDHGALA
		1	Į.		1	NROLGGTRLSLGTGSSYGLQVPWMDSTPEEK
1				2		OT WOALL FORCEWVDGLLPLRTNLAPKI
L _					392	APGIGSI GRDHSGSGGGTGMAGAWVRKAAD
775	2125	A	6191	2	372	VVDSKDFRDYLMSTHFWGPVANWGLPIAAIT
1		1				DMK\KSPEIISRRMTFAL*CYSLTFVRFAHYVQ
1		[		1		PWNWLMLGCHTAVDFDQLISSMPCISHGMT
1	1	- 1	{	(	{	TARASA
L					827	FRGYWGVREAFTDASWSGGLGPGKPGMKIT
776	2126	A	6217	1	021	POVHAKKHI GFFRNNFGVREPYOILLDGTFC
			j			OAALRGRIOLREOLPRYLMGETQLCTTRCVL
			1			KELETLGKDLYGAKLIAOKCOVRNCPHIKNA
						VSGSECLLSMVEEGNPHHYFVATQDQNLSVK
1						VKKKPGVPLMFIIONTMVLDKPSPKTIAFVKA
						VESG/RLSOCMRKKVSNISKRNRV**KTLNRG
	}	1				RRKKRKKISGPNPLSCLKKKKKAPDTQSSASE
1	Ì					KKRKRKRIRNRSNPKVLSEKQNAEGE
1		ŀ				KKKKKKKKKNKONYKALOE

				<del>15 11 4 4 4</del>	Predicted end	Amino acid sequence (A=Aianine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-Aspertic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	I-Icoleucine K=Lvsine L=Leucine,
eotide	seq-	l	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	09/496	correspondi	acid residue	O-Glutamine R=Arginine, S=Serine,
uence		1	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
40	{	1	<b>\</b>	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ	ł	residue of	sequence	/=possible nucleotide deletion, \=possible
	ł	1		peptide		nucleotide insertion
	•		1	sequence		YYQISSLPSIVGNGIFLWLLICIFLAKQGGSRL*
777	2127	A	6236	1038	1402	FQPFGRPRGGGHLRSGVLGQPGQHGETP/SFF
111	212/			1	1	FQPFGRPRGGGHLRSG & LOQI OQIIGLITATI
	l		1	1		YNSKISPALWGPPVIPSALGGEAGKSL*PRRQ
	1	1	1	1		RFQRGGIAPLPSRVRGRAKLFLKKK
	2130	A	6237	422	913	ASFFHHHRGAFLLLLAIPGS*GQDQSLIHWSN
778	2128	Α	0237	,		ASTATION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE ST
	1	1	l	1		PQVL\SEPN*RSGGCFSAPSFEVPPWTGEVKP/
	1		i	1	1	SPQRDGGALG\QGPLGIPSDSILALLKKQT*RA
	1		Ĺ	1	1	LLNWPLGSLRRSSCFGGQDGQDLKPRSGLGC
	}	Ì	1		1	NCERVER
				120	36	AD ADSPES VR DVELSDPARERGEMPVAVGP
779	2129	Α	6249	420	30	VGOSOPSCEDRVKMGFVMGCAVGMAAGAL
		1	1	l l	ì	LCTESCI SSILVSSSG/SGMRGRELMGGIGKIM
	1	1		1		MQSGGTFGTFMAIGMGIRC*PWLPTTSVPSH
	l l		ļ.	Ì	İ	OSOPMY
	1	1	l		1.000	PIMPMCDRGIOMLITTVGAFAAFSLMTIAVG
780	2130	A	6263	415	1380	TOVIA VSRGVCRTKSTSDNETSRKNEEVM1
	1		1		1	TIPGI WOTCCI EGAFRGVCKKIDHFPEDADYE
l		1	1			QDTAEYLLRAVRASSVFPILSVTLLFFGGLCV
	1	-	1	1	1	AASEFHRSRHNVILSAGIFFVSAGLSNIIGIIVYI
	1		1	İ	<b>(</b>	S\ANAGRTPGQR\DSKKSYSYGWSF/YFSGAFS
	1			1		FIIGR/IIC*GVGLPWHIYIEKHQQLRAKSHSEF
ļ	1	l	1	Ì		LKKSTFARLPPYRYRFRRRSSSRSTEPRSRDLS
Ì	1			1		PISKGFHTIPSTDISMFTLSRDPSKITMGTLLNS
1	1	1	1			DRDHAFLQFHNSTPKEFKESLHNNPANRRTT
1				1		
	1	1				PV RIIKVKDLKQTLAIKTAYPRCKCLVEMDQIFH
781	2131	A	6274	832	318	LQVKQKQLACLCTWQARDPDCPPSTKVVL/L
101	2131					VGPGMGCMVALFQDSIAWSNKSMPSSLSAIS
	1	1.				QSPCQVQAPEGPSSFHLPTLSFTTCLSWQGGD
	)	1	- (	(		LEFLGDLKGCSELKNFQELITQSALVHPKADV
1	l l		-	1		LEFLGDERGCSELRINGEBITQUID TITLE
ł	Į.	- 1	1			WWYCGRPLLGTLPSN WISLPSSLLCRKNGSSAEDDRRIGEPSAEEAEG
782	2132	+	6281	1324	393	WISLPSSLLCRKNGSSAEDDRKIGE SAEDS EREDWGIGSA*SVGAVSKVPSARF*RTYPS\(\text{L}\)
102	2132	11	1	}		EREDWGIGSA-SVOAVSKVI SAKI KI I I SE
		- 1				DEEEVTHQKSSSSDSNSEEHRKKKTSRSRNK KKRKNKSSKRKHRKYSDSDSNSESDTNSDSD
	{	- 1		1		KKRKNKSSKRKHRK I SUSUSINSESDI INODUS
			1			DDKKRVKAKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
	ì		1	ł		ESSDSSCKDSEEDLSEATWMEQPNVADTMDL
	ł	1	ł	ļ	]	IGPEAPUHTSQDEKPLKYGHALLPGEGAAMA
1		1	1			EYVKAGKRIPRRGEIGLTSEEIGSFECSGYVM
1						SGSRHRRMEAVRLRKENQIYSADEKRALASF
						NOGERRKRESKILASFREMVHKKIKGKDDK
		<del></del>	(205	201	1032	WDDYPQGALRREAAEGLHFLGPPGRVRGQ
783	2133	A	6305	201		T DGITGPA WYCHSPSHSLLSAFCHLP I PSKCP
				ļ		ANA PPDVPGSVVVPNWHES/RRGQGVPGLHS
1						A OEDDA GUWA A*AASAAAA\LSIDTASYKIFV
	1		1	1	1	- CCVCCVCKTALVAKLAGLEYPVVHHEIIGIQ
[	l	İ				TTVVFWPAKLOASSRVVMFRFEFWDCGESA
		l	1			I KKEDHMI LACMENTDAFLFLFSFIDRASFE
	1	1				DI PGOLARIAGEAPGVVRMVIGSKFDQYMHI
		Ì				DVPFRDLTAFROAWELPLLRVKSVPGRRLG
1	1	- 1				GSSPDPASLITMKNQDKKNGAAKQSNPKSSP
	ŀ			86	96	GSPDPASETIMINADIOMATALOGICAL
794	2134	A	6308			LAMPERITECIALEM SUMM A LIMES SUCCE
784	2134	A	6308			THE CARTAOSCAL PROSESS SPOLEDIL
784	2134	A	6308			DDKDEGAGARTAOSGALRDVSEELSKQLEDIL
784	2134	A	6308			PRKPEGAQARTAQSGALRDVSEELSRQLEDIL
784	2134	A	6308			PRKPEGAQARTAQSGALRDVSEELSRQLEDIL STYCVDNNQGGPGEDGAQGEPAEPEDAEKSR TYVARNGEPEPTPVVNGEKEPSKGDPNTEEIR
784	2134	A	6308			PRKPEGAQARTAQSGALRDVSEELSKQLEDIL STYCVDNNQGGPGEDGAQGEPAEPEDAEKSR TYVARNGEPEPTPVVNGEKEPSKGDPNTEEIR
784	2134	A	6308			PRKPEGAQARTAQSGALRDVSEELSRQLEDIL STYCVDNNQGGPGEDGAQGEPAEPEDAEKSR TYVARNGEPEPTPVVNGEKEPSKGDPNTEEIR

SSQ ID NO: of nucleotide sequence with the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the seq				1.050	D 11 44 4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	SEQ iD	SEQ ID	Met	SEQ	Predicted		D-Aspertic Acid F=Glutamic Acid
Test contact sequence      Sequence	NO: of	1	hod				D-Aspartic Acid, E. Glucine Hallistidine
### 1949   Open	nucl-	peptide	ļ				remenylatable, G-Glychic, if Installe,
1949   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493   1493	eotide	seq-	i	USSN	location		l=Isoleucine, K=Lysine, L=Leucine,
914   ng to first amino said residue of peptide sequence   peptide of peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   pept			ŀ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Profine,
mino acid residue of peptide sequence peptide sequence peptide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq			İ	914		acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of poptide   sequence	uciicc	Ì	1	1		of peptide	T=Threonine, V=Valine, W=Tryptophan,
Peptide	Į			Į.			Y=Tyrosine, X=Unknown, *=Stop codon,
		1 .				Sequence	/=possible nucleotide deletion. \=possible
RSKLESLCRELQRINKSLKEBGVQRAREEEE	l .	1	1			1	nucleotide insertion
RKKEVTSHFQVTLNDIQLQMEQHNERNSKIK   QENMELAERIKKILEQVEREEHIDKVYKHIK   QENMELAERIKKILEQVEREEHIDKVYKHIK   DIQQQLVDAKIQQAQEMIKEAEEHIQREKT   LIKEKAMESQNACHIKQQI-ALIY   TEKFEEFQNTI.SKSSEVFITIKQEMEKMTIKJ   TEKFEEFQNTI.SKSSEVFITIKQEMEKMTIKJ   RDKELEGLQVKIQRI.EKLCRALQTIGAQ*PVR   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   SPQQFLLRSVSPVSAGASSVTPGGAQFYVT   TEKPELGOLQVKIQRI.EKLCRALQTIGAQ*PVR   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAVIFS   GORWGSHRTSAV	l	1	L		sequence		DON'T EST COET OF PUNDST KEEGVOR ARFEFE
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PSELVAVAPAGGSAGPAAGWO,*HAGCRWT KLPWSWGMRPMKIFSEEPTSISTRISHDAL* EKCTOPAKPLSMIRITGSSVSPGPJLVWNWT RREFRINGTVVSSCCOKSCMYSFLGHCSVS QDLPLVHVDVGWQPPLGPTVGLRPGLLPHD TTPCQKLVVDDLDWA REHGQCADVDECSLAEKTCVRKNENCYNTP GSYVCVCPDOFFEETTRECLCAAGRG*SHRRK PDTAALPRRPVMCRTYPLNYSEGCPVENVAL RMSPAVDSGGERLPAL  787 2137 A 6530 1693 227 DYVLTAELHRQRSPGVSFGLSVFNLMAIMG SGRIGLAVYMANTGVFGFFFLLTVALLASYS VHLLLSMCIOTAYLOP*TNYFMVLPAH*LTCL PLEFILQSL*NSL*AVTSYEDLGJFAFGLPGKL VVAGTHIQNIGAMSSYLLHITELPAALAEFLT GDYSRYWYLDQGTLLHICVGIVFPLALEKIG FLGYTSSLSFFFMMFFALVVIKKWSJFCPLTL NYVEKGFQISNYTDDCKFKLPHTSKESAYALP TMAFSFLCHTSLLPTYCLGSPSKKRMQNVTN TAIALSFLJYFISALFGYLTTYD/GTTAQRGE VTCHRIKDKVESELLKG**IP*SHDVVVMTV KLCILFAVLLJYYPLHFPARKAYTMFFSNFF FSWRFHEITLALMIVLLALAYVPDRNVFGVV GASTSTCLFIFFGLFYLKLSREDFLSWKLLGV GCGCOLLSFKTSLRNSLSVYLLBASRKSJYFKI TMYQKKFMSAPLFPYTEGDLYLLTIT TMYOKKMEGCRMDFPANAVLCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGBNAVLCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGNAVALCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGNAVALCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGNAVALCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGNAVALCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGNAVALCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGNAVALCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGNAVALCFSKAVH NLLERCLMNRNFVRIGKWFVKPYEKDEKPIN KSEHLSCSFTFHLIGGNAVALCFSKAVH NLSEPHTLAQQSNSPPQVLCAFGRINCLSCCLKEMSE EKQEDMDWEDDSLAAVEVLVAGVRMTPPAC FVLVPQSDIPTPSFVGSTHCSSCCLGHQVPAS TRDPAMSSVTLTPTTSEEVQTVDPGSVGKW VKFSSVSDGFNSDSTSHIGGKPRKLANHVV DRVWQCCMNRAQORKKYSASSGGLCEBAT AAKVASWDFVBATORTNCSCLRRINLKSRN AGQGGAPSLGQQQQLRFKNINLKSRN AGQGGAPSLGQQQQLRFKNINLKSRN AGQGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFKNINLKSRN AGGGGAPSLGQQQQLRFCHTTFSTPQS QHFYQMFTPDPLVYSKPMEDRDSLSQSFPPQ VQEAVEFTVVYGTAVVLEEDEANIAWKYYX FPKKMDFLFLEDEANIAWKYYX FPKKM	i	1	1	1 _			GURWGSHRISAVRIFS
PSELVAVAPAGSAAGRAAG WY PROCESSE  KLPWSWGMRPMKIFFSESPRSISTRISHDAL* EKCTQPAKPLSMIRITGSSVSPGPJLVWNWT RREFRNSGTVVSCCGMSCMYSFLGHCSVS QDLPLVHVDDUGWOPPLGPTVGLRPGLLPLHD TTPCOKLVVDDLDWA  786 2136 A 6320 551 135 RWLPVAECDSSCVGCTGEGPGNCKECLIGGVA REHGQCADVDECSLAEKTCVRXMENCYNTP GSVVCVCPDGFEET/RRCLCAAGRG*SHRRK PDTAALPRRPVMCRTYPLNYSEGCPVENVAL RMSPSPAVDSGGELPAL  787 2137 A 6330 1693 227 DYVLTAELHRQRSPGVSFGLSVFNLMNAIMG SGLGLAYVMANTGVGFSFFLLLTVALLASYS VHLLLSMCIQTAYLOP*INVFMVLPAH*LTCL PLIFELQSL*PNSL*NATYSPEDLGLPAFGLPOKL VVAGTIIIQNIGAMSSYLLIKTELPAALAFFLT GDYSRYWYLDGOTLLILICGPSKKRMQNVTN TAIALSFLIYFISALFGYLTFYD/GTTAQRGE VTCHRIKDKVESELLKG**IP*SHDVVVMTV KLCILFAVLLTVPLIHFPARKAVTMMFSNTF FSWIRHFLITALMIIVLLAIYVPDIRNVFGVV GASTSTCLFFFGGFYLKLSREDFLSWKLIGV GCFGLLSFYTSIRRNSLSVILDASKKSIVFKI TSWSTPLAUSTPLHPTEDFILSSFSKCLKADV LGVWRDQRPERREL*FTWEDFLISHSKKLIGK VVQGPTSAPLIFFVTEGDFLISHSKKLIGK VVQGPTSAPLIFFVTEGDFLISHSKKLIGK LGVWRRDQRPERREL*FTWEDFLISHSKKLIGK VVQGPTSAPLIFFVTEGDFLISHSKKLIGK VVQGPTSAPLIFFVTEGDFLISHSKKLIGK VVQGPTSAPLIFFVTEGDFLISHSKKLIGK VVQGPTSAPLIFFVTEGDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSKCLKADV LGVWRRDQRPERREL*FTWEDFLISHSCLKADV VKPSSYSDGFNSDSTSHIGGKIPKLANHVV DRVWQCGMNAGNOKKRYASSGGLCEAT AAKVASWDFVEATORTNCSCLRRINLKSRN AGQGGAPSLGQQQQLKPKNINLSRN AGQGGAPSLGQQQQLKPKNINLSSSCLUCHESTE AAKVASWDFVEATORTNCSCLRRINLKSRN AGQGGAPSLGQQQQLKPKNINLSSSCLUCHESTE AAKVASWDFVEATORTNCSCLRRINLKSRN AGQGGAPSLGQQQQLKPKNINLSSSCRIPQ VYGAVETVYGTAVNLEDEANILAKYYX FPKKKDVEFLPPQLPSNKFNDDVAKTPQMGTE MANSQCPPLSNIPCDVDEGVTKTPSTPQS QHFYQMTTPDPLVPSKPMEDRDSLSQSFPPQ VQEAVETVYDGTAVLEEDEANIAWKYYX FPKKKDVEFLPPQLPSNKFNDDVQFGQESVEK FSVTEMVQCKKPLKVSDELVQQPQKKNQCL	785	2135	A	6319	1493	889	SPQGPLLRSVSPVSAGASSVIPGGAQPGVIII
EKCTQPAKPLSMIRITGSSVSPGPLVKWNWT     RREFRINSGTVVSSCCOMSVYSFLGHCSVS     QDLPLHYDVDWQWPLGFTVGLRPGLLPHD     TTPCOKLVVDILDWA     RWLPVAECDSSCVGCTGEGPGNCKECIGGYA     REIGQCADVDECSLAEKTCVRKNENCYNTP     GSYVCVCPDGEET/RRCLCAAGRG*SHRRK     PDTAALPRRPVMCRTYPLNYSEGCPVENVAL     RWSPAVDSGGELPAT     RWSPAVDSGGELPAT     RWSPAVDSGGELPAT     A 6530 1693 227     DYVLTAELHRQRSPGVSFGLSVYNLMNAIMG     GSIGLGAYVMANTGVFGSFFLLLTVALLASYS     VHLLISMCIQTAYLOP*INYEMVLPAH*LTCL     PLIEFLOSL*INSL*A*ATYS*PDLGLPAFGLPGKL     VVAGTIIIQNIGAMSSYLLIKTELPAALAFLT     GDYSRYWYLDOJTLLIIKCVGIVFPLALLPKIG     FLGYTSSLSSFFFMMFFALVVIKKWSIPCPLTL     NYEKGFQISNYTDDCKFKLHFTSKESAYALP     TMAFSFLCHTSLIPTYCELGSPSKKRMQNVIN     TAIALSFLIYFISALFGYLTTYPJCTTTAQRGC     VTCHRIKDKVESELLKG**IIP*SHDVVVMTV     KLCILFAVLLTYPLHFPARKAYTMFSNFP     FSWRRFILTLALNIIVLLAILYVPDRNVFGVV     GASTSTCLFFFGLFTLKSSEDSLEXKLGV     GCFCALLSFKTSLRNSLSVILD-SSKKLKGV     GCFCALLSFKTSLRNSLSVILD-SSKKSLKADV     LGVWRRDQRFERREL*FFWGEDFILSSSKCLKADV     LGVWRRDQRFERREL*FFWGEDFILSSSKCLKADV     LGVWRRDQRFERREL*FFWGEDFILSSSKCLKADV     LGVWRRDQRFERREL*FFWGEDFILSSSKCLKADV     LGVWRRDQRFERREL*FFWGEDFILSSSKCLKADV     LGVWRRDQRFERREL*FFWGEDFILSTSKCKADV     LGSEHITLAQOSNSFPQVILCPFGINGTLTGQ     AFKMSDSATKKLIGEWKQFYPISCCLKEMSE     EKCEDMOWEDDSLAAVEVLVAGVRMTYPAC     FVLVPQSDIFTPSVGSTHCSSCCLGHQVPAS     TRIPAMSSVTLTPFTSSEEVQTVDPQSVQK     VKFSSVSDGFNSDSTSHIGGKIPRKLANHVV     DRVWQCEMNAQQNKKYSASSGGLCEAT     AAKVASWDFVEATORTNCSCLRRIKNLKSRN     AGQGGAPSLGQQQQLRFKKTNLKSRN     AGQGGAPSLGQQQQLRFKKTNLKSRN     AGQGGAPSLGQQQQLRFKKTNLKSRN     AGQGGAPSLGQQQQLRFKKTNLKSRN     AGQGGAPSLGQQQQLRFKKTNLKSRN     AGQGGAPSLGQQQQLRFKKTNECCERSEK     QKRPLTPFHHRVSVSDDVGMDMADSASQRL     VISAPDSQVRFSNRTNDDVAKJTPQMHGTI     MANSQCPLPJSNFTCDVVDEGVTKTFSTPS     QHFVQMTTPDPLVPSKPMEDRDSLSQSFPPO     YQCAVETVYVGTAVNLEEDEANIAWKYY     FPKKKDVEFLPPQLPSDKFKDDPVQFFQCES     VTSTYLEMVCCKFLKVSDELVQQYQKNCC	1						PPSLVAVAPAPGSAAGPAAGWQ*HAGCR/WI
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						/A-Alorino C-Cysteine
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
	1	1		peptide		nucleotide insertion
				sequence		RONSEREAGKKHKVEDGTSSVTVLSHEEDA
						MSLFSPSIKODAPRPTSHARPPSTSLIYDSDLA
		ļ				VSYTDLDNLFNSDEDELTPGSKRSANGSDDK
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		1				CIYRQSWTVGKLELLSSGPSMPFIKEGDGSNM
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		{	1	1	1	VKYENSDLYSPASTPSTCRPLNSVEPATVPSIP
ì	1	1	1		1	EAHSLYVNLILSESVMNLFKDCNSDSCCICVC
			1			NMNIKGADVGVYIPDPTQEAQYRCTCGFSAV
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		1	1			KRFEALRATSAEHVNGGLKESEKLSDDLILLL ODQCTNLFSPFGAADQDPFPKSGVISNWVRV
i	1	1				QDQCTNLFSPFGAADQDFFFRSGVISIW VRV EERDCCNDCYLALEHGRQFMDNMSGGKVDE
		1				ALVKSSCLHPWSKRNDVSMQCSQDILRMLLS
		1	1			LQPVLQDAIQKKRTVRPWGVQGPLTWQQFH
		1				KMAGRGSYGTDESPEPLPIPTFLLGYDYDYLV
ļ				İ		LSPFALPYWERLMLEPYGSQRDIAYVVLCPE
1	į		i	1		NEALLNGAKSFFRDLTAIYESCRLGQHRPVSR
						LLTDGIMRVGSTASKKLSEKLVAEWFSQAAD
1		1		1		GNNEAFSKLKLYAQVCRYDLGPYLASLPLDS
1	1	1				SLLSOPNLVAPTSOSLITPPQMTNTGNANTPS
				Į.	1	ATLASAASSTMTVTSGVAISTSVATANSTLTT
			1			ASTSSSSSSNLNSGVSSNKLPSFPPFGSMNSNA
1	İ					AGSMSTQANTVQSGQLGGQQTSALQTAGISG
		1				ESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH
1						AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTL
					1	GLLRCFLEMVQTLPPHIKSTVSVQIIPCQYLLQ
				İ	1	PVKHEDREIYPQHLKSLAFSAFTQCRRPLPTS
		j			1	TNVKTLTGFGPGLAMETALRSPDRPECIRLYA
1		1		Į		PPFILAPVKDKQTELGETFGEAGQKYNVLFV GYCLSHDQRWILASCTDLYGELLETCIINIDVP
1						NRARRKKSSARKFGLQKLWEWCLGLVQMSS
İ						LPWRVVIGRLGRIGHGELKDWSCLLSRRNLQ
			1	Ì		SLSKRLKDMCRMCGISAADSPSILSACLVAM
					1	EPQGSFVIMPDSVSTGSVFGRSTTLNMQTSQL
					1	NTPODTSCTHILVFPTSASVQVASATYTTENL
J		1		]	1	DLAFNPNNDGADGMGIFDLLDTGDDLDPDII
	1	1		1	1	NILPASPTGSPVHSPGSHYPHGGDAGKGQSTD
1		1			1	PLI STEPHEEVPNILOOPLALGYFVSTAKAGP
1				1		LPDWFWSACPOAOYQCPLFLKASLHLHVPSV
		i	1	1		OSDELLHSKHSHPLDSNQTSDVLRFVLEQYN
						ALSWLTCDPATQDRRSCLPIHFVVLNQLYNFI
		1	1	1		MNML
		A	6359	+,	2002	TGTLTEDGLDVMGVVPLKGQAFLPLVPEPRR
789	2120	, 4	وردن ا	1 *		LPVGPLLRALATCHALSRLQDTPVGDPMDLK
	2139	1	1	1		
1	2139				Ì	MVESTGWVLEEEPAADSAFGTQVLAVMRPP
	2139					LWEPOLOAMEEPPVPVSVLHRFPFSSALQRM
	2139					LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATOPEAYVKGSPELVAGLCNPET
	2139					LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAOMLOSYTAAGYRVVALASKPLPSVP
	2139					LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SI FAAOOLTRDTVEGDLSLLGLLVMRNLLKP
	2139					LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP OTTPVIOALRRTRIRAVMVTGDNLQTAVTVA
	2139					LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPOEHLIIVHATHPERGQPASLEFLP
	2139					LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA
	2139					LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP
	2139					LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA

					T 10 10 10 10 10 10 10 10 10 10 10 10 10	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in	nucleotide	location	r=pnenylalanine, d=diyene, ii iiisissine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence	]	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1		314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	Į.				sequence	/=possible nucleotide deletion, \=possible
		1	1	peptide		nucleotide insertion
	j	ł	1	sequence	<u> </u>	VIREGRCSLDTSFSVFKYMALYSLTQFISVLIL
	+					VIREGROSLDISTSVIKI WALLISETQUISTED
		1	i	1		YTINTNLGDLQFLAIDLVITTTVAVLMSRTGP
	1	1	1	1		ALVLGRVRPPGALLSVPVLSSLLLQMVLVTG
		I				VQLGGYFLTLAQPWFVPLNRTVAAPDNLPNY
	1		1		1	ENTVVFSLSSFQYLILAAAVSKGAPFR\RPLTN
	1	-	1		l .	NVPFLLASAL*SSVLVVLVLSPGLLHGPLALR
		İ	l	!		NITDTGFKLLLVGLVTLNFVGGLHAGERARP
		1				VPPRLPAPPPAQAG\SKKRFKQLERELAEQPW
		1			1	
						PPLPAGPLR
	1 22.10	+	6380	76	1059	SSAGSARKLQVMALAARLWRLLPFRRGAAP
790	2140	A	0300	"		GSRI PAGTSGSRGHCGPCRFRGFEVMGNPGT
ĺ		1	1	1		FKRGI I I SALSYLGFETYOVISQAAVVHATA
1	1			l		KVEEILEQADYLYESGETEKLYQLLTQYKESE
}	1	1	1	1		DAELLWRLARASRDVAQLSRTSEEEKKLLVY
		1				EALEYAKRA/L/EKNESSFASHKWYAICLSDV
}		1	1		1	GDYEGIKAKIANAYIIKEHFEKAIELNPKDATS
1	1	<b>\</b>	1		ļ	GDYEGIKAKIANA YIIKEHPEKATELIYADA 13
1	1					IHLMGIWCYTFAEMPWYQRRIA*NACLQLPP
	1				}	*FPPYEKALG\YFHRAEQVDPNFYSKNLLLLG
}		1	1			KTYLKLHNKKLAAFWLMKAKDYPAHTEED
1		1	1			KOIOTEAAOLLTSFSEKN
					1460	IALLIVDGLAWDDQGGLALLHISPSKLIL*QDS
791	2141	A	6434	3	1460	SGMS/YVMVRCTITRAFFKSLLCHICQYSIGPQ
17.	1					SUMS/ I VM V KCITI KATI KSEEDOTTOO TOTOO
1	1	1	1		ļ	*VT\CPGQDACKE*KSTAN*GG*RE**PQVLFF
1	1		1			AFLSNPAVKFGRMSKKQRDSLYAEVQKHQQ
		İ				RLQEQRQQQSGEAEALARVYSSSISNGLSNLN
1						NETSGTYANGSVIDLPKSEGYYNVVSGQPSP
	1					DOSGLDMT\GIKOIKQEPIYDLTSVPNLFTY\SS
1	1					ENINGOLAPGIT\MTEIDRIAONIIKSHLETCQY
1	1			1		TMEELHQLAWQTHTYEEIKAYQSKSREALW
ł					1	QQCAIQITHAIQYVVEFAKRITGFMELCQNDQ
	1		ł	ļ	ļ	ILLKSGCLEVVLVRMCRAFNPLNNTVLFEG
<b>\</b>	1		ł	1		ILLEASURE AL CODDI MEADEAKNI CSI
				ļ		KYGGMQMFKALGSDDLVNEAFDFAKNLCSL
ł	ľ		ļ			QLTEEEIALFSSAVLISPDRAWLIEPRKVQKLQ
1		1	1		Ì	EKIYFALQHVIQKNHLDDETLAKLIAKIPTITA
			l l			VCNLHGEKLQVFKQSHPEIVNTLFPPLYKELF
1	l l	1	1			NPDCATACK
				<del> </del>	701	SRGTERCECRDFFPCFSNMRLFLWNAVLTLFV
792	2142	Α	6440	92	781	TSLIGALIPEPEVKIEVLQKPFICHRKTKGGDL
				1	ł	MLVHYEGYLEKDGSLFHSTHKHNNGQPIWFT
1	1			1	j	WLAHAEG I TEVTASTELIST LIMITAGE I ALL
	1		1	1	1	LGILEALKGWGPGA*K/DMCVGEKRKLIIPPA
1	1			1	1	LGYGKEGKGKIPPESTLIFNIDLLEIRNGPRSH
1			1	1		ESFQEMDLNDDWKLSKDEVKAYLKKEFEKH
1					1	GAVVNESHHDALVEDIFDKEDEDKDGFISAR
1				1	1	FFTYKHDEL
	1	1	1		<del></del>	PRLKRLVVTEEDGGARPEALGKIAPRTPAELG
793	2143	A	6446	3201	152	ARADQELVTALMCDLRPAAGGMMDLAYV
.,,,		1				AKADUELV IALMODERICAAOOMINDATI
1		i				CEWEKWSKSTHCPSVPLACAWSCRNLIAFTM
1	1					DLRSDDQDLTRMIHILDTEHPWDLHSIPSEHH
}	1					FAITC\LEWDOSGFPGFLFSRWPTGQIK\CWS
1	1	- 1		1		MGVSTLA\NSWE\SSVGSL\VEGGPHLWALS\
ĺ	1	- 1				WLH/NGVKLALHVEKSGASSFGEKFSR/VKFS
[	1			1		P\SLTLF\GGNAMEGWIAVTVSGLVTVSLLQ\P
1	1	-				SGQVL\TST\ESLCRLRARVALADIAFTGGGNI
1	1		Ì			SGQVL/151/E5LCKLKAKVALADIAF166611
1	Į.					VVATADGSSA\SPVQFYKVCVSVVSEKCRIDT
1				1		DILPSLFMRCTTDLNRKDKFPAITHLKFLARD
1			1.	]		MSEOVILCASSOTSSIVECWSLRKEGLPVNNI
1	1		1	1		FQQISPVVGDKQPTILKWRILSATNDLDRVSA
1		-		1.		VALPKLPISLTNTDLKVASDTQFYPGLGLAL
1	1		1	1		VALIALISEITIERA AL CTALLENCE LA PROVID
1						
						AFHDGSVHIVHRLSLQTMAVFYSSAAPRPVD
		i				AFHDGSVHIVHRLSLQTMAVFTSSAAFRFVD EPAMKRPRTAGPAVHLKAMQLSWTSLALVG

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		}	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1			amino acid	of peptide sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		<b>!</b>	Ì	residue of	sequence	/=possible nucleotide deletion, \=possible
			1	peptide	1	nucleotide insertion
		ļ	ļ	sequence	<del>                                     </del>	IDSHGKLSVLRLSPSMGHPLEVGLALRHLLFL
		Į .				I FYCMVTGYDWWDILLHVQPSMVQSLVEKL
	ŀ	{	1			HEEYTROTAALOOVLSTRILAMKASLCKLSP
		ł				CTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNT
		ļ				PDKSPGDRLTEICTKITDVDIDKVMINLKTEEF
		]		İ		VI DMNTLOALOOLLOWVGDFVLYLLASLPN
	1	i	İ			OPCPTSEPCPTSEPSPTSEPSPTSEPSSP*SLC\G
			1			SLIRPGHSFLRDGTSLGMLRELMVVIRIWGLL
				j	}	KPSCLPVYTATSDTQDSMSLLFRLLTKLWICC
			1	1		RDEGPASEPDEALVDECCLLPSQLLIPSLDWL
						PASDGLVSRLQPKQPLRLQFGRAPTLPGSAAT
		1				LQLDGLARAPGQPKIDHLRRLHLGACPTEEC
		1	1		}	KACTRCGCVTMLKSPNRTTAVKQWEQRWIK
	1					NC/LVRWALVAGAPQLPLSPAAPQLLLSYPSA
					1	APEPGCCKSHRSPWTLLGAVNLSPPCRAVEG
			1			RGPDACVTSRASEEAPAFVQLGPQSTHHSPRT
			1			PRSLDHLHPEDRP NGDKADLENESCRAQVLMPVVPALWEAEGG
794	2144	A	6490	418	585	GSIEPRDLRLQ*AVITPL\TPAWVTQ
		1	1			KLLWLPPHSEQKRSPLYHPQGPSGTTPSAP\FS
795	2145	Α	6499	395	1027	SHSPPPSLLQAVPSIAAFLRTHGHISASGPLRMP
1				İ		FPH/H*NAFLLVFPGQRSQLTS/PSHYLCREVFP
		i		}		DHHHHLCRLSLESSPLFHHRVLFCVPKQNVN
			i			STRAQIFCLFVHIVGCRCINTFPLHLFRLHLWL
		İ				HFLQIPLCKKNKSVKLGKTVVGRGCQSAAGS
		1		1		DTRVRAAVGAPGLPVEPLV
		A	6503	68	936	HSALLTHSSECVETLCODFFTYSSMSEEVTYA
796	2146	A	0303	100		DLOFONSSEMEKIPEIGKFGEKAPPAPSHVWK
ļ		1		1		PAALFLTLLCLLLLIGLGVLASMFHVTLKIEM
						KKMNKLQNISEELQRNISLQLMSNMNISNKIR
Ì			ļ			NLSTTLQTIATKLCRELYSKEQEHKCKPCPRR
		}	]			WIWHKDSCYFLSDDVQTWQESKMACAAQN
ľ						ASLLKINNKNALEFIKSQSRSYDYWLGLSPEE
}		1		ļ		DS/YSWYESG*YNQ\PSAWVIRNAPDLNNMY CGYINRLYVQYYHCTYKQRMICEKMANPVQ
ļ	1	}	1	ŀ		
}						LGSTYFREA PGSTHASARSQVPRSAGEAAPHSRRPPGLLPH
797	2147	A	6507	1	881	APRAASAQLEERMRDPHPGMTLQEGDCRGS
		-				QTVSLTMGTADSDEMAPEAPQHTHIDVHIHQ
1		1			1	FSALAKILLTCCSALRPRATOARGSSRLLVAS
				ĺ		WVMQIVLGILSAVLGGFFYIRDYTLLVTSGA
		l.		ļ		AIWTGAVAVLAGAAAFIYEKRGGTYWALLR
1			-			TLLALAAFSTAIAALKLWNEDFRYGYSYYNS
1				1		ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM
}		1		-		DMLKALFRTLOAMLLGVWILLLLASLTPLWL
1					1	/SI_/RGECSOPKG*VPKKRDQKEMLEVSGI*PG
						STHASARSOVPRSAGEAAPHSRRPPGLLPHAP
	-	1		1		RAASAOLEERMRDPHPGMTLQEGDCRGSQT
				1		VSLTMGTADSDEMAPEAPOHTHIDVHIHQES
	1					ALAKLILITCCSALRPRATOARGSSRLLVASW
1		l		1	1	VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI
		1	(	1	ı	WTGAVAVLAGAAAFIYEKRGGTYWALLRTL
}	- {	1		1		LALAAFSTAIAALKLWNEDFRYGYSYYNSAC
			1	<b>+</b>		
				}		RISSSDWNTPAPTQSPEEVRRLHLCTSFMDM
						LKALFRTLQAMLLGVWILLLLASLTPLWLYC
						LKALFRTLQAMLLGVWILLLLASLTPLWLYC WRMFPTKGVSP
798	2148	A	6528	912	2287	LKALFRTLQAMLLGVWILLLLASLTPLWLYC WRMFPTKGVSP VPNYLPSVSSAIGGEVPQRYVWRFCIGLHSAP
798	2148	A	6528	912	2287	LKALFRTLQAMLLGVWILLLLASLTPLWLYC WRMFPTKGVSP

					32 3 3 - 4	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	!	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uchec	ł	ł	l	amino acid	of peptide	I=Inreonine, v=vainte, v=itypropriam,
	1	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ļ	1	peptide		/=possible nucleotide deletion, \=possible
	Ì	ļ		sequence	ì	nucleotide insertion
		ļ	<del> </del>	Sequence		EVFPEGTGLPLPHSDLPTSWCGHSLQCGSQSS
	1	l	<b>!</b>			EDDAIHENAFIVEIASSLGHMLLTCILWRLTKK
	1	ì	ł	ļ		HTVSOE\DGLSLAGAPROPRRKSRTSVLKIKV
		1		ļ	İ	MVRWELSSNGNPGRGVLGLGLGLGNKLRVV
			ì	İ		GQNLGL*HCVWVVWETGE*KRWRLQMGIE*
	l	l	1	1		GVASRRQ*VRNSVRGLVCHNSSAPPMYMGFF
	}	ł	1	1		SPTVFGGGVGG*LHVTFILHPPEVEAAGIPLLL
		i	1	1		SPIVEGGVGG*LHVIFILITIE VERTOR *WEP
	1	1	1	Į		GPSLPQRQGREHIVVILAAPACAPFHDR*WEP
	i	1	ĺ			REIRPSP*ELGLRGEPTLSYPASCRVIRQPIP*D
		1	ĺ			RKSYSWKQRLFIINFISFFSALAVYFRHNMYC
Ì			1			EAGVYTIFAILEYTVVLTNMAFHMTAWWDF
ļ .			i	ì		GNKFI LITSOPEEKRF
					874	FFFFQRINFIEHSGSVSLLALACDLGWCEDWS
799	2149	Α	6529	1	0/7	CCL VOGGGDLVDVVOTNHGEDEAGGDIDSV
}		1	1	1		DEARCKESQQEAQENLREDLCLESFAKDKIL
1			1	1	1	QIIEGSEREHEETRTKQAALDGEPLGGGQLTA
		1	1			VHLHPSKEQQGQEGGERQRGARTHHWRGW
1		1	1			EKGRRVRLRPPSGKLRADQPVRKLGGPTPS/T
ļ	1	-	1			EKGKKVKLKPPSGKLKADQI VIQADGGI II SI
ì						ELPGLQPHAPTPHTA/PATPTYSPAPDTPNPPV
1	Ì		İ			RWKCPLPVEPRTRQLCRERTRKACPPKPRPPL
j	Į		1			GLPGDPTGPVTHHAPPVSPTGASGQERRAEP
	-		]		1	GAVSYAHASATK
l			- 1 6544	2	662	SAQRWAAVAGRWGCRLLALLLLVPGPGGAS
800	2150	Α	6544	1 2	002	FITTEI PONAKOCFYEDIAOGIKCILEFQVIIG
1	1	l	<b>\</b>			CHYDYDCRLEDPDGKYLYKEMKKQ 1D3F1F
l		1	1			TASKNGTYKFCFSNE\FSTFTHKTVYFDFQVG
1		1		1		E\THLCFLVR/DRVSALTQMESACVSIHEALKS
1	Ì				i	VIDYQTHFRLREAQGRSRAEDLNTRVAYWSV
1	Ì	ļ				GEALILLVVSIGQVFLLKSFFSDKRTTTTRVGS
1	1	1	1	1		GEALILLY VSIQ VI LENGT TO DELL'ANTE CONTROLL SECONDE POTE GSM
901	2151	A	6556	1	1319	TPCMECIKGEGLREPQNLSGSQREPQTEGSM
801	2131	1 "	1			DGWRRMPRWGLLLLLWGSCTFGLPTDTTTF
1	1	İ	1	Ì		KRIFLKRMPSIRESLKERGVDMARLGPEWSQP
1	Į.	- [	1	İ		MKRLTLGNTTSSVILTNYMDTQYYGEIGIGTP
1	1	ļ	ł	1		POTFKVVFDTGSSNVWVPSSKCSRLYTACVY
i		l	1			HKI FDASDSSSYKHNGTELTLRYSTGIVSGFL
	1				ļ	SODITYGGITYTOMFGEVTEMPALPFMLAEF
1	ļ	- 1	Į.		<b>\</b>	DGVVGMGFIEOAIGRVTPIFDNIISQGVLKED
1		1	1	1		VESEVVNR DSENSOSLGGOIVLGGSDPQH I E
1	l	1		}		CNEHVINI IKTGVWOIOMKGVSVGSSTLLCE
1		- [	1	1		DGCLALVDTGASYISGSTSSIEKLMEALGAKE
		1	1	1		KRLFDYVVKCNEGPTLPPTFLFLLGGKDTPLT
		1				KKLFDY V VKCNEUT ILFT ITELEBOOKDTTDT
				1		SADYLFQESYSSKKLSTLAIHAMYIPPPTGPTL
1	1	1		ı	\	\ALGATF\IRKFYTEFDRGNNPHGFALAR
			6567	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSL
802	2152	A	0307	13	1 ***	I AVVVII ALPVAWGOCNAPEW\LPFARPINL
}		- 1	-			TDEFEEPIGTYLNYECRPGYSGRPFSHCLKNS
	1					VWTGAKDRCRRKSCRNPPDPVNGMVHVIKG
1	[	1				IOFGSOIKYSCTKGYRLIGSSSATCHSGDTVIW
1	i			ļ	1	DNETPICDRIPCGLPPTITNGDFISTNRENFHY
		- 1				GSVVTYRCNPGSGGRKVFELVGEPSIYCTSND
				1		DONOTHE CONTROLLING ALTONOMY AND ACTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
				-		DQVGIWSGPAPQCIIPNKCTPPNVENGILVSD
	1					NRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA
1				1		LNKWEPELPSCSRVCQPPPDVLHAERTQRDK
	1			1		DNESPGOEVEYSCEPGYDLRGAASMRCTPQG
j	1		1			DWSPAAPTCEVKSCDDFMGQLLNGRVLFPV
			i	1		
						NI OLGAK VDEVCDEGFOLKGSSASYCVLAG
						NLQLGAKVDFVCDEGFQLKGSSASYCVLAG MESI WNSSVPVCEOIFCPSPPVIPNGRHTGKP
						NLQLGAKVDFVCDEGFQLKGSSASYCVLAG MESI WNSSVPVCEOIFCPSPPVIPNGRHTGKP
						NLQLGAKVDFVCDEGFQLKGSSASYCVLAG MESLWNSSVPVCEQIFCPSPPVIPNGRHTGKP LEVEPEGKAVNYTCDPHPDRGTSFDLIGESTIR
						NLQLGAKVDFVCDEGFQLKGSSASYCVLAG MESI WNSSVPVCEOIFCPSPPVIPNGRHTGKP

Seq III orazion peptide sequence de la cation incucleotide control peptide sequence de la cation periode sequence de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation corresponding de la cation ca	250 th	CEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nociculation of the period could be sequence of the period corresponding to the period could be sequence of period and the period could be sequence of period and the period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of period could be sequence of peri	SEQ ID	SEQ ID	. :			_	D=Aspartic Acid, E=Glutamic Acid,
norte coulde seq. 09445 914 914 916 917 918 918 918 918 918 919 918 919 919 918 919 919		t ·	noa		, ,		F=Phenylalanine, G=Glycine, H=Histidine,
conce sequence  914  914  914  914  914  914  914  91					1		I=Isoleucine, K=Lysine, L=Leucine,
uence    1914		, -	1		1	to last amino	M=Methionine, N=Asparagine, P=Proline,
amino acid relider of peptide relider of peptide sequence of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of peptide insertion of	•	uence	1				O=Glutamine, R=Arginine, S=Serine,
residue of peptide sequence   Y=Tyrosine, X=Unknown, **Stop podon, /-possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion, *possible nucleotide tellion	uence	İ		714			T=Threonine, V=Valine, W=Tryptophan,
Pepide   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence		ł	l	]	1		V=Tyrosine, X=Unknown, *=Stop codon,
nucleotide insertion  STICLDIN, VMSSPROVEKRRSCETFPDPVNG MYHVTDIQVGSRNYSCTTGHRLIGHSSAECI LISGNAAHWSTRPFICQRFGCJPFTIANODFIS THENPHYGSVVTYRCHOSGGRKVFELVGE PSYCTSDDDQVGINSGPAGCLIPNKCTPNN ENGILVSDNSSLFSLNEVVERCQFGYMKGP RVKCQALNKWEPELFSCSRVCQPPDVLHA ERTORDEDNSFGGEVTYSCEPGYDLRGAAS MCCTPQGWSPAAPTCEVKSCDDEPMGQLN GRVLFPVNLQLGAKVDFVCEGIFCRSPPVIPNO RRTIGKPLEVFFGKAVNYTCDPHPDRGTSPD LIGESTIRCTSDPQONGWSSPAPRCGIGHC QAPDHELFAKLKTOTNASDFFJGTSLKYECRP EYYGRPSTICLDIN, WSSPKDVCKRSCKTP PDPNNGMYHVTDIQVGSRNYSCTTGHRLIG HSAACLISGNTAHWSTKPPCQRFTGGFDT ANGOPISTNRENPHYGSVVTYRCNLGSRGKK VEIL VGBFSTCTSDDQVGIWSSPAPCGLPTI ANGOPISTNRENPHYGSVVTYRCNLGSRGKK VEIL VGBFSTCTSDDQVGIWSSPAPCGLPTI ANGOPISTNRENPHYGSVVTYRCNLGSRGKK VEIL VGBFSTCTSDDQVGIWSSPAPCCLBN KCTPPNVENGILVSDNRSLFSLNEVVEFRQQP GFVMKGPRKVKQALNKWEPELFSCSRVCQ PSPELHAGEHTSHQDVGIWSGPAPCLIPN KCTPPNVENGILVSDNRSLFSLNEVVEFRQQP GFVMKGPRKVKQALNKWEPELFSCSRVCQ PSPELHAGEHTSHQDVGIWSGPAPCLIPN KCSSVSIKCHV, GMRSJSCLEDL, WSSVEDNC RRKSCGPPEPFNGMVHINTDTOFGSTVNYSC LSVRAGHCKTPEQPFPASPTIENDFEPFVGTS LNYRCGRYGFGKMSSICLENLWSSVEDNC RRKSCGPPEPFNGMVHINTDTOFGSTVNYSC NGGFRLIGSSTTCTLSVNSVEDNC RRKSCGPPEPFNGMVHINTDTOFGSTVNYSC NGGFRLIGSSTTCTLSVNSVEDNC RRKSCGPPEPFNGMVHINTDTOFGSTVNYSC NGGFRLIGSSTTCTLSVNSVEDNC RRKSCGPPEPFNGMVHINTDTOFGSTVNYSC NGGFRLIGSSTTCTLSVNGOVGWWS PPPRCISTNKCTAPEVENARVYGNRSFPSI,TEL RFRCQPFGVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPELHAGEHTLSNQDMSSPPSI,TEL RFRCQPFGVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPELHAGEHTLSNQDMSSPPSC SCEPSTYDLRGAASLHCTYQGDVSRSPRFSI,TEL RFRCQPFTWFINGTSTRTSTEEPHONGVWS SPAPRCELPVGAACPHPRLIQNGHYIGGHVSL LKIRKGNNAHENFEVAUHLHSGGSSVHP RTLQTNESSTRVLP HGRSARLAGVFASAAHVGSPLITARGSSSVHP RTLQTNESSTRVLP HGRSARLAGVFASAAHVGSPLITARGSSSVHP RTLQTNESSTRVLP HGRSARLAGVFASAAHVGSPLITARGSSVHALLILL LLIPILLILLIGSSBAGGSVHP RTLQTNESSTRVLP HGRSARLAGVFASAAHVGSPLITARGSPSALGLLUG LLIPILLILLIGSSBAGGALTVAVVLPLANTSY VWSWARVGGAVELALAGVAKARVDLKWE HNPAVFLOFGCVYAAAHVSYPLL TAGAPALGFGVKDEVALITARGFSYAKLLGDF VAALHREGWBRQAALMITYAPLEDLFONT VRIVLGSSENALGVCSSTAPLAAVDLKWE HNPAVFLOFGCVYAAAHVSYPLL TAGAPALGFGCKAAAMTYARVPLL TAGAPALGFGCKAAAMTYACAAFGRFTAHAVDLL TAG		1	ļ			Sequence	/=possible nucleotide deletion, \=possible
SITCLDNI,VMSSRLDVCKRISCKTPPDPVNG WMYNTDIQVGSRNYSCTTGIRLIGIESSACI LSGNAAHWSTKPPCQRIPCGLPPTIANGDFIS TNRENFYGSVOTYRCNPOSGGRAYCELVGE PSIYCTSNDDQVGINSGPAPGCIPNKCTPPNV BEGILVSDNSRJSISLNEVVEFRCOPGPVMKGP RRVKCQALNKWEPELPSCSRVCQPPPDVLHA BETORDKDNFSSGGEVFYSCEPGYDLRGAS MRCTPGGBWSPAPTCEVKSCDDFMGQLLN GRVLFPVNLQGASVMYSCPCHGCRSSAY VCHLAGMESLWNSSVPVCEGIFCRSPVPVNG RTTKEPLEVPFEGKANVTCDPHEDGTSFD LIGESTIRCTSDPQONGVWSSPAPCGLIGHC QAPBELPAKLKTOTHASPPFGTSLEVFECK EYVGRPSTITCLDNI,VMSSRKDVCKKKSCKTP PPPVNQMWHVTDJQVGSRNYSCTFOHBLIG HSSAGCLISGNTAHWSTKPPLOGREGLPPTI ANGDPSSTVRENHETYGSVVTYRCALGSGRK VFELVGEPSYTCTSNDDQVGIWSGPAPCCTP HSSAGCLISGNTAHWSTKPPLOGREGLPPTI ANGDPSSTVRENHETYGSVVTYRCALGSGRK VFELVGEPSYTCTSNDDQVGIWSGPAPCCTP GVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVMKGPRAVKCQALNKWEPELPSCSSVCQ GPVERGRAVATARVACALNKSCDDF LGQLPHGRVLTGMAVACACACACACACACACACACACACACACACACACACA		1	ľ		1		nucleotide insertion
MYHYTDIQUGRSRNYSCTTGHRLIGHSSAGE  I SIGNAAHWSTKPIQQRFCGLPTTIANGDE'S TYRENFHYGSVYTYRCNPGSGGRKYELUG ESTYCTSNDDQVGIWSGPAPQCIIPNCTPPN ENGILVSDNSSLFSLNEVVERCQPFDWLFA RETORDKDNTSPGGEVFYSCEPGYPLRGAA MCTCTGGDWSPAAPTCEVKSCDDFMGQLAN GRVLFVNLQLGAKVDFVCDEGFQLKGSSA YCVLAGMESL UNSSVPVCDEGFCSPFVPNSA RTTGRPLEVPFFGKAVNTTCDHPDRGTSPF LIGESTRCTSDPGGWVSSSAPRCGILGHC QAPDHELFAKLKTQTNASDFPIGTSLKYEGEP EYGRPSTICLDLN WSSSFWDCGLFGT ANGDFISTNENFHYGSVVTYRCNLGSBGRK VELLVGEFSYCTSDDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLREVVEFRCQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVKCQALNK WEELPFSCSRVQQ GFVMKGFRVLFPLNQLGAKVSFVCDEGFFT KGSSTBCLUCK WSSVEDNC RGFRLIGSSFTICLSDPHGNVWSSPAPRCE LSVRAGHCKTFEGPFFASFTIFINDFEFFVCIC LGQLPHGRVLFPLNQLGAKVSFVCDEGFFT NEGRETION WSSVEDNC RRSSCGPPFFSNGMYHNTDTOFGSTVTYNSV NEGFFLLGSSFTICLVSGNVTVWBKAPICELL SCEPPFTISNGFYSNNRTSFHNOTVVTVQCL TGFDGGQLFELVERSINCTSXDQVGWWSS TPPRCISTIKCTAFEVENAREVPGNSFFSLLT LIL PRCGGGFVMVGSTPQCQTVGSSFFSLTV CSCPPFTISNGFYSNNRTSFHNOTVVTVQCL TGFDGGQFFKGRSASHCVLAGMKAKALWSSVPVC DGGFRLKGRASHCVLAGMKAKALWSSVPVC DGGFRLKGRASHCVLAGMKAKALWSSVPVC DGGFRLKGRASHCVLAGMKAKALMNSSVPVC DGGFRLKGRASHCVLAGMKAKALWSSVPVC DGGFRLKGRASHCVLAGMKAKALWSSVPVC DGGFRLKGRASHCVLAGMKAKALWSSVPVC DGGFRLKGRASHCVLAGMKAKALWSSVPVC DGGFRLKGRASHCVLAGMKAKALWSSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC DGGFRLKGRASHCVLAGMKAKALMNSVPVC					sequence	<b></b>	SITCI DNI VWSSPKDVCKRKSCKTPPDPVNG
LISGNAAHWSTKPPICQRPCGLPPTIANGGIST THRENFHYGSVYTYCROPGSGRKYELVIG PSIYCTSNDDQVGIWSGPAPQCIIPNKCTPNN BGILVSDNRSLSLSLNEVVERPCOPGTVMKGP RRVKCQALNKWEPELPSCSRVCQPPDVLHA BETQDKUNTSPGVFYSCEPGFYDLGGAAS MRCTPQGDWSPAAPTCEVKSCDDFMGQLU GRVLPVNLGLGAKVPYCDEGFCLKGSSAS YCVLAGMESLWNSSVPVCEDIFCGSPPVISNG RHTGKPLEVPFPGAAVNTCDPHDPBGTSPD LIGESTIRCTSDPQGGWSSPAPRCGILGHI QAPDHELPARLKTYNASDPPIGTSPD LIGESTIRCTSDPQGGWSSSPAPRCGILGHI QAPDHELPARLKTYNASDPPIGTSPD LIGESTIRCTSDPQGGWSSSPAPRCGILGHI QAPDHELPARLKTYNASDPPIGTSPD LIGESTIRCTSDPQGGWSSSPAPRCGILGHI QAPDHELPARLKTYNASDPPIGTSPD LIGESTIRCTSDPQGGWFCSCFSFPVINN KCTPTNVENGILVSSVENOLGKRSCKTIC PSYGRFSTICLDALVWSSPKDVCKRSCKTIC PSYGRRYNCQALNKWEPELPSCSRVCQ PSYELLVGEPSTYCTSNDDQVGWSGPAPQCTIC ANGDESTTRESPHYGSVYTYRCTGHIBLIG HSAACCLSGNTAHWSTKPPICQRPCGGPFACPTICHTSCHIGHT KCFSTNVENGILVSSVENOLGSRGK VEELVGEPSTYCTSDDDQVGWSGPAPQCTIC ANGDESTTRESPHYGSSVYTYCDEPGD QCFVMKQBRRVKCQALNKWEPELPSCSRVCQ PSYELLHGBHTTSHQDNTSPGGEVYCCHOEPGR KCFSTNVENGILVSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK VEELVGEPSTYCLNGANSSVENOLGSRGK RTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT							MVHVITDIOVGSRINYSCTTGHRLIGHSSAECI
THRENFHYGSVYTYRCNPGSGRKVFELUGE PSIYCTSNDDQVGIWSGPAPQCIPNKCTPPNV ENGILVSDNSSLFSLNEVVERCCQFGFWKGF RIVKKQALNKWEPLPYSCRYCQPFDVLHA ERTQRDKDNTSPGQEVFYSCEPCYDLRGAS, MRCTPGGDWSPAAPTCEVKSCDDFMGQLAN MRCTPGGDWSPAAPTCEVKSCDDFMGQLAN MRCTPGGDWSPAAPTCEVKSCDDFMGQLAN MRCTPGGDWSPAAPTCEVKSCDDFMGQLAN MRCTPGGDWSPAAPTCEVKSCDDFMGQLAN MRCTPGGDWSPAAPTCEVKSCDDFMGQLAN MRCTPGGGWSPAAPTCEVKSCDDFMGQLAN RWSLFWYLOLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWANSSVPVCDEGFCSPPVIPNS RHTGRPLEVFPFGKAVNYTCDPHDRGTSLKYECRP EYYGRPFSTICLDNLVWSSRDVACTGGHLIG HSSABCILSGNTAHWSTKPPLCQRFCGLPTI ANADDFSTNREWFHYGSVYTXCNLGSBGRK VFELUGBPSTYCTSNDDQVGIWSGPAPCGIPN KCTPPNVENGILVSDNRSLFSLNSVEFRCQP GFVMKGPRRVKCQALNKWEPELPSCRXVCQ PFPELHGBHTTSHDNSTSQGEVFYSCEPGY DLRGASALGTPGGDWSFEAPRCAVKSCDDP KGPPNVENGILVSDNRSLFSLNSVVCEHFCPG PPALINGRHGTPFSDDPYGKSLSYTCDPHEDR GMTNLJGGSTRCTSDPHGRUSYTCDPHEDR GMTNLJGGSTRCTSDDPHGRUSYTCDPHEDR GMTNLJGGSTRCTSDDPHGRUSYTCDPHEDR RRSSCSVSHCVLVGMRSLWNNSVPVCEHFCPG PPALINGRHTGTPSDDPYGKSLSYTCDPHEDR RRSSCSPPFPPRGMVHNDTDTQFGSTVNYSC NEGFRLIGSSTTCLVSGNNVTWDKKAPICEL SCEPPFPTISNGDPYSNNSTSHDDFEFFVGTS LNYECRPGYPGKMFSISCLENLVWSSVEDDN RRSSCGPPFFPFNSNDTPFSHDFEFFVGTS LNYECRPGYPGKMFSISCLENLVWSSVEDDN RRSSCGPPFFFNSNDTFSNNTYTVQCH CSRVCOPPELHGEHTLSHQDPGSFSTLTEI RFRCQPGFVMVGSHTVCQCNNGRSFFSLTEI RFRCQPGFVMVGSHTVCQCNNGRSFFSLTEI RFRCQPGFVMVGSHTVCQCNNGRSFFSLTEI RFRCQPGFVMVGSHTVCQCNNGRSFFSLTEI RFRCQPGFVMVGSHTVCQCNNGRSFFSLTEI RFRCQPGFFMPALINGRHGTPLQDIPYGKEVSYT CDHPDRGMTFNLIGESTRRTSEPHGNGVWS SPAPRGELPVGAACAPPRKUNGNYGMYSGVP CEGFCFNPPALINGRHGTPLQDIPYGKEVSYT CDHPDRGMTFNLIGESTRRTSEPHGNGWS SPAPRGELPVGAACAPPRKUNGHYGHWS VPLAKCTSRTDALIVGLGAKVSFVC DGGFRLKGRSASHCVLAGKALWNSVPV DGGFRLKGRSASHCVLAGKALWNSVPV DGGFRLKGRSASHCVLAGKALWNSVPV CDGFRFRFALIHFLLIHLSW RLHKRGNNAHEWFEVAHLLHSQGGSSVHP RNILQTHEENSRVLIP LLLTPLLLLLLRGSPWSQCQADDRWS PHACCTSRTDALIVGLGFGCTDQGUS PPRGELPVGAACAPAAKTIVTAVVLPLANTSY PWSWARVGPAVAAPVGCSBACATAHWVNLL LAGAPALGGGVAAAAVGCAAAVGCSDAACHALAYVPLL TAGAPALGGGVAAAPACAMPTCMPPTHALHTSPYAKLGU VAALHRLGWRGAALMAAVPLENFUNDEPFY CUGGLDWSARAGAAAAVALAKVPLL LLCGLEDVYFFILDIFGGODVSARAGAAAAVALAKPUL RLLCGGCDVYFFILDIFGG		ļ	ì				I SGNAAHWSTKPPICORIPCGLPPTIANGDFIS
PSIYCTSNDDQVGIWSGPAPQGIPNKCIPN HOGILVSDNRSLSLSNEVVERPCOPGYMKGP RRVKCQALNKWEPELPSCSRVCQPPDVHAG RRVKCQALNKWEPELPSCSRVCQPPDVHAG RRVKCQALNKWEPELPSCSRVCQPPDVHAG RRVKCQALNKWEPELPSCSRVCQPPDVHAG RRVKCQALNKWEPELPSCSRVCQPPDVHAG RRVGPVGDVFYSCEPCJUEGASAS YCVLAGMESLWNSSVPVCEQIECPSPPVIPNG RRTGRPLEVFFGKAVNYTCDPHPDRGTSFD LIGESTIKCTSDPGORGVWSSPAPRCGILGHO QAPDHFLFAKLKTQTNASDPFOTSLKYECRP EYYGRFSTICLINLVWSSYRDVCKRKSCKTP PDPVNGMWIVITDIQVGSRINTSCTTGHRLIG HSAACLLSGNTAHWSTKPPCGRCILPTI ANGDFISTNRENFHYGSVVTYRCNLGSRGKK VFELUGEPSYCTSTDDQVGIWSGPAPQGIIPN KCTPPNVENGILVSDNRSLFSLNEVVEFRCQ GFVMKCPRVKVCQALNKWEPELPSCSRVCQ PPPELLHGEHTTSHQDNTSPQGEVTYSCEPGY DLRGAASLHCTPGQDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVFSCDEGFRL KGSSVSHCVLVGMRSLWNNSVFSCDEGFRL KGSSVSHCVLVGMRSLWNNSVFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVFVCDEGFRL LSVRAGHCKTPEGPPFASPTIPINDEFFFVCI RGFPLIGSSFTICTSDPHGNOVSSPAPRCE LSVRAGHCKTPEGPPFASPTIPINDEFFFVCI KGSCDPPFPFRMMHNTDTGFGSTVTYNSV NEGPFLIGSSFTICLVSGNVTVMSKSPAPRCE LSVRAGHCKTPEGPPFASPTIPINDEFFFVCI SCEPPFTISNGDFYSNNRTSHNGTVVTVOC NEGFFLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNNRTSHNGTVVTVOC NEGFFLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNNRTSHNGTVVTVOC NEGFFLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNNRTSHNGTVVTVVC NEGFFRLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNNRTSHNGTVVTVVC NEGFFRLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNNRTSHNGTVVTVVC NEGFFRLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNRTSFHNGTVVTVVC NEGFFRLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNRTSFHNGTVVTVVC NEGFFRLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNRTSFHNGTVVTVVC NEGFFRLIGSSFTICLVSGNNVTWBKAPICEI SCEPPFTISNGDFYSNRTSFHNGTVVTVVC NEGFFRLIGSSFTICLVSGNNVTWSSVPAPRC SCEPSYDLRGASSLHCTLOSGNSVDOWSS PPRCEIPYGAACAPHPKLYQHALLGAVSNVV DEGFRLKGRSASHCVLAGKARWLDHANTSV SCEPSYDLRGASSLHCTLOGDWSFSARRCVL SCEPSYDLRGASSLHCTLOGDWSFSARRCVL SCEPSYDLRGASSLHCTLOGDWSFSSNRTSHNGTLHILIFLSWN LIKHKGNNAHENFKEVAHLHSQGGSSVHP RTJCDSSSNALGCSGNAAPHTRAGFYAKLGD VAALHRLCWRQAALMVAYPLANTSY PWSWARVGFAVELALAQVKARPDLLPGWT RTLVLGSSBNALGCSDAAP						\ \	TNDENEHVGSVVTYRCNPGSGGRKVFELVGE
ENGILYSDNESLESLNEVVEERQOPGPYMKGP RRVKCQALNKWEPELPSCSKVCQPPPDVLIAL ERTQRDKDNFSPGGEVTYSCEPGYDLRGAAS MRCTPOGDWSPAAPTCEVKSCDDFMGQLLN GRVLFYVLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSVPVCDEGFQLKGSSAS YCVLAGMESLWNSVPVCDEGFQLKGSSAS YCVLAGMESLWNSVPVCDEGFOLKGSSAS YCVLAGMESLWNSVPVCDEGFOLKGSSAS YCVLAGMESLWNSVPVCDEGFOLKGSSAS YCVLAGMESLWNSVPVCDEGFOLKGSSAS YCVLAGMESLWNSVPVCDEGFOLKGSSAS YCVLAGMESLWNSVPVCDEGFOLKGSSAS YCVLAGMESLWNSVPVCDEGFOLKGSSAS YCVLAGMESLWNSVPVCDEGFOLKGSSAS PYCVLAGMESLWNSVPVCDEFOLPDIL GAPDHFLAKLKTOTNASDFJGTSIFD EGYRFSTCLDNLWSSPKDVCKRKSCKTP BYVGRFSTCLDNLWSSPKDVCKRKSCKTP BYVGRFSTCLDNLWSSPKDVCKRKSCKTP BYVGRFSTCTNASDFJGTSTALLG HSSACLLSCNTAHWSTKPFLGVCFGCDFGTL ANGDFISTNRENHTYGOVTYCNLGSGRGK VFELVGERSTCTSNDDQVGWSGPAPQCIPN KCTPPNVENGLVSDNASLFELNEVVEFRCOP GFWKGRRWKCQDWSGPAPQCIPN KCTPPNVENGLVSDNASLFELNEVVEFRCOP GFWKGRRWKCQDWSSEPAPCAVXSCDDF LGQLPHGRVLPLALQGAKSFVCDEGFUL KGSSVSHCVLVGMRSLWNSVPVCEHIFCPN PPALLNGRHTGFTBODIPYGKESYTCDPHFDR GMTSNLIGESTIRCTSDPHONGVWSSPARCE LSVRAGHCKTPGOPFASPITINDFEFPYGTS LNYECRFGYFGGFFNGWYHINDTQFGSTVNYSC REGFRLIGSPSTTCLVSGNNVTWDKKARICEII SCEPPPTISNIGPTSNNTUTNTOTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKARICEII SCEPPPTISNIGPTSNNTUTNTOTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKARICEII SCEPPPTISNIGPTSNNTUTNTOTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKARICEII SCEPPPTSNGDFYSNNTSFHOTVYTYQCH TGPDGEQLFELVGERSYTCTSKDDQVGWSS PPPRCISTNKCTAPEVENARIVYGNRSFFSLTEII IRFRCQFGFWMGSHTVQCQTNORWGFKLPH CSRVQPPFELINGERTTLNQLQGAKVSPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC DEGFRLKGRSASHCVLAGMKALUNSSTPLILITL LLLPHTLLLLLLTGRSHAGRLTTAVVLPLLATNSY PWSWARKOFAVELALGORVARPDLLFGMT UTAGAPAAGGFGCVVDCYVAADPGGEHCFF LVEGFRWVABRAGFGAAMTYDDDNESCFLIFUT RLLTTMFKCGFGAVLAGWARPDLLWTY RLLETTMFKCGFAVELAGA	l	1					PSTYCTSNIDDOVGIWSGPAPOCIJPNKCTPPNV
RRVKCQALNKWEPELPSCSRVQCPPPDVIHA ERTQRNENDFSFGGEVTYSEGFOTNLRGAAS MRCTPQRDWSFAGPTCEVKSCDDFMQGLIN GRVLFVVLLQLGAKVDFVCDEGFOLKGSSAS YCVLAGMESLWNSSVPVCEQFCPSPVPNG RHTGKPLEVFPFGKAVNYTCDFBPDRGTSEF) LIGESTIRCTSDPQGNGWSSPAPRCGLIGHC QAPDHFLFAKLKTQTMASDFPIGTSLKYECRP EYVGRFSTICLDRLWSSPKDVCKRKSCKTP PDFVNGMVHVITDIQVGSRNYSCTTGHELIG HSSAECLISONTAHWSTRFPIGREGLPPTI ANGDFISTNRENHYGSVYTYRCNLGSGRGK VFELVGEPSIYCTSNDDQVGJWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLRSVVEFRCQP GFVMKGPRRVKCQALNKWEPLFSCSRVCQ PFPELLIGEHTTSHQDNTSPGQEVFYSCEPGY DLRGAASLHCTPQGDWSSPAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFTL KGSSVSHCVLVGMRSLWNSVPVCEHFCCPN PPALINGHTGTPSGDIPYGKEISYTCDPHDR GMTNLIGESTIRCTSDPHGRVWSSPAPRCE LSVRAGHCKTPROPFASPTIPNDFEFPVGTS LNYRCHGFFFINGVWSSPAPRCE LSVRAGHCKTPROPFASPTIPNDFEFPVGTS LNYRCHGFFFINGVWSSPAPRCE LSVRAGHCKTPROPFASPTIPNDFEFFVGTS LNYRCHGFFFINGVWSSPAPRCE LSVRAGHCKTPROPFASPTIPNDFEFFVGTS LNYRCHGFFFINGVWSSPAPRCE LSVRAGHCKTPROPFASPTIPNDFEFFVGTS LNYRCHGFFFINGVWSSPAPRCE LSVRAGHCKTPROPFASPTIPNDFEFFVGTS LNYRCHGFFFINGVWSSPAPRCE LSVRAGHCKTPROPFASPTIPNDFEFFVGTS LNYRCHGFFFINGVWSSPAPRCE USPPERINGDFYSNRTSFHNGTVYTYQCH GGFFRLIGBSTTCLVSGNNVTWDKKAPICEII SCEPPTISNGDFYSNRTSFHNGTVYTYQCH GGFFRLIGBSTTCLVSGNNVTWDKKAPICEII SCEPPTISNGDFYSNRTSFHNGTVFTVGCH CSRVCQPPFEILNGGHTSLAVFNVTWDKKAPICEII SCEPPTISNGDFYSNRTSFHNGTVFTVGCH CSRVCQPPFEILNGGHTSLAVFNVTWDKKAPICEII SCEPPTISNGDFYSNRTSFHNGTVFTVGCH CSRVCQPPFEILNGGHTSLAVFNVTWDKKAPICEII SCEPPTISNGDFYSNRTSFHNGTVTYQCH CSRVCQPPFEILNGGHTSLAVFNVTWDKKAPICEII RFRCQFGFVMVGSHTVLCGTNGTWGFKSLT VKSCDDFLGGLJGGFTLAVFNVTWDKAPICEHCFF CDHPDRGMTFTLLIGESTIRRTSEPHGNOWWS SPAPRCELPVGAACHPPRINLGLGAKVSFVC DGGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCNPPALINGHTGTHVLJUFGKEVSTY CDPHDPRGMTFTLLIGESTIRRTSEPHGNOWWS SPAPRCELPVGAACHPFRUNGHTSLIFLLIIFLSWI LHRKGNNAHENPEVAHLIHSOGGSSVHP RILOTNEENSRVLP PHAKCTSSTPLANGGRGSSVHP RILOTNEENSRVLP HPRAVTLGFGCCVYAAAPVGARGHTGGHVSL HRHRKGNNAHENPEVAHLIHSOGGSSVHP RILOTNEENSRVLP HPRAVTLGFGCCVYAAAPVGARGHTGHVSL HRHRKGNNAHENPEVAHLIHLIFLLIIFLSWI LLEFTMFRKGRVYIVCSSPDAFRTLMLLLEH LLEFTMFRKGRVYIVCSSPDAFRTLMLLALEH LLEFTMFRKGRVYIVCSSPDAFRTLMLLALEH LL	l				l .	1	ENGIL VSDNPSI ESI NEVVERCOPGEVMKGP
ERTORDKDNFSPGGEVTYSCEPGYDLRAAS   MRCTPOGDWSPAAPTCEVKSCDDFMGQLLN   GRVLFYVLQLGAKVDFVCDEGTGLKGSSAS   YCVLAGMESLWNSVPVCDEGTGLKGSSAS   YCVLAGMESLWNSVPVCDEGTGLKGSSAS   YCVLAGMESLWNSVPVCDEGTGLKGSSAS   YCVLAGMESLWNSVPVCDEGTGLKGSSAS   YCVLAGMESLWNSVPVCDEGTGLKGSSAS   YCVLAGMESLWNSVPVCDEGTGLKGSSAS   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   GROWN   G		1				ł	PRVKCOALNK WEPEL PSCSR VCOPPPDVLHA
MRCTPGGDWSPAAPITCEVKSCDDFMGQLIN GRVLFVVNLQLGAKUPVEVDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQFCPSPPVPNO RHTGKPLEVFPFGKAVNYTCDPHPDRGTSFD LIGESTIRCTSDPGONGWSSPAPRGLIGHC QAPDHFLFAKLKTOTNASDPGTSTLKYECRP BYYGRPFSITCLDNLWSSPKDVCKRKSCKTP PDPVNGMYHVITDIQVGSRNYCTTGHRLIG HSSAECILSCNTAHWSTKPPLCORPCGLPTI ANGDFISTNRENFHYGSVVTYCHGSRGKK VFELVGEPSIYCTSNDDQVGIWSGPAPCCIIPN KCTPPNVENGILVSDNRSLFSLRSVEFRCPY GGYMKGPRRVKCQALNKWEPELFSCSRVCQ PPPELHGBHTTSHQDNRSHGSERKK VFELVGEPSIYCTSNDDQVGIWSGPAPCCIIPN KCTPPNVENGILVSDNRSLFSLRSVEFRCPY DLRGAASLHCTPQGDWSFEAPRCAVKSCDDF LGQLPHGGHTVFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNSVSPVCEHFCFN PPALINGRHTGTPSGDIPYGKEISYTCDPHDR GMTNLIGESTIRCTSDPHGRGVWSSPAPRCF LSVRAGHCKTPEQFPFASPTIPNDFEFPVGTS LNYECRRGVFGKMFSISCLENLVWSSVEDNC RRSSCGPPEFPSNGWVHINTDTQGGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGESSYTCTONTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGESSYTCTONTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGESSYTCTONTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGESSYTCTONTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGESSYTCTONTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGESSYTCTONTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGERSYTCTONTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGESSYTCTONTVDKKAPICEIL SCEPPTISNGDFYSNNTSFHNCTVVTYQCH TGPDGEOLFELVGESSYTCTONTVDKKAPICEIN SCEPSTURGAASLHCTTPQDWSPEAPRCTV KSCDDFLGGJEHGWLLIPLNLQLGAKVSPVC DEGFRLKGRSASHCVLAGMKALWNSSYPVC EQIFCNNPALINGRHTGTHTUGHTST TCDPGTLLVGGFRYCTONGWS SPAPRCELPVGAACHPHPKINGTWYSL YLPGMTISTTCDPGYLLVGKGFRTGTHSL YLPGMTISTTCDPGYLLVGKGFRTGTHSL YLPGMTISTTCDPGYLLVGKGFRTGTHSL YLPGMTISTTCDPGYLLVGKGFRTGTHSL YLPGMTISTTCDPGYLLVGKGFRTGTHSL YLPGMTISTTCDPGYLLVGKGFRTGTHFILLIIFLSWI HTRAGNAHAPEADAPGFRFTAGSRIRLLLL LLLIPLLLLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVVAAAPVGARGSSVHP TLAGAPAAGFGCVVAAAPVGARTAAWRVPLL TAGAPAAGFGCVVAGAPGTAAWRVPLL TAGAPAAGFGCVAACHPROTATHAURLALEA HNPAVFLGPGCVAAAPVGARTAAWRVPLL TAGAPAAGFGCVAALGGGAGAPAPRPW FEGGGODVSAAGAGAAGAAAATHTVADPNSPPY			1	1	i		ERTORDY DNESPGOEVEYSCEPGYDLRGAAS
GRVLFYNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQICPSPPVTPNG RHTGKPLEVFFGKAVNTCDPHDPGGTSPD LIGESTIRCTSDPQGNGWSSPAPRCGLIGHC QAPDHELFAKLKTQTNASDFPIGTSLKYECRP EYVGRPFSTLCLDRLWSSPKDVCKRKSCKTP PDPVNGMVHVITDIQVGSRRNYSCTTGHRLIG HSSAECILSGNTAHWSTKPPICORIPCGLPPTI ANGDFISTNRENPHYGSVVTYRCNLGSRGRK VFELVGERSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVERGILSONTAHWSTKPPICORIPCGLPPTI ANGDFISTNRENPHYGSVVTYRCNLGSRGRK VFELVGERSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVERGILSONTAHWSTKPPICORIPCGLPPTI ANGDFISTNRENPHYGSVVTYRCNLGSRGRK VFELVGERSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVERGILSONTSNEWSPVCEHIFCPN PPRLINGHTFINDONSFSPCVEGEGFL KGSSVSHCVLVGMRSLWNSVPVCEHIFCPN PPALINGHTGPISDIPYGRESIYCTDPHEPR GMTSNLIGESTTRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQPPASPTIDFEPFVGTS LNYECRPGVPGKMPSISCLENLVWSSVEDNC RRKSCGPPEFFRGMVHINDFEFFVGTS LNYECRPGVPGKMPSISCLENLVWSSVEDNC RRKSCGPPEFFRGMVHINDFEFFVGTS LNYECRPGVPGKMPSISCLENLVWSSVEDNC RRKSCGPPEFFRGMVHINDFEFFVGTS LNYECRPGVPGKMPSISCLENLVWSSVEDNC RRKSCGPPEFFRGMVHINDFEFFVGTS LNYECRPGVPGKMPSISCLENLVWSSVEDNC RRKSCGPPEFFRGMVHINDFEFFVGTS LNYECRPGVPGKMPSISCLENLVWSSVEDNC RRKSCGPPEFFRGMVHNTDFEFFVGTS LNYECRPGVPGKMPSISCLENLVWSSVEDNC RRKSCGPPEFFRGMVHNTDVGSTVNYSC NEGFRLIGSPSTTLLVSGNNNTWDKKAPICEII SCEPPTISNGDFYSNNNTSFHRGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNRCTAPEVENARVPGNSFTSLTEI RRRCQPGFVMYGSHTVQCTNORWGFKLPH CSRVCQPPFELLHGEHTLSHQDMPSGCVFY SCEPSYDLRGAASHCTPGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPINLQLGAKVSPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVLAGMKUNSSVPVC DEGFRLKGRSASHCVL		1	ì	j	1	1	AMCTROGOWSPA APTCEVKSCDDFMGOLLN
YCVLAGMESLWNSSYPYCEQICFEPPVIPMOR RHTGKPLEVPFGKAVNYTCDPHPDRGTSFD LIGESTIRCTSDPQGRGVWSSPAPKGLIGHG QAPHHELFAKLKTOTHASDPIGTSLKYECRP EYYGRPFSITCLDRLVWSSPKDVCKRKSCKTP PDPVNGMYHVITDIQVGSMYSSPAPKGLGHGK VFELVGEPSIVTSNDDQVGIWSGPAPQCIIPM RANGDFISTNRENFHYGSVYTYRCHLGRGKK VFELVGEPSIVCTSNDDQVGIWSGPAPQCIIPM KCTPPNVENGILVSDNRSLFSLNEVVEFRCQP GFVMKGPRAVKQALIKBVEPLSSGSRVCQ PPEHLHGEHTPSHQDNFSRGQEVFYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLILQLGAKVSFVCDEGFRL KGSSVSHEVU JVGMSSL WANSPVVCEHIFCPN PPALINGRHTGTPSGDIPVGKEISYTCDPHEDR GMTPNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKYTEOFPFASPTIPRIDFEFPVGTS LNYECRGVYFGKMFSISCLERLVWSSVEDING RRKSCGPPPFSPNGMYHINITDTGGSTVNYSC NEGFRLIGSPSTTCLVSGNNYTWKAPICEI SCEPPTISNGDFYSNNKTSHINGTVVTYQCI TGPDGEQLFELVGGRSIVCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVQQPPEBLHGEHTLSGNNSTSHRGTVYTYQCI KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFFLKGRSSHCVLAGMKALWNSSVPVC EQIFCTNPPALINGRHTGTPLGDIPYGKEVSTY CDPHEPDRGMTFNLIGESTIRRTSEPHGNOVWS SPAPRCELVGAACHPPKIQNGHYGGHVSL VLPGMTISTYCDGFYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSPLPMGISKELEMKLVYH YGDVYTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENTREVAHLHISQGGSSVHP VGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENTREVAHLHISQGGSSVHP VGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENTREVAHLHISQGGSSVHP VGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENTREVAHLHISQGGSSVHP VGDYVTLKCEDGYTLEGGRSWCLALLL LLIPPILLLILLIGGHAGNALTVAVVLPLANTSY PWSWARVQFAVELALAQVKAPDALDFWT VTXTUGSSENALGVCSTAAPLAAVDLKWE HNPAVFLGPGCVVAAAPVGRTAHWRVPLL TAGAPALGFGVKDEYALTTRAGFSYAKLGDF VAALHRRLGWRQALMULAYRRGDEHCFF LVEGLFMRVRRUNITVDHLEFAEDDLSHTT RILLRTMPRKGRWYTICSSPAAFLAMVLLALEA GLCGEDYVFFHILDIFQGSLQGGGGPAPRRPW REGDGGDVSARGAFGAAMITTKXDPDNPEYL	i		1				CRIM EDIVIT OF GAKADEACHER CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CON
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PDPYNGMYHVITDIQVGSRNYSCTIGHALIGH HISSAECL SGNTAHWSTKPPICORPEGL.PPTI ANGDFISTNRENHYGSVVTYRCNLGSRGKK VFELVGEPSTYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGIL NSDNRSLFSLNEVVEFRCQP GFVMKGPREVKCQALNKWEPLEPSCSRVCQ PPFELLIGEHTTSHQDNFSPGQEVTYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCODF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PAILNGRHTGTISGDIPYGKEISYTCDPHEPD GMTFNLIGESTIRCTSDPHGNOVWSSPAPRCE LSVRAGHCKTPEQPFFASPTIFINDFEFFVGTS LNYECRPGYFGKMFSISCLENLWSSVEDNC RRKSCGPPPEPFNGMVHNIDTOFGSTVNYSC NEGFRLIGSFSTTCLVSGNNVTWDKKAFICEII SCEPPPTISNGDFYSNNTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGGLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGGLFELVGERSIYCTSNRTSPHNGTVVTYQCH TGPDGGLFELVGERSIYCTSNRTSPHRGYBYFL SCEPSYDLRGAASLACTPAGDWSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC DEGFRLKGRSASHCVLAGMKALWALIGHTSKDPHACH UKTVLGSSENALGVCGGSVHALTTRAGFSYAKLGDF VAALHRALGWEQALMLVAYRGDEHCFF LVEGLFMWRVGRAVALTIVALDALBA GLCGEDVYFHLDIFGGSLGGGGPAPRRTM RLLLTMPRGGRVVITCSSPDAFRTIMLLALEA GLCGEDVYFHLDIFGGSLGGGGPAPRAFT FROGGOGGPAPRTW FROGGODDVSAROAFALTTYKDPDNPEYL							CALCULATION ON ANGERLUACE FOR A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULATION OF A CALCULAT
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VEELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGIL VSDNRSLFSLNEVVEFRCOP GFVMKGPRRVKCQALNKWEPELPSCSRVCQ PPPELLHGEHTPSHQDNTSPROQEVTYSCEPGY DLRGAASHLCTTPQDWSSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGARVSFVCDEGFRL KGSSVSHCVL.VGMRSLWNNSVPVCDEHIFCPN PPALLNGRHTGTPSGDIPYGKEISYTCDPIPDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEGPFPASPTIPINDFEFFVGTS LNVECRPGYPGKMFSISCLENLVWSSVEDNC RRKSCGPPPEPFNGMYHINDTOTFGSTVMYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHOTTVYTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGR WGPKLPH CSRVCQPPPELHGHTLSHQDNFSPGQEVFY SCEPSYDLRGAASHLCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPFKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS SPAPRCELPVGAACPHPFKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKXYH YGDVYTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIGTSTIRFILLIHELSWI ILKHRKGNNAHENFKEVAIFILHSQGGSSVHP RTILQTNEENSRVL) HGRSARLAAVFAEAMPGPRRPAGSRLRLLLL LLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWARVGPAVELAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLLWBE HNRAVFLGPGCVYAAAPVGRTTAHWRVPLL TAGGPALGFGVKACPAVALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLITTVDHLEFAEDDLSHYT RLLRTMFRKGRVTYICSSPDAFRTLMLLALEA GLCGEDYYFFHLDIFGQSLOGGQGPAPRRPW FRGDGDOVSAROAGOAAKITTVKDPLSPRAFR			ì				HSSAECILSUNTARWSTAFFICQAI COEFF II
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DLRGAASLHCTPQODWSPEAPR.CAYKSCDDF LGQLPHGRVLFPLINLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PPALINGHGTGTPSGDIPYGKEISYTCDPHDDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEOFPFASPTIPNDFEFPVGTS LNYECRPGYPGKMFSISCLENLVWSSVEDNC RRKSCGPPPEPNGMVHINITDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGFYSNNRTSFINGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTINKCTAPEVENAIRVPGNRSFFSLTEI IRPRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGFPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIECTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENFEVAHLHLSQGGSSVHP RTLQTNEENSRVLP BTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRAGSRLRLLLL LLLPPLLLLLRGISHAGNLTVAVVLPLANTSV PWSWARVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEBLCFF LVEGLFMRYDRINTTVDFLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQAPRRPP FRGDGGDDVSAROAFQAAKIITYKDPDNFEYL					1		GFYMKGPKKVKCQALINK WEI EEI SCSKVCQ
LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHFCPN PPALLNGRHTGTPSGDIPYGKEISYTCDPHDDR GMTFNLIGESTIRCTISDPHGNGVWSSPAPRCE LSVRAGHCKTPEQPFPASPTIPNDFEFFVGTS LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEPFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPTISNGDFYSNNRTSFHNGTVYTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTINKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDMFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSSHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIECTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSVLP RTLQTNEENSVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALATRAGPSYAKLGDF VAALHRRLGWERQALMLYAYAYRODEEHCFF LVVGLFMRWRDRLITVDHLEFAEDDLSHYT RLLRTMPRKGRVIVICSSPDAFRTIMLLALEA GLCGEDYVFFHLDIFGQSLQGGGGPAPRRPW FRGDGGDDVSAROAFQAAKIITYKDPDNFEYL	1	Į.				1	PPPEILHGEHTPSHQDNPSPOQLVI TSCLIGT
KGSSVSHCVLVGMRSLWNNSVPVCEHIFCN PPAILNGRHTGTPSGDIPYGKEISYTCDPHDDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEOFPFASPTIPNDFEFPVGTS LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVGGNNVTWDKKAPICELI SCEPPPTISNGDFYSNNRTSFINGTVYTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVWGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGGEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKLQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENFKEVAHLHSQGGSSVHP RTLQTNEENSRVLP RTLQTNEENSRVLP HRRAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYAALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYVRPGDEEHCF LVEGLFMRVRDRLNITVOPHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRILMLLALEA GLCGEDYVFTHLDIFGQSLQGGGGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL	j	1					DERGAASEHCTPQQDWSFEAFRCAVRGCDDI
PPAILNGRHTGTPSGDIPYGKEISYTCDPHPDR GMTFNLIGESTTRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFFPASPTIPINDFEFPVGTS LNYECRPGYPGKMFSISCLENLVWSSVEDNC RRKSCGPPPEPFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTICLVSGNNVTWDKKAPICEII SCEPPTISNGGFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLLGSFWSQCQADDRWD PPLAKCTSTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  ### HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLIPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLFGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRGRINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTIMLLALEA GLCGEDYVFFHLDIFGQSLQGGGPAPRRPW FRGDGGODYSAROAFQAAKIITYKDPDNFEYL RTGDGGODYSAROAFQAAKIITYKDPDNFEYL FRGDGGODYSAROAFQAAKIITYKDPDNFEYL FRGDGGODYSAROAFQAAKIITYKDPDNFEYL FRGDGGODYSAROAFQAAKIITYKDPDNFEYL FRGDGGODYSAROAFQAAKIITYKDPDNFEYL FRGDGGODYSAROAFQAAKIITYKDPDNFEYL FRGDGGOVSAROAFQAAKIITYKDPDNFEYL FRGDGGOVSAROAFQAAKIITYKDPDNFEYL FRGDGGOVSAROAFQAAKIITYKDPDNFEYL FRGDGGOVSAROAFQAAKIITYKDPDNFEYL FRGDGGOVSAROAFQAAKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL FRGDGGOVSAROAFQAKKIITYKDPDNFEYL	i						LGQLPHGKVLFPLNLQLGAKVSFVCDLGFIECPN
GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFPFASPTIPINDFEPPVGTS LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEPFNGMYHINTDTOFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIVCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEII IRFRCQPGTVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPELHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SFAPRCELPVGAACPHPFKIQNGHYIGGHVSL YLPGMTISYTCDPGYPLLVGKGFIFCTDQGIWS QLDHYCKEVNCSPPLFMNGISKELEMKKVYH YGDVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRPAGSRLRLLLL LLPFLLLLLGRSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAPRPGDEEHCFF LVEGLFMRVRGRUTITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTILMLALAEA GLCGEDYVFFHLDIFQSLLOGGGGPAPRRPW FRGDGODVSAROAFQAAKIITYKDPDNPEYL					1		RGSSVSHCVLVGMRSLWMVSVI VCLIM CITY
LSYRAGHCKTPEQFPFASPTIPNDFEFPVGTS LNYECRPGYPGKMFSISCLENLVWSSVEDNC RRSCGPPPEPFNGMVHINITDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGWSS PPPRCISTNKCTAPEVENARVPGNRSFFSLTEI IRFRCQPGFVMYGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFEKRBASSHCVLAGMKALWNSSVPVC EQFFCNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTILQTNEENSRVLP HGSSARLAAVPAEAMPGFRRPAGSRLRLLLL LLLPPLLLLLRGISHAGNLTVAVVLPLANTSY PWSWAIRVGFAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLK WE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEBCFF LVGGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFHLDIFGQSLQGGQGPAPRRPW FRGDGGDVSARQAFQAAXIITYKDPDNPEYL	1	1			(	ļ.	PPAILNGKHIGIPSUDIFIGKEISTICDIII DK
LNYECRPGYFGKMFSISCLERLVWSSVEDNC RRKSCGPPPEPFNGMVHINTDTQFGSTVNYSC NEGRELIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENARRYPGNRSFFSLTEII IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQFCPNPPAILNGRHTGTPLIGDIPYGKEVSYT CDPHPDRGMTTPNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP WSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGFTAHWRVPLL TAGAPALGFGVWDEYALTTAGGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRW FRGDGGDVSARQAFQAAXIITYKDPDNPEYL	1			1	1	1	GMTFNLIGESTIKCTSDFHONGV WSSI AI KCD
RRKSCGPPPEPRIOMYHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNODFYSNNRTSFINGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTINKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSFAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DGFFLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKVYH YGDVYTLKCEDGYTLEGSFWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAHHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLVAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGGGODVSARQAFQAKIITYKDPDNPEYL			-		1		LSVRAGHCK IPEQFFFASFIIFIIADIEIT VOIS
NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTINGR WGPKLPH CSRVCQPPPEILHGEHTLSHQDNRSPGGVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLVAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGGGODVSARQAFQAKKIITYKDPDNPEYL	1						LNYECRPGYFGRWF313CLENLYW337LDNC
SCEPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPARCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLL LLLPPLLLLLRGISHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSAROAFQAAKIITYKDPDNPEVL	ł			1			RRKSCGPPPEPFNGMVHINTDTQFGSTVNTSC
TGPDGEQLFELVGERSIYCTSKDDQVGVWSS PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFYMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSSRLRLLLL LLLPPLLLLLRGISHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYPRGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRPW FRGDGODVSAROAFQAAKIITYKDPDNPEVL		i		1	}		NEGFRLIGSPSTICLVSGNNVIWDRRATICEI
PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDMFSPGGEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDVYFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSAROAFQAAKIITYKDPDNPEYL			1				SCEPPPTISNGDF YSNIKISPHNGI VVI I QCH
IRFRCQPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGFPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQFAPRRPW FRGDGGODVSARQAFQAAKIITYKDPDNPEYL	1				1		TGPDGEQLFELVGERSIYCISKDDQVGVW33
CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKAL WNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQFAPRRPW FRGDGGODVSARQAFQAAKIITYKDPDNPEYL	ì	i	i		1		PPPRCISTNKCI APEVENAIKVPUNKSFISLIEI
SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPINLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFHMGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWARVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGQGPAPRRPW FRGDGODVSAROAFQAAKIITYKDPDNPEYL							IRFRCQPGFVMVGSH1VQCQ1NGRWGFXLF11
KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRGSHAGNLTVAVVLPLANTSY PWSWAIRVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSAROAFQAAKITTYKDPDNPEYL	ļ	1					CSRVCQPPPEILHGEHTLSHQDNF5FQQEVFT
DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYPRGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGGPAPRPW FRGDGGODVSARQAFQAAKIITYKDPDNPEYL	1	j			1		SCEPSYDLRGAASLHCIPQGDWSPEAPRCIV
EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRINITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSAROAFQAAKIITYKDPDNPEYL	1		1			J	KSCDDFLGQLPHGKVLLPLNLQLGAKVSFVC
CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL	1		1	1	1		DEGFREKGRSASHCVLAGMKALWNSSVPVC
SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL			1	1			EQIFCPNPPAILNGRHIGTPLGDIPYGKEVSYT
YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGFTTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL					1		CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS
QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL			ł		1		SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL
YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGFTTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQARQAFQAAKIITYKDPDNPEYL	1						YLPGMTISYTCDPGYLLVGKGFIFCIDQGIWS
PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQARQAFQAAKIITYKDPDNPEYL			1	1	J		QLDHYCKEVNCSFPLFMNGISKELEMKKVYH
ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNEENSRVLP  803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQARQAFQAAKIITYKDPDNPEYL			[		1		YGDYVTLKCEDGYTLEGSPWSQCQADDRWD
RTLQTNEENSRVLP  803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQARQAFQAAKIITYKDPDNPEYL	1	1	- [	1	1		PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI
803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL	1	1	1		1		ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP
803 2153 A 6574 2 3233 HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL	1		1		1		RTLOTNEENSRVLP
LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL	000	- 2:52		6574	12	3233	HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL
PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSAROAFQAAKIITYKDPDNPEYL	803	2153	A	05/4	-	1 3233	LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY
VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL							PWSWA\RVGPAVELALAQVKARPDLLPGWT
HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL						{	VRTVLGSSENALGVCSDTAAPLAAVDLKWE
TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL						1	HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL
VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL							TAGAPALGEGVKDEYALTTRAGPSYAKLGDF
LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL							VAALHRRLGWERQALMLYAYRPGDEEHCFF
RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL						*	I VEGLEMRVRDRLNITVDHLEFAEDDLSHYT
GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW FRGDGODVSARQAFQAAKIITYKDPDNPEYL							RURTMPRKGRVIYICSSPDAFRTLMLLALEA
FRGDGODVSARQAFQAAKIITYKDPDNPEYL					1		GLCGEDYVFFHLDIFGOSLOGGOGPAPRRPW
EFLKQLKHLAYEQFNFTMEDGLVNTIPASFH	ŀ						FRGDGODVSAROAFOAAKIITYKDPDNPEYL
El Piderer 1941							FELKOLKHLAYEOFNFTMEDGLVNTIPASFH
	I						Dr. Dr. Arean

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	иепсе		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
			]	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		}		residue of	sequence	/=possible nucleotide deletion, \=possible
		Ì		peptide		nucleotide insertion
			<u> </u>	sequence	ļ	DGLLLYIQAVTETLAHGGTVTDGENITQRMW
			}		1	NRSFQGVTGYLKIDSSGDRETDFSLWDMDPE
		ļ			1	NGAFRVVLNYNGTSQELVAVSGRKLNWPLG
			1	1	ļ	YPPPDIPKCGFDNEDPACNQDHLSTLEVLALV
		1	1	Į	1	GSLSLLGILIVSFFTYRKMQLEKELASELWRVR
		\		]		WEDVEPSSLERHLRSAGSRLTLSGRGSNYGSL
				1		LTTEGQFQVFAKTAYYKGNLVAVKRVNRKR
			1	1		IELTRKVLFELKHMRDVQNEHLTRFVGACTD
				1		PPNICIL TEYCPRGSLODILENESITLD WMFRY
	1	1				SLINDIVKGMLFLHNGAICSHGNLKSSNCVV
		1	1		ł	DGREVLKITDYGLESFRDLDPEQGHTVYAKK
				1	1	I WTAPELLRMASPPVRGSQAGDVYSFGIILQE
		1		1		IAIRSGVFHVEGLDLSPKEHERVTRGEQPPFR
1			1			PSLALOSHLEELGLLMQRCWAEDPQERPPFQ
	Ì	1		i		OIRLTLRKFNRENSSNILDNLLSRMEQYANNL
	1	1			1	EELVEERTQAYLEEKRKAEALLYQILPHSVAE
		1				QLKRGETVQAEAFDSVTIYFSDIVGFTALSAE
1		}			1	STPMQVVTLLNDLYTCFDAVIDNFDVYKVET
{	ĺ					IGDAYMVVSGLPVRNGRLHACEVARMALAL
	}	İ	1			LDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGV
		}	1		1	VGLKMPRYCLFGDTVNTASRMESNGEALKI
			1			HLSS\ETKAVL\EEFGGFELELRGDVEMKGKG
		1				KVRTYWLLGERGSSTRG DAPGRPPVRLPTMELEDGVVYQEEPGGSGAV
804	2154	A	6585	2	3837	MSERVSGLAGSIYREFERLIVRYDEEVVKELIP
				1		LVVAVLENLDSVFAQDQEHQVELELLRDDNE
			1		1	QLITQYEREKALRKHAEEKFIEFEDSQEQEKK
	-	ł		1		DLQTRVESLESQTRQLELKAKNYADQISILEE
		1		1	1	REAELKKEYNALHORHTEMIHNYMEHLERT
	1	1				KLHOLSGSDOLESTAHSRIRKERPISLGIFPLP
}	1				1	AGDGLLTPDAOKGGETPGSEQWKFQELSQPR
		1				SHTSLKDELSDVSQGGSKATTPASTANSDVA
					}	TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV
	1					QVAQETRNYSTGSAENEEKSEVQAIIESTPEL
						DMDKDLSGYKGSSTPTKGIENKAFDRNTESL
		Ì				FEELSSAGSGLIGDVDEGADLLGMGREVENLI
1			İ			LENTQLLETKNALNIVKNDLIAKVDELTCEK DVLQGELEAVKQAKLKLEEKNRELEEELRKA
į	}	ł			1	RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE
					1	MARVLMERNQYKERLMELQEAVRWTEMIR
		1				ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK
}		1		i		KPEPPVNLKYNAPTSHVTPSVKKRSSTLSQLP
1		1			ļ	GDKSKAFDFLSEETEASLASRREQKREQYRQ
i		ļ		į.	1	VKAHVQKEDGRVQAFGWSLPQKYKQVTNG
ł	-	1	1			QGENKMKNLPVPVYLRPLDEKDTSMKLWCA
		1		Į.		VGVNLSGGKTRDGGSVVGASVFYKDVAGLD
1		1	1			TEGSKQRSASQSSLDKLDQELKEQQKELKNQ
1	1	1				EELSSLVWICTSTHSATKVLIIDAVQPGNILDS
						FTVCNSHVLCIASVPGARETDYPAGEDLSESG
				1		OVDKASLCGSMTSNSSAETDSLLGGITVVGC
ì		1				SAEGVTGAATSPSTNGASPVMDKPPEMEAEN
	1	1		1		SEVDENVPTAEE\ATEATEGNAGSAEDTV\DIS
	ļ	1		1	1	THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
					ı	OTGVYTEHVETDPLG\VUIPEDLSEV IUSSND
						QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND SDAYKDOISVLPNEODLVREEAQKMSSLLPT
						SDAYKDQISVLPNEQDLVREEAQKMSSLLPT
						SDAYKDQISVLPNEQDLVREEAQKMSSLLPT
						SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SII SIVHVKGIVLVALADGTLAIFHRGVDGQW
						SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVOPKAMKIEKSFDAHPRKESQVRQ
						SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG YRNKIYVVOPKAMKIEKSFDAHPRKESQVRQ
						SDAYKDQISVLPNEQDLVREEAQKMSSLLPT MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD SILSIVHVKGIVLVALADGTLAIFHRGVDGQW DI SNYHLLDLGRPHHSIRCMTVVHDKVWCG

			LCEA	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide		l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginne, 3-30 me,
derice	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	ì	peptide		/-possible nucleotide deletion, \-possible
	Ì		{		1	nucleotide insertion
			<b></b>	sequence	<del></del>	NRLWVGTGNGVIISIPLTETVILHQGRLLGLR
				!		ANKTSGVPGNRPGSVIRVYGDENSDKVTPGT
	1	1	ì	ļ	1	ANK ISO VPOINT OF OFFICIAD ANK EEVA VPGOV
	1	1	ì			FIPYCSMAHAQLCFHGHRDAVKFFVAVPGQV
		}	1	ļ		ISPQSSSSGTDLTGDKGRGHLHRSLVVRRP
	1	<del> </del>	6605	469	2602	FGRLLWGTAFKSWKMKAPIPHLILLYATFTQ
805	2155	A	0003	403	2002	SLKVVTKRGSADGCTDWSIDIKKYQVLVGEP
		1	İ	]		VRIKCALFYGYIRTNYSLAQSAGLSLMWYKS
				1		SGPGDFEEPIAFDGSRMSKEEDSIWFRPTLLQ
	1	ì	ì		Ì	DSGLYACVIRNSTYCMKVSISLTVGENDTGL
	}		Į	1		DSGLYACVIRNS I I CWR VSISLI V GENDIGE
	1	1		1		CYNSKMKYFEKAELSKSKEISCRDIEDFLLPT
			1	1	ļ	REPEILWYKECRTKTWRPSIVFKRDTLLIREV
		1		1		REDDIGNYTCELKYGGFVVRRTTELTVTAPL
		1		1	Į.	TDKPPKLLYPMESKLTIOETQLGDSANLTCRA
		1				FFGYSGDVSPLIYWMKGEKFIEDLDENRVWE
	1	1	1	i		SDINKILKEHLGEQEVSISLIVDSVEEGDLGNYS
				1	ľ	CYVENGNGRRHASVLLHKRELMYTVELAGG
	1	1	1			CYVENGNGKKHASVLLIKKELWIIIVELA
	İ	1		1	1	LGAILLLLVCLVTIYKCYKIEIMLFYRNHFGA
	1	1	ļ	İ		EELDGDNKDYDAYLSYTKVDPDQWNQETGE
		1	i	1	1	EERFALEILPDMLEKHYGYKLFIPDRDLIPTGT
	1	1	l l		1	YIEDVARCVDOSKRLIIVMTPNYVVRRGWSIF
	j	1	ļ	)		ELETRLRNMLVTGEIKVILIECSELRGIMNYQE
			i i			VEALKHTIKLLTVIKWHGPKCNKLNSKFWKR
				İ		LQYEMPFKRIEPITHEQALDVSEQGPFGELQT
	1	1	1			LOYEMPERRIEPTTHEOALD VSLOOT GEEQT
	1	1				VSAISMAAATSTALATAHPDLRSTFHNTYHS
ĺ	ì	l				QMRQKHYYRSYEYDVPPTGTLPLTSIGNQHT
1	į	- }	1	4		YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA
İ	-			İ		I ILPLLPRETSISSVIW
		4		3	1584	NSARGGVGVRGARAMATVQEKAAALNLSAL
806	2156	Α	6614	3	1304	HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT
		ì	ł	1	1	QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
		1	1	j	ļ	IQNKYFGDVDIPRAKVVRVCQALMDYKVFE
			į.	1		AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD
İ	1	i	1		1	AVPIKYFGKDKKPIFEDSSCSETIA TILITYED
	1		1	1	ļ.	SQLGKENKLYSPARYADALFKSSDIRSASLED
İ	İ	1		1		LWENLSLKPANSPHVNISTTLSPQVINEVWQE
1		<b>I</b>				ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK
	- 1	'	1	1		ROSTMVNSSNYLDRGILKAYSDSQEDEWLSA
Ì	1			1		AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE
1	ļ	1				LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV
	1	- 1				NGKTEIALEATQLLLKLLDFQNREEFRRLLYF
1		1		1	[	NUK I EIALEAT QUEEN DE CARRESTACE IT
1		1			1	MAVAANPSEFKLQKESDNRMVVKRIFSKAIV
1	1				1	DNKNLSKGKTDLLVLFL\MDHQKDVFKIPGT
		1		1	1	L\HKIVS\VK\LMAIQNGRDPNRDAGYIYCQRI
1	i	1		1	1	DORDYSNITEKTTIDELLYLLKTLDEDSKLSA
				1		KEKKK\LLGOFYKCHPDIFIEHFGD
		İ			+	FGIVGTFALETDELDSDRDPAIFSLCDFGAMR
807	2157	A	6615	4198	2094	PQILLLALLTLGLAAQHQDKVPCKM/VKML
						POLLLIALLILGUAAQUQUAVICANI VANIL
		ļ				CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD
		1				LSGNQLRSILASPLGFYTALRHLDLSTNEISFL
	İ					OPGAFOALTHLEHLSLAHNRLAMATALSAG
		1				GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS
1		ı		l		LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS
1			ĺ	1		NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD
1	1	1	1	1		NVLMDIEDUATEGLEKLI ILLINGSKISCH CISD
1	1	(	1			FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT
		l l			1	WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR
			1	1		WLDLKENKLLIH I BEITGET EN 1201 1121
						I PTGPPODSKGIHAPSEGWSALPLS\APSGNAS
						I PTGPPODSKGIHAPSEGWSALPLS\APSGNAS
						LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSOLLNLDLSYNEIELIPDSFLEHLTSLCFL
						LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NI SRNCLRTFEARRLGSLPCLMLLDLSHNALE
						LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NLSRNCLRTFEARRLGSLPCLMLLDLSHNALE TI FI GARALG\SLRTLLLOGNALRDLPPYTFA
						LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL NI SRNCLRTFEARRLGSLPCLMLLDLSHNALE

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N-Asparagine, 1-1 forme,
uence		Ì	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uchice		Į.		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	ĺ	[	Ĭ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ı			ł	peptide		/=possible nucleotide deletion, \=possible
	1	ļ	1		1	nucleotide insertion
			ļ	sequence	ļ <del>`</del> -	LDLSSNPGLEVATGALGGLEASLEVLALQGN
	}	}	1	1	1	GLMVLQVDLPCFICLKRLNLAENRLSHLPAW
	1	İ		· ·		TOAVSLEVLDLRNNSFSLLPGSAMGGLETSLR
	}	1				TOAVSEEVEDERINGS SEEF OF A OF HOCE AND A
	1			1		RLYLQGNPLSCCGNGWLAAQLHQGRVDVDA
	l	}		ļ		TQDLICRFSSQEEVSLSHVRPEDCEKGGLKNI
	1	}	1	Į.	İ	NLIIILTFILVSAILLTTLAACCCVRRQKFNQQ
1	1	1				YKA
		<b></b> _	+	167	1852	FKALSQYIYTNTHLEREAAFEVAILLRRMEEG
808	2158	A	6619	153	1032	ARHRNNTEKKHPGGGESDASPEAGSGGGGV
1	Į.	l	1	1		ALKKEIGLVSACGIIVGNIIGSGIFVSPKGVLEN
1		1		i		AGSVGLALIVWIVTGFITVVGALCYAELGVNI
	1	1		1	•	AUDANTHALIA MIA IOLII A LOUTCI UTTANI ALAD
1				1		PKSGGDYFYVKDIFGGLAGFLRLWIAVLVTYP
		1	1	1		TNQAVIALTFSNYVLQPLFPTCFPPESGLRLLA
1		1		1	1	AICLLLTWVNCSSVRWATRVQDIFTAGKLL
		1		1	1	ALALIIIMGIVQICKGEYFWLEPKNAFENFQEP
1		1	1	1	1	DIGLVALAFLOGSFAYGGWNFLNY\VTEELV
1		1				DP\YKNI\PRAIFISIP\LVTFVYVFANV/ALYVT
1		1	ļ	1		AMSPOFL/LAS/NAVAVTFGEKLLGVMAWIM
1	1	ì			1	PISVALSTEGGVNGSLFTSSRLFFAGAREGHLP
· ·		1	1			SVLAMIHVKRCTPIPALLFTCISTLLMLVTSD
	1	1	1	l	l .	MYTLINYVGFINYLFYGVTVAGQIVLRWKKP
	1	1				DIPRPIKINLLFPITYLLFWAFLLVFSLWSEPVV
1		1		1		CGIGLAIMLTGVPVYFLGVYWQHKPKCFSDFI
	1			1		ELLTLVSQKMCVVVYPEVERGSGTEEANED
	}		ı	1		ELLILVSQKMCVVVIFEVERGSGIEERINDS
						MEEQQQPMYQPTPTKDKDVAGQPQP
809	2159	A	6621	1041	223	QDSRKMLPSTSVNSLVQGNGVLNSRDAARH
809	2139	1 ''	002.			TAGAKRYKYLRRLFRFRQMDFEFAAWQMLY
ì		1	1			LFTSPQRVYRNFHYRKQTKDQWARDDPAFL
		İ	1		1	VLLSIWLCVSTIGFGFVLDMGFFETIKLLLWV
1	1	-	i	1	1	VLIDCVGVGLLIATLMWFISNKYLVKRQSRD
1			1		1	YDVEWGYAFDVHLNAFYPLLVILHFIQLFFIN
		ļ			1	HVILTDTFIGYLVGNTLWLVAVGYYIYVTFL
{			1	}		GYSVGLLFFSVALPFLKNTVILLYPFAPLILLYG
1	· I		1			LSLALGWNFTHTLCSFYKYRVK
1	1					SPASGHCRLNGAAVAMFGCLVAGRLVQTAA
810	2160	A	6623	160	822	SPASGHCKLINGAAVAINI GCEVAGGEVQTEL
1		1			1	QQVAEDKFVFDLPDYESINHVVVFMLGTIPFP
		1	1	1		EGMGGSVYFSYPDSNGMPVWQLLGFVTNGK
	1		1			PSAIFKISGLKSGEGSQHPFGAMNIVRTPSVAQ
		1			Į.	IGISVELLDSMAQQTPVGNAAVSSVDSFTQFT
		- {			ſ	OKMLDNFYNFASSFAVSQ/VPDDTQ/RPSEMF
		1		1		IPANVVLKWYENFQRRTSTEPSLLENIIWIKIN
	1				]	F
					3367	LEGSLNTERAKYYLTITMPHFTVTKVEDPEEG
811	2161	Α	6627	18	3301	AAASISQEPSLADIKARIQDSDEPDLSQNSITG
1				1		EHSQLLDDGHKKARNAYLNNSNYEEGDEYF
		-			1	EMOULLUUMAAANAA LUMAAN LEGUULT
1		1	1			DKNLALFEEEMDTRPKVSSLLNRMANYTNLT
	1	1				QGAKEHEEAENITEGKKKPTKTPQMGTFMG
	;	i		1		VYLPCLQNIFGVILFLRLTWVVGTAGVLQAF
1		- {		1		AIVLICCCCTMLTAISMSAIATNGVVPAGGSY
		1	1	1		FMISRALGPEFGGAVGLCFYLGTTFAAAMYIL
1	1	1		1		GAIFIFLVYIVPRAAIFHSDDALKESAAMLNN
			1		1	MRVYGTAFLVLMVLVVFIGVRYVNKFASLFL
					1	TOTAL DISTRIBUTION OF THE COURT
İ						ACVIVED AIVAGAIK SCHAPPHERVUMI UNKI
						ACVIVSILAIYAGAIKSSFAPPHFPVCMLGNRT
						LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS
						LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS OFFNATCDEYFVHNNVTSIQGIPGLASGIITEN
					į	LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS QFFNATCDEYFVHNNVTSIQGIPGLASGIITEN LWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL
						LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS QFFNATCDEYFVHNNVTSIQGIPGLASGIITEN LWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL VDITTSFTLLVGIFFPSVTGIMAGSNRSGDLKD
						LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS QFFNATCDEYFVHNNVTSIQGIPGLASGIITEN LWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL VDITTSFTLLVGIFFPSVTGIMAGSNRSGDLKD AOKSIPIGTII.AILTTSFVYLSNVVLFGACIEGV
						LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS QFFNATCDEYFVHNNVTSIQGIPGLASGIITEN LWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL VDITTSFTLLVGIFFPSVTGIMAGSNRSGDLKD AQKSIPIGTILAILTTSFVYLSNVVLFGACIEGV VI RDKFGDAVKGNLVVGTLSWPSPWVIVIGS
						LSSRHIDVCSKTKEINNMTVPSKLWGFFCNSS QFFNATCDEYFVHNNVTSIQGIPGLASGIITEN LWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL VDITTSFTLLVGIFFPSVTGIMAGSNRSGDLKD

	····	<u> </u>	CCC	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ŧ - I	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496		acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	ļ		914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	}		amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1			residue of	sequence	/=possible nucleotide deletion, \=possible
	1			peptide	l	nucleotide insertion
	1	}	_	sequence		FGHSKANGEPTWALLLTAAIAELGILIASLDL
	<del></del>					VAPILSMFFLMCYLFVNLACALQTLLRTPNW
						VAPILSMFFLING I LFV NEACAEQTEERT IV
	}	)	1		1	RPRFRYYHWALSFMGMSICLALMFISSWYYA
	1	ļ	1	1		IVAMVIAGMIYKYIEYQGAEKEWGDGIRGLS
	1	l	1	ļ	1	LSAARFALLRLEEGPPHTKNWRPQLLVLLKL
	1		İ			DEDLHVKHPRLLTFASQLKAGKGLTIVGSVIV
		l .	1			GNFLENYGEALAAEQTIKHLMEAEKVKGFCQ
	Ĭ	ĺ				I VVAAKI REGISHLIOSCGLGGMKHNTVVM
	1	1				GWPNGWROSEDARAWKTFIGTVRVTTAAHL
		1				ALLVAKNISFFPSNVEQFSEGNIDVWWIVHDG
	i	ĺ			J	GMI MI LPFLLK\OHKVWRKCSIRFF\TVAQLE
						DNSIOMKKDLATFLYHLRIEAEVEVVEMHDS
						DISAYTYERTI MMEORSOMLRHMRLSKIER
		}			1	DREAQLVKDRNSMLRLTSIGSDEDEETETYQ
		1				EKVHMTWTKDKYMASRGQKAKSMEGFQDL
	1	1	l l			LNMRPDQSNVRRMHTAVKLNEVIVNKSHEA
	l l					KLVLLNMPGPPRNPEGDENYMEFLEVLTEGL
		1			!	KLVLLNMPGPPKNPEODEN I WIELEEVE LEGE
	1	ľ				ERVLLVRGGGSEVITTYS
812	2162	A	6628	66	640	AVCTMSEMAELSELYEESSDLQMDVMPGEG
012	2102	1 '`	3322			DLPQMEVGSGSRELSLRPSRSGAQQLEEEGP
		1		1		MEEEEAQPMAAPEGKRSLANGPNAGEQPGQ
				1		VAGADFESEDEGEEFDDWEDDYDYPEEEQLS
		1	l		Į.	GAGYRVSAALEEADKMFLRTREPALDGGFQ
	1		1			MHYEKTPFDQLAFIEELF\SLMVVNRLTEELG
1			1	1		CDETIORE
		<del></del>	6630	708	1355	AKMGAYKYIOELWRKKOSDVMRFLLRVRC
813	2163	A	0030	708	1333	WOVROLSALHRAPRPTRPDKARRLGYKAKQ
ĺ	[		Ì			GY/VYIYIGFVFAVIYRIRVRRGGRKRPVPKG
Ì			1			ATYGKPVHHGVNOLKFARSLQSVAEERAGR
	ì				1	HCGALRVLNSYWVGEDSTYKFFEVILIDPFHK
	1	1				AIRRNPDTQWITKPVHKHREMRGLTSAGRKS
1	1	ĺ	ĺ			RGLGKGHKFHHTIGGSRRAAWRRRNTLQLH
	1	ì				
		1		<u> </u>		RYR KGTEMNKSRWQSRRRHGRRSHQQNPWFRLR
814	2164	A	6635	201	1705	DSEDRSDSRAAQPAHDSGHGDDESPSTSSGT
1		-				AGTSSVPELPGFYFDPEKKRYFRLLPGHNNCN
				i		AGTSSVPELPGF YFDPERRKTFREET GIMMEN
		-			}	PLTKESIRQKEMESKRLRLLQEEDRRKKIARM
	1	1		1		GFNASSMLRKSQLGFLNVTNYCHLAHELRLS
1				1	Į.	CMERKKVQIRSMDPSALASDRFNLILADTNS
		)		1	1	DRLFTVNDVTVGGSKYGIINLQSLKTPTLKVF
		1		1		MHENLYFTNRKVNSVCWASLNHLDSHILLC
		1	}			LMGLAETPGCATLLPASLFVNSHPAGIDRPG\
						MT CSFR IPGAWSCAWSLNIOANNCFSTGLSR
1		1		}		RVLLTNVVTGHROSFGTNSDVLAQQFALMA
1		Ĭ		1		DITENGORSGETFAIDLRCGNOGKGWKATRLF
		Į.		1		HDSAVTSVRILODEOYLMASDMAGKIKLWD
			}	1	1	LRTTKCVRQYEGHVNEYAYLPLHVHEEEGIL
1	1			1		VAVGQDCYTRIWSLHDARLLRTIPSPYPASKA
1		}	1	}		DIPSVAFSSRLGGSRGAPGLLMAVGQDLYCY
				1		
		-			<u> </u>	SYS SYSTEM OF THE PLANT OF THE PLANT OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE
815	2165	A	6643	659	3282	NKNILEVPSARTTRIMGDHLDLLGVVLMAG
1 013	2103	1 ''				PVFGIPSCSFDGRIAFYRFCNLTQVPQVLNTTE
				,		RLLLSFNYIRTVTASSFPFLEQLQLLELGSQYT
	1	ĺ				PLTIDKEAFRNLPNLRILDLGSSKIYFLHPDAF
1		ı	1		1	OGLEHLEELRLYFCGLSDAVLKDGYFRNLKA
1		1				
						LTRLDLSKNOIRSLYLHPSFGKLNSLKSIDFSS
						LTRLDLSKNQIRSLYLHPSFGKLNSLKSIDFSS NOIFLYCEHELEPLOGKTLSFFSLAANSLYSR
ļ						NOIFLYCEHELEPLQGKTLSFFSLAANSLYSR
						NQIFLVCEHELEPLQGKTLSFFSLAANSLYSR VSVDWGKCMNPFRNMVLEILDVSGNGWTV
						NOIFLYCEHELEPLQGKTLSFFSLAANSLYSR

		1 1 4 .4	CTO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	1	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ł	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	l	09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence		Į	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	}	1	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		1	residue of	sequence	/=possible nucleotide deletion, \=possible
		<b>,</b>		peptide	1	/=possible nucleotide detector, /-possible
	1	i		sequence	1	nucleotide insertion
	<del> </del>		<del></del>			RVFETLKDLKVLNLAYNKINKIADEAFYGLD
	ł	1		•		NLQVLNLSYNLLGELYSSNFYGLPKVAYIDL
i			1			QKNHIAIIQDQTFKFLEKLQTLDLRDNALTTIH
		ì	1			FIPSIPDIFLSGNKLVTLPKINLTANLIHLSENR
		1	1			LENLDILYFLLRVPHLQILILNQNRFSSCSGDQ
	1	1	1			TPSENPSLEQLFLGENMLQLAWETELCWDVF
		1	1			EGLSHLQVLYLNHNYLNSLPPGVFSHLTALR
			1			GLSLNSNRLTVLSHNDLPANLEILDISRNQLL
		1				GLSLNSNKLI VLSIHIDDI ANDBIDDIGITAZIO
	İ				1	APNPDVFVSLSVLDITHNKFICECELSTFINWL
i	i	1	ļ		1	NHTNVTIAGPPADIYCVYPDSLSGVSLFSLSTE
(		1	1			GCDEEEVLKSLKFSLFIVCTVTLTLFLMTILTV
		1				TKFRGFCFICYKTAQRLVFKDHPQGTEPDMY
1		1			1	KYDAYLCESSKDFTWVQNALLKHLDTQYSD
					1	ONRENT.CFEERDFVPGENRP\ANIQDALWNSK
ŀ				1	1	KIVCLVSRHFLRDGWCLEAFSYAQGRCLSDL
		1				NSALIMVVVGSLSOYQLMKHQSIRGFVQKQQ
		1				YLRWPEDLQDVGWFLHKLSQQILKKEKEKK
	j		1			KDNNIPLQTVATIS
İ					100	RDRAGVRPAGKQHAAAAFYDVGGDRPWDS
816	2166	A	6646	1	3811	GNTQLPPRNPVKANAMFGAGDEDDTDFLSPS
1				1		GGARLASLFGLDQAAAGHGNEFFQYTAPKQP
ì	ì				ì	GGARLASLIGLDQAAAGHONEITQTTA NQI
	1	]				KKGQGTAATGNQATPKTAPATMSTPTILVAT
	1	1	1		]	AVHAYRYTNGQYVKQGKFGAAVLGNHTTR
ł	1		1	1		EYRILLYISQQQPVTVARIHVNFELMVRPNNY
1	1			Į.		STFYDDQRQNWSIMFESEKAAVEFNKQVCIA
	1					KCNSTSSLDAVLSQDLIVADGPAVEVGDSLE
1		-				VAYTGWLFQNHVLGQVFDSTANKDKLLRLK
		1	1			LGSGKVIKGWEDGMLGMKKGGKRLLIVPPA
1			1		ĺ	CAVGSEGVIGWTQATDSILVFEVEVRRVKIA
l		1	l.			KDSGSDGHSVSSRDSAAPSPIPGADNLSADPV
	1					VSPPTSIPFKSGEPALRTKSNSLSEQLAINTSPD
1						AVKAKLISRMAKMGQPMLPILPPQLDSNDSEI
}						EDVNTLQGGGQPVVTPSVQPSLQPAHPALPQ
	ļ					MTSQAPQPSVTGLQAPSAALMQVSSLDSHSA
1	i	1		i		VSGNAQSFQPYAGMQAYAYPQASAVTSQLQ
1			İ			PVRPLYPAPLSQPPHFQGSGDMASFLMTEAR
	1			1		PARPLYPAPLSQPPHPQGGGDMASI EMIDIN
1		.	ł	ł		QHNTEIRMAVSKVADKMDHLMTKVEELQKH
i	1			\	1	SAGNSMLIPSMSVTMETSMIMSNIQRIIQENER
		1		ĺ		LKQEILEKSNRIEEQNDKISELIERNQRYVEQS
						NLMMEKRNNSLQTATENTQARVLHAEQEKA
1				j		KVTEELAAATAQVSHLQLKMTAHQKKETEL
1		1				OMOLTESLIKETDLLRGOLTKVOAKLSELQET
				1		SFOAOSKFKSEKONRKQLELKVTSLEEELTDL
1				1		RVEKESLEKNLSERKKKSAQERSQAEEEIDEI
1	1	-		· l		RKSYOFELDKLROLLKKTRVSTDQAAAEQLS
1		1		1	1	LVQAELQTQWEAKCEHLLASAKDEHLQQYQ
		-		-		EVCAQRDAYQQKLVQLQEKSVCFA\CLALQA
						QITALTKQNEQHIKELEKNKSQMSGVEAAAS
						QITAL I KUNEUHIKELEKINASUMSU VEKAKAS
						DPSEKVKKIMNQVFQSLRREFELEESYNGRTI
}		}	}			LGTIMNTIKMVTLQLLNQQEQEKEESSSEEEE
		- 1				EKAEERPRRPSQEQSASASSGQPQAPLNRERP
1		1				ESPMVPSEOVVEEAVPLPPQALTTSQDGHRR
1						KGDSEAEALSEIKDGSLPPELSCIPSHRVLGPP
1				1		TSIPPEPLGPVSMDSECEESLAASPMAAK\PDN
		1	1	1	1	PSGK\VCVREVAPDGPLQESSTRLSLTS\DPEE
1		i				GDPLALGPESPGEPQPPQLKKDDVTSSTGPHK
1		1	1		*	ELSSTEAGSTVAGAALRPSHHSQRSSLSGDEE
1					1	ELSSTEAUST VAUAALKYSHISQKSSLSUDEL
1		1		İ		DELFKGATLKALRPKAQPEEEDEDEVSMKGR
1	1	- 1				PPPTPLFGDDDDDDDDDDDWLG
817	2167	A	6649	63	1073	FFRSSDNGSPIRQYE/HSTPAHQGPVMGLEG
		, ,	1 0042	1 00		

Section   D. No.   for the periods of executions   D. No.   for the periods of executions   D. No.   for the periods of executions   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the periods   D. No.   for the peri		660 10	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
No control   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   S	SEQ ID	SEQ ID	Met				D=Aspartic Acid, E=Glutamic Acid,
USSN ocation of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of			noa				F=Phenylalanine, G=Glycine, H=Histidine,
### Service of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction o		1	1				I=Isoleucine, K=Lysine, L=Leucine,
### 1914 in the first amino acid residue of peptide peptide peptide peptide peptide sequence per per per per per per per per per pe		, -	1	_			M=Methionine, N=Asparagine, P=Proline,
amino acid residue of speptide requence propriet and propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequence propriet sequ	seq-	uence		1			O=Glutamine, R=Arginine, S=Serine,
residue of peptide sequence      Poptible periodice	uence	į	}	914			T=Threonine, V=Valine, W=Tryptophan,
Peptide   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence		ì	Ì		1		V=Tyrosine X=Unknown, *=Stop codon,
nucleotide inscrition  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQUENCE  SEQ		1		1		Sequence	/=possible nucleotide deletion. \-possible
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### PYVQRGLQRVGLDPQLENLAALQAHLAQE" RVVAFFSLALLLAPLVETILLDRLLYLQEQ, LSPGFHAELLFIFSPELSPRNLVLVATKMPLG QALSVLETEDS  #### SQGFHCAEAASMGPWGWKLRWTVALLLA AGGTAVGDRCERNEFQQQDGKCISYKWVC GSAECQDGSDESQETCLSVTCKSGDFSCGGI VNRCIPQFWRCDGQVDCDNGSDEQGCPPKI SQDEFRCHDGKGISRQFVCDSDRDCLDGSDI ASCPVLTCGFASFQCNSSTCPQLWACDNDI CEDGSDEWPQRCRGLYVFQGDSSPCSAFFF CLSGECHISSWRCDGGPDKCMCKSDEENCAV TCRPDEFQCSDGNCHHGSRQCDREYDCKDW DEVGCVNVTLCEGPNKEKCHSGECTLDKV NMARDCRDWSDEPIKEGGTNECLDNNGGC HVCNDLKIGYECLCPDGFQLVAQRRCEDID CQDPDTCSQLCVNLEGGYKCQCEGGFQLDF TKACKAVGSIAYLFFTNRHEVRKIMTLDRSE TSLIPNLRNVVALDTEVASNRTYWSDLSQRR CSTQLDRAHGVSSYDTVISRDIQAPDGLAVI WHISNTYWTDSVLGTVSVADTKGVKRKTLE ENGSKPRATVVDPVHGFMYWTDWGTPAKI KGGLNGVDIYSLVTENIQWPNGITLDLLSGF YWVDSKLHSISIDVNGGNRKTLEDEKRLA PFSLAVFEDKVFWTDINEAHFSANRLTGSDD NLLAENLLSPEDMVLFHNLTQPRGVNWCEI TLSNGGCQYLCLPAPQNPHSFKFTCACPDG LLARDMRSCLTEGEAAVATQETSTVRLKV STAVRTQHTTTRPVPTSRLPGATPGLTTVV VTMSHQALGDVAGRGNEKKPSSVRALSIV PIVLLVFLCLGVFLLWKNWRLKNINSINFDI VYQKTTEDEVHICHNQDGYSYPSRQMVSLE DVA  ##################################				1	1		PAAI ETVIRRARPELRRPGVOGIPRVHELKIEE
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AAGTAVGDRCERNEFQCQDGKCISYKWVC GSAECQDGSDESQETCLSVTCKSGDFSCGGI VNRCIPQFWRCDGQVDCDNGSDEQGCPPKT SQDEFRCHDGKCISRQFVCDSDRDCLDGSDI ASCPVLTCGPASFQCNSSTCIPQLWACDNDF CCDGSDEWPQRCRGLYVFQGDSSPCSAFEF CLSGECHSSWRCDGGPDCKDKSDEENCAV TCRPDEFQCSDGNCIHGSRQCDREFVDCKDN DEVGCVNVTLCEGPNKFKCHSGECITLDKV NMARDCRDWSDEPIKECGTNECLDNNGGC HVCNDLKIGYECLCPDGFQLVAQRRCEDID CQDPDTCSQLCVNLEGGYKCQCEEGFQLDF TKACKAVGSLAYLFFTNRHEVRKMTLDRSE TSLIPNLRNVVALDTEVASNRIYWSDLSQRN CSTQLDRAHGVSSYDTVISRDIQAPDGLAVI WIHSNIYWTDSVLGTVSVADTKGVKRKTLF ENGSKPRAIVVDPVHGFMYWTDWGTPAKII KGGLNGVDIYSLVTENIQWPNGITLDLLSGF YWVDSKLHSISSIDVNGGNRKTILEDEKRLA PFSLAVFEDKVFWTDIINEAIFSANRLTGSDN NLLAENLLSPEDMVLFHNLTQPRGVNWCEI TLSNGGCQYLCLPAPQINPHSPKFTCACPDC LLAR\DMRSCLTEG\EAAVATQETSTVRLKV STAVRTQHTTTRPVPDTSRLPGATPGLTTVF VTMSHQALGDVAG\RGN\EKKPSSVRALSIV PIVLLVFLCLGVFLLWKNWRLKINSINFDI VYQKTTEDEVHICHNQDGYSYPSRQMVSLI DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSFTSLWGLLFLSA LSILWPTSGEIGGPGIDIRNDYQQLKRLENCT EGYLHILLISKAEDYRSYRFFKLTVITEYLLI			1	·			QALSVLETEDS
GSAECQDGSDESQETCLSVTCKSGDFSCGGI VNRCIPQFWRCDGQVDCDNGSDEQGCPPXT SQDEFRCHDGKCISRQFVCDSDRDCLDGSDI ASCPVLTCGPASFQCNSSTCIPQLWACDNDI CEDGSDEWPQRCRGLYVFQGDSSPCSAFEF, CLSGECHSSWRCDGGPDCKDKSDEENCAV TCRPDEFQCSDGNCIHGSRQCDREYDCKDW DEVGCVNVTLCEGPNKFKCHSGECITLDKV NMARDCRDWSDEPIKECGTNECLDNNGGC HVCNDLKIGYECLCPDGFQLVAQRRCEDID, CQDPDTCSQLCVNLEGGYKCQCEEGFQLDF TKACKAVGSLAYLFFTNRHEVRKMTLDRSE TSLIPNLRNVVALDTEVASNRIYWSDLSQRN CSTQLDRAHGVSSYDTVISRDIQAPDGLAVI WHSNIYWTDSVLGTVSVADTKGVKRKTLF ENGSKPRAIVVDPVHGFMYWTDWGTPAKI KGGLNGVDIYSLVTENIQWFNGITLDLLSGF YWVDSKLHSISSIDVNGGNRKTILEDEKRLA PFSLAVFEDKVFWTDIINEAIFSANRLTGSDN NLLAENLLSPEDMVLFHNLTQPRGVNWCEI TLSNGGCQYLCLPAPQINPHSPKFTCACPDC LLARVDMRSCLTEGVEAAVATQETSTVRLKV STAVRTQHTTTRPVPDTSRLPGATPGLTTVE VTMSHQALGDVAGRGNEKKPSSVRALSIV PIVLLVFLCLGVFLLWKNWRLKNINSINFDI VYQKTTEDEVHICHNQDGYSYPSRQMVSLI DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSFTSLWGLLFLSA LSLWPTSGEIGCPGIDIRNDYQQLKRLENCT EGYLHILLISKAEDYRSYRFFKLTVITEYLLL	819	2169	A	6661	65	2686	SUSUHULAEAASMUF WU WALKWI WILDDIN
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HVCNDLKIGYECLCPDGFQLVAQRRCEDID. CQDPDTCSQLCVNLEGGYKCQCEGGFQLDF TKACKAVGSIAYLFFTNRHEVRKMTLDRSE TSLIPNLRNVVALDTEVASNRIYWSDLSQRN CSTQLDRAHGVSSYDTVISRDIQAPDGLAVI WIHSNIYWTDSVLGTVSVADTKGVKRKTLF ENGSKPRAIVVDPVHGFMYWTDWGTPAKII KGGLNGVDIYSLVTENIQWPNGITLDLLSGF YWVDSKLHSISSIDVNGGNRKTILEDEKRLA PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NILAENLLSPEDMVLFHNLTQPRGVNWCEI TLSNGGCQYLCLPAPQINPHSPKFTCACPDG LLAR\DMRSCLTEG\(\text{EAAAVATQETSTVRLKV}\) STAVRTQHTTTRPVPDTSRLPGATPGLTTVE VTMSHQALGDVAG\(\text{RGN\(\text{EKKPSSVRALSIV}\) PIVLLVFLCLGVFLLWKNWRLKNINSINFDI VYQKTTEDEVHICHNQDGYSYPSRQMVSLF DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSA LSLWPTSGEICGPGIDIRNDYQQLKRLENCT FGYLHIILISKAEDYRSYRFPKLTVITTEYLLI		1			1	1	NMARDCRDWSDEPIKECGTNECLDNNGGCS
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TSLIPNLRNVVALDTEVASNRIYWSDLSQRN CSTQLDRAHGVSSYDTVISRDIQAPDGLAVI WIHSNIYWTDSVLGTVSVADTKGVKRKTLF ENGSKPRAIVVDPVHGFMYWTDWGTPAKII KGGLNGVDIYSLVTENIQWPNGITLDLLSGF YWVDSKLHSISSIDVNGGNRKTILEDEKRLA PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCEI TLSNGGCQYLCLPAPQINPHSPKFTCACPDG LLAR\DMRSCLTEG\EAAVATQETSTVRLKV STAVRTQHTTTRPVPDTSRLPGATPGLTTVE VTMSHQALGDVAG\RGN\EKKPSSVRALSIV PIVLLVFLCLGVFLLWKNWRLKNINSINFDI VYQKTTEDEVHICHNQDGYSYPSRQMVSLF DVA  820 2170 A 6666 17 4146 ERGISSQIKGMKSGSGGGSPTSLWGLLFLSA LSLWPTSGEICGPGIDIRNDYQQLKRLENCT EGYLHIL ISKAEDYRSYRFPKLTVITEYLLL					1		TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY
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nucle colide sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	SEQ ID	SEQ ID					D-Aspartic Acid E=Glutamic Acid.
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entide  USSN 105496 1914  1916  1916  1916  1916  1916  1917  1916  1917  1916  1917  1916  1917  1917  1917  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918  1918		pentide		in	nucleotide		F=Phenylalanine, G=Olychic, ri-ilistidile,
### Unifice   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   1949   19				USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
914 a maino acid residue of peptide residue of peptide sequence while, we'l'rpyrophan, we'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l'ropyrophan, ye'l		•		l	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence    1914   amino acid residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of peptide sequence   residue of residue of peptide sequence   residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of residue of resi	•	uence					O=Glutamine, R=Arginine, S=Serine,
residue of poptide sequence    Y=Tyrosine, X=Unknown, "-Stop codon, possible nucleotide tissertion   Fyrosible nucleotide tissertion   Fyrosible nucleotide tissertion   Fyrosible nucleotide tissertion   Fyrosible nucleotide tissertion   Fyrosible nucleotide tissertion   Fyrosible nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotid	uence	1	ļ	914			T=Threonine V=Valine, W=Tryptophan,
### peptide sequence		Ì		ľ			V-Torogina V-IInknown *=Ston codon
nucleotide insertion  EMTILAUDIGI TYNLENTIRGAIRIEKNADLCYL SITVDWSLILDAVSNNYIVGNKPPKECGDLCP GTMEERPMCEKTITINSTYNRCWTNRCK MCPSTCGRRACTENNECCHPECLGSCSAPDN DTAGVACRHYYYAGCVPACPPNTYNRCWTNRCK MCPSTCGRRACTENNECCHPECLGSCSAPDN DTAGVACRHYYYAGCVPACPPNTYNRCWTNREGW RCVDRDPCANILSAESSDSEGFVIHDAGEMOG CPSFIRMSGSMYLCPGFGPCFVCVEGEKKI KTIDSVTSAGMLOGCTIFKONLLINIRRGNNIA SELNFMGLIEVTGYVKIRHSHALVSLSFLK NLRLILGEEQLEGNYSFYVLDNONLQQLWD WHRNILTIKAGKMYPARPNKLCVSETYMEE VTGTKGRQSKGDNTRNNGERASCESDVLHF TSTTTSNRIITIWHRYAFPNYKLDSTYMEE VTGTKGRQSKGDNTRNNGERASCESDVLHF TSTTTSNRIITIWHRYAFPDYRADLSTYTYK EAPFRNVTEYDGQDACGSNSWMMVDVDLPP NCDVEPGLILBGLKPWTQYAVYVXAVTLTM VENDHIRGAKSELLYIRTNASVSPIPLDVLSAS NSSQLVKWPPSLPKONLSYYIYRWGRQP QDGYLYNENYCSKDKIPRKYADGTIDIEEVT EPKTEVCGGKEGPCCACPKTLEAKGAEKEE AFYKKVFENFLINSIFVPRFEKRRDVMQVA NTIMSSRSNITAADTNITDFELETETYPF ESRYDNKEETVISNLRPFILYRDHISCNHEAE KJGCSASNIVPARTMPGGADDIPGYTWEP RPENSIFLKWPEPENFNGLLMYFEKYGGVE DORECVSROPTRXYGGAKINELNPGHTYWIGH GATSLSGNOSWTDPVFFYVQAKRYENFHILLI ALPVAVLLVOGGLWINLVYHTRKRYNSELGN GGVLYASNIPEYFSAADVYVPDEWEVAREKTI MSRLGGGSFGMYVTGVAKGVXCDPETRY AIKTVNEAASMRERIEFINEASSYMKEPNCHH VYRLLGCGSFGMYVTGVAKGVXCDPETRY AIKTVNEAASMRERIEFINEASSYMKEPNCHH VYRLLGVSGGGFGHAVTYMEGGLLSKYLR SLRPEMENPVLAPPSLSKMIGMAGEIADGM AYLNANKFYHRDLAARNCMVAEDFPTKIGG FGMTRDTYSDWWSPGSLLKSHERPGFRE VSFYYSEENKLPPERSLEISIKEREMFERPGFRE VSFYYSEENKLPPERSLEISIKEREMFGRE VSFYYSEENKLPPERSLEISIKEREMFERPGFRE VSFYYSEENKLPPERSLEISIKEREMFGRE VSFYYSEENKLPPERSLEISIKEREMFGRE VSFYYSEENKLPPERSLEISIKEREMFGRE VSFYYSEENKLPPERSLEISIKEREMFGRE VSFYYSEENKLPPERSKRYN ESKKIDRHMYHSLYLKVKGNVKNNKRILMEH RIKLADARAKKLLADAGARASKKTARAR RAPEKVTWARGRANLRRLRLRYRSFKAYR ESKKIDRHMYHSLYLKVKGNVKNNKRILMEH RIKLADAARAKKLLADAGARASKKTARAR RAPERLQAKKEEINTLSKEETTK SGDICNACVLLLKRKKLPAGSKKNWN VVDARAGPSLKTTLKPKKVKTLSGNRIIST PTWRQGCCGGVIKGFGEVLLDTHLFKKNC SGNKAAAABKPEGGFGFRHISTINGENTINSSCTINEA  822 2173 A 6715 772 21 DFREGCTGOSGGCFGFGSRNRIPPYSSLOLV VVDARAGGPSLKTTLKPKKVKTLSGNRIIST PTWRQGCCGGTGGGGFTHISTOGWVTEVFM NAGPLARNGSAAPGGGGGTHTSNSSCTINGS SSASSSSFTOSGTGFOSSTRIPPYSSLOCC SNKKAAAABKPEGGFELLITINGEW		ļ	İ	1	residue of	sequence	Y=1 yrosine, x=0 indiowii, = 5top codon,
sequence   mouleoidé insection		ì	{	i	peptide	ĺ	/=possible nucleotide deletion, \=possible
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IHKLKADKARKKLLADQAEARRSKTKEARK   RREERLQAKKEEIIKTLSKEEETKK   RREERLQAKKEEIIKTLSKEEETKK   RREERLQAKKEEIIKTLSKEEETKK   DFRPGLLLPRKKKMFGFHKPKMYRSIEGC\CI   SGAKSSSS\RFTDSKRYEK\DFQ\SCFGLHETR\  SGDI\CNA\CVLL\LKR\WKKLPAGSKK\WNH   VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST   QISKLQKEFKR\HNSDDAHSTTS\SASP\AQSPLF   TV\QFR\WTGSDTGVGFPGSNR\HPVFSFLDL\  TY\WKRQKICCG\UYKGRFGEVLIDTHLFKPCC   S\NKA\AAEKPEEQGPEPLPISTQE\WYTEVFM   S\SSASGS\SVPP\SSLI\PPKYQTPPAAAQGQATPG   NAGPLAP\NGSAAPPAGSAF\PTS\NSSST\PAA   S\SSASGS\SVPP\SSSASGS\SVPP\SSSASGS\SSGSS\SSGSS\SGSS\SGSS\SGSS\SG			1		1	1	ARMPEKVTWMRRMRILKRLLRRYRES/KRYR
IHKLKADKARKKLLADQAEARRSKTKEARK   RREERLQAKKEEIIKTLSKEEETKK   RREERLQAKKEEIIKTLSKEEETKK   RREERLQAKKEEIIKTLSKEEETKK   DFRPGLLLPRKKKMFGFHKPKMYRSIEGC\CI   SGAKSSSSURFTDSKRYEK\DFQ\SCFGLHETR\   SGDI\CNA\CV\LL\KRWKKLPAGSKK\WNH   VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST   QISKLQKEFKR\HNSDAHSTTS\SASPAQSPLF   TV\QFRWTGSDTGVGFPGSNRNHPVFSFLDL\   TYWKRQKICCG\IYKGRFGEVLIDTHLFKPCC   SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM   SSSASGSSVPPVSSSASAPGSAFNPTSNSSSTNPAA   SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS	ŀ	1	1	1	1		ESKKIDRHMYHSLYLKVKGNVFKNKRILMEH
RREERLQAKKEEIIKTLSKEEETKK  822 2172 A 6715 772 21 DFRPGLLLPRKKKMFGFHKPKMYRSIEGC\CI SGAKSSSS\RFTDSKRYEK\DFQ\SCFGLHETR\ SGDI\CNA\CVLL\LKR\WKKLPAGSKK\\WNH\ VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST QISKLQKEFKR\H\SDAHSTTS\SASP\AQSPLF TV\QFR\WTGSDTGVGFPGS\RNHPVFSFLDL\ TY\WKRQKICCG\\YKGRFGEVLIDTHLFKPCC S\RKA\AAEKPEEQGPEPLPISTQE\WYTEVFM S\RKA\AAEKPEEQGPEPLPISTQE\WYTEVFM \ PYLATLQLDSSLIPPKYQTPPAAAQGQATPG\ NAGPLAP\RGSAAPPAGSAF\RTS\SSST\PAA\ SSSASGSS\YPYSSSASAPGISQISTTSSSGFSGS		1		1	1		IHKLKADKARKKLLADOAEARRSKTKEARK
822 2172 A 6715 772 21 DFRPGLLLPRKKKMFGFHKPKMYRSIEGC\CI SGAKSSS\RFTDSKRYEK\DFQ\SCFGLHETR\ SGDI\CNA\CV\L\L\KR\WKKLPAGSKK\WNH\ VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST QISKLQKEFKR\HNSDAHSTTS\SASP\AQSPLF TV\\QFR\WTGSDTGVGFPGS\RNHP\FSFLDL\ TY\\WKRQKICCG\LYKGRFGEV\LIDTHLFKPCC S\RKA\AAE\KPEE\QFPEPLPIST\QE\WYTE\FM\ PYLATL\QLDSSL\LIPPKY\QTPPAAA\QG\ATPG\ NAGPLAP\\GSAAP\PAGSAF\\PTS\NSST\\PAA\ SSS\ASGS\VP\YSS\ASAP\GIS\OISTTSSS\GFS\GS\	1	1		l	ì		DDEEDI OAKKEFIKTI SKEFETKK
SGAKSSSS\RFTDSKRYEK\DFQ\SCFGLHETR\ SGD\CNA\CVLL\LKR\WKKLPAGSKK\\WNH\ VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST\ QISKLQKEFKR\H\NSDAHSTTS\SASP\AQSPLF\ TV\QFR\WTGSDTGVGFPGS\NR\HPVFSFLDL\ TY\WKRQKICCG\NYKGRFGEVLIDTHLFKPCC\ S\NKA\AAEK\PEEQGPEPLPISTQE\WYTEVFM\ PYLATLQLDSSLIPPKYQTPPAAAQGQATPG\ NAGPLAP\NGSAAPPAGSAF\PTS\NSSST\NPAA\ SSSASGSS\PP\SSSASGSFSGSS\SGSS\SGSS\SGSS\SGSS\SGSS\S	1	1	1	1		L	AKEEKLYAKKELIKI LOKULUI KK
SGAKSSSSRFTDSKRYEK\DFQ\SCFGLHETR\ SGDI\CNA\CVLL\LKR\WKKLPAGSKK\\WNH\ VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST\ QISKLQKEFKR\H\NSDAHSTTS\SASP\AQSPLF\ TVNQFR\WTGSDTGVGFPGSNR\HPVFSFLDL\ TYWKRQKICCGI\!YKGRFGEVLIDTHLFKPCC\ S\NKA\AAEKPEEQGPEPLPISTQEWVTEVFM\ PYLATLQ\LDSSL\IPPKYQTPPAAAQGQATPG\ NAGPLAP\NGSAAPPAGSAF\PTS\NSSST\\PAA\ SSSASGSSVPP\SSSASAPGISQISTTSSSGFSGS\	822	2172	A	6715	772	21	DFRPGLLLPRKKKMFGFHKPKMYKSLEGCICI
SGDI\CNA\CVLL\LKR\WKKLPAGSKK\\WNH\ VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST\ QISKLQKEFKR\HINSDAHSTTS\SASP\AQSPLF\ TVNQFR\WTGSDTGVGFPGSNRNHPVFSFLDL\ TY\WKRQKICCGI\YKGRFGEVLIDTHLFKPCC\ SNKKA\AAEKPEEQGPEPLPISTQE\WYTEVFM\ PYLATLQLDSSL\IPPKYQTPPAAAQGQATPG\ NAGPLAP\NGSAAPPAGSAF\NPTS\NSSST\NPAA\ SSSASGSS\VPP\SSSASGSFSGSS\SGSS\SGSS\SGSS\SGSS\SGSS\S	022	1 21/2	1.	1	1		SGAKSSSS\RFTDSKRYEK\DFQ\SCFGLHETR\
VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST QISKLQKEFKR\HINSDAHSTTS\SASP\AQSPLF TVNQFR\WTGSDTGVGFPGSNRNHPVFSFLDL\ TY\WKRQKICCGI\YKGRFGE\VLIDTHLFKPCC SNKKA\AAEKPEQGPEPLPISTQE\WYTE\VFM PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSS\VPP\SSASAPGISQISTTSSSGFSGS	1	ł	1				SGDI\CNA\CVLL\LKRWKKLPAGSKK\NWNH
QISKLQKEFKR\HNSDAHSTTS\SASP\AQSPLF TVNQFRWTGSDTGVGFPGSNRNHPVFSFLDL\ TYWKRQKICCGN\YKGRFGEVLIDTHLFKPCC SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM  823 2173 A 6727 3 4063 PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS	!	1	i			1	VVDARAGPS\LKTTLKPKKVKTL\SGNRIK\ST
TVNQFRWTGSDTGVGFPGSNRNHPVFSFLDL\ TYWKRQKICCGINYKGRFGEVLIDTHLFKPCC SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM  823 2173 A 6727 3 4063 PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS	:	1	1	1		[	OTOM ONE ENDINIST A DETTE SA SENA OSEI F
TYWKRQKICCGINYKGRFGEVLIDTHLFKPCC SNKKANAAEKPEEQGPEPLPISTQEWVTEVFM  823 2173 A 6727 3 4063 PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS	i			1	1		CIPKTOVELVVALIADAUDI 19/9491 AGREDI.
SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM  823 2173 A 6727 3 4063 PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS		ļ		t .		1	TVNOFRWTGSDTGVGFPGSNKNHPVF3FLDL\
SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM  823 2173 A 6727 3 4063 PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS						1	
823 2173 A 6727 3 4063 PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS							TYWKROKICCGNYKGRFGEVLIDTHLFKPCC
NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS							TYWKROKICCGNYKGRFGEVLIDTHLFKPCC
NAGPLAPNOSAAPPAOSAFNY ISINSSITU AA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS						1063	TYWKRQKICCGNIYKGRFGEVLIDTHLFKPCC SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM
SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS VGGONPSTGGISADRTQGNIGCGGDTDPGQS	823	2173	Ā	6727	3	4063	TYWKRQKICCGINYKGRFGEVLIDTHLFKPCC SNKKANAAEKPEEQGPEPLPISTQEWVTEVFM PYLATLOLDSSLLIPPKYOTPPAAAOGQATPG
VGGONPSTGGISADRTQGNIGCGGDTDPGQS	823	2173	A	6727	3	4063	TYWKRQKICCGINYKGRFGEVLIDTHLFKPCC SNKKANAAEKPEEQGPEPLPISTQEWVTEVFM PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA
	823	2173	Ā	6727	3	4063	TYWKRQKICCGINYKGRFGEVLIDTHLFKPCC SNKKANAAEKPEEQGPEPLPISTQEWVTEVFM PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS

						/A Alorina C-Custeine
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	ļ		914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	residue of	sequence	/=possible nucleotide deletion, \=possible
,	]			peptide	1	nucleotide insertion
			<u> </u>	sequence		SSQPSQDGQESNVPSVGSLADPDYLNTPQMN
					1	TPVTLNSAAPASNSGAGVLPSPATPRFSVPTP
		ì			1	RTPRTPRTPRGGGTASGQGSVKYDSTDQGSP
		1		Í		ASTPSTTRPLNSVEPATMQPIPEAHSLYVTLIL
	1	1	l	İ		SDSVMNIFKDRNFDSCCICACNMNIKGADVG
				Į.		LYIPDSSNEDQYRCTCGFSAIMNRKLGYNSGL
		1	1		ļ	FLEDELDIFGKNSDIGQAAERRLMMCQSTFL
	1	1		1		POVEGTKKPOEPPISLLLLLQNQHTQPFASLN
			}	+	}	FI DYISSNNROTLPCVSWSYDRVQADNNDY
				l	}	WTECENALEOGROYVDNPTGGKVDEALVRS
		1				ATVHSWPHSNVLDISMLSSQDVVRMLLSLQP
					Ī	FLODAIOKKRTGRTWENIQHVQGPLTWQQFH
					J	KMAGRGTYGSEESPEPLPIPTLLVGYDKDFLT
		1	1	1	1	ISPESI PEWERLLLDPYGGHRDVAYIVVCPEN
						FALLEGAKTFFRDLSAVYEMCRLGQHKPICK
		1		Ì		VI RDGIMRVGKTVAOKLTDELVSEWFNQPW
	1	1	1	1		SGEENDNHSRLKLYAQVCRHHLAPYLATLQL
	-		1			DSSLLIPPKYQTPPAAAQGQATPGNAGPLAPN
	1	1				GSAAPPAGSAFNPTSNSSSTNPAASSSASGSSV
			1	1		PPVSSSASAPGISQISTTSSSGFSGSVGGQNPST
		1	1	1		GGISADRTQGNIGCGGDTDPGQSSSQPSQDG
	1	1				QESVTERERIGIPTEPDSADSHAHPPAVVIYM
				l	1	VDPFTYAAEEDSTSGNFWLLSLMRCYTEMLD
						NLPEHMRNSFILQIVPCQYMLQTMKDEQVFY IQYLKSMAFSVYCQCRRPLPTQIHIKSLTGFGP
ļ	ļ	ļ		ļ		AASIEMTLKNPERPSPIQLYSPPFILAPIKDKQT
1						ELGETFGEASQKYNVLFVGYCLSHDQRWLL
4.	1		ļ			ASCTDLHGELLETCVVNIALPNRSRRSKVSAR
			1		1	KIGLQKLWEWCIGIVQMTSLPWRVVIGRLGR
]		ì		1		LGHGELKDWSILLGECSLQTISKKLKDVCRM
j		1	1		1	CGISAADSPSILSACLVAMEPQGSFVVMPDAV
						TMGSVFGRSTALNMOSSQLNTPQDASCTHIL
1						VEPTSSTIOVAPANYPNEDGFSPNNDDMFVDL
			1	1		PEPDDMDNDIGILMTGNLHSSPNSSPVPSPGSP
			1			SGIGVGSHFOHSRSOGERLLSREAPEELKQQP
						I ALGYFYSTAKAENLPOWFWSSCPQAQN\QC
						PLFLKASLHIHHISVAQTDELLPARNSQRVPHP
			,	1		
,			1	,	1	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD
1						LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTOLYNAIMNIL
924	2174	Δ	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGG
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGOTTYOHPGVAEPSAYGGRDVAC
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASI VEGRLOHRGGDRKRGLLGRSSGDAASD
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD OPERCRSGSTAGRLVKOMDFTEAYADTCSTV
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNILLCSRRRGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTEFGFCALHLAASOGHWKIVQILLEAGADP
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNILLCSRRRGGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLNADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTI EFTTPLFLAVENGOIDVLRLLLQHGAN
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHOASFOENAEIIKLLLRK
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKFCODDFGITPLFVAAQYGKLESL\SILIS
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL  VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SGIANVNCOALDKATPLFIAAQEGHTKCVELL
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRTTPFGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLKK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SG\ANVNCQALDKATPLFIAAQEGHTKCVELL LSGADPPLLYCNEDSWOLPIHAAAQMGHTKI
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRTTPFGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SG\ANVNCQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDILTPLTNRACDTGLNKVSPVYSAVFGGHE
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SG\ANVNCQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCI_FII_LRNGYSPDAOACLVFGFSSPVCMAFQ
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL  VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SG\ANVNCQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL  VEEGLGRRTTPFGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SG\anvncQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPIHAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQINELHLAYCLKYEK
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL  VEEGLGRRTTPFGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SG\anvncQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQINELHLAYCLKYEK FSIFRYFLRKGCSLGPWNHIYEFVNHAIKAQA
824	2174	A	6732	2440	365	LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL  VEEGLGRRTTPFGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHNLLCSRRRGGGGGG GGGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SG\anvncQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPIHAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQINELHLAYCLKYEK

						(A. Alarina Ca-Custaina
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	l	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uciico				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
Į.		Ì		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ	1	ļ	]	peptide	1	/=possible nucleotide deletion, \=possible
1	{	1	ì	sequence	ļ	nucleotide insertion
	<del> </del>	+				QLPLPRSLHNYLLYEDVLRMYEVPELAAIQD
1	1	}	1			G
925	2175	A	6735	277	1252	RIMGLFDRGVQMLLTTVGAFAAFSLMTIAVG
825	21/3		0,33			TDYWLYSRGVCKTKSVSENETSKKNEEVMT
		1			}	HSGLWRTCCLEGNFKGLCKQIDHFPEDADYE
						ADTAEYFLRAVRASSIFPILSVILLFMGGLCIA
						ASEFYKTRHNIILSAGIFFVSAGLSNIIGIIVYIS
1	l l		1		ļ	ANAGDPSKSDSKKNSYSYGWSFYFGALSFIIA
		1		]		EMVGVLAVHMFIDRHKQLRATARA\TDYLQ
į				1		ASAITRIPSYRYRYORRSRSSSRSTEPSHSRDA
1		1	1			SPYGIKGENTLPSTEISMYTLSRDPLKAATTPT
		1	1			ATYNSDRDNSFLQVHNCIQKENKDSLHSNTA
1	1	1				NRRTTPV
	-	-	6744	+3	5177	SDDLRTGLFODVODAESLKLPGVYEVLFYNE
826	2176	Α	0744	,	1 31	TEDCPGMMLWRYPEPRGLTLVRITPVPFNTT
	İ	1		1		EDPDISTADLGDVLQDPCSLEYWDELQKVFV
		1	1			AFREFNI SESKVCELOLPDINLVNDQKKLVSS
		1	ŀ			DLWRIVLNSSONGADDQSSASESGSQSTCDPL
ì		<b>\</b>				VTPTALAACTRVDSCFTPWFVPSLCVSFQFAH
Ì	Ì	1	]			1 EFHI CHHLDOLGTAAPQYLQPFVSDRNMPS
}	1	1	ì	1		FLEYMIVSFREPHMYLROWNNGSVCQEIQFL
				1		AOADCKLLECRNVTMQSVVKPFSIFGQMAVS
1						SDVVEKLLDCTVIVDSVFVNLGQHVVHSLNI
			l			AIOAWOONKCPEVEELVFSHFVICNDTQETL
1						REGOVOTDENILLASLHSHQYSWRSHKSPQL
ļ	}	}	ł		Í	LHICIEGWGNWRWSEPFSVDHAGTFIRTIQYR
İ		1		İ		GRTASLIKVOOLNGVOKQIIICGRQIICSYLSQ
l l	İ	1	1	į.		SIELKVVQHYIGQDGQAVVREHFDCLTAKQK
						LPSYILENNELTELCVKAKGDEDWSRDVCLE
ļ						SKAPEYSIVIQVPSSNSSIIYVWCTVLTLEPNS
i	į	ł	f	1		QVQQRMIVFSPLFIMRSHLPDPIIIHLEKRSLGL
1			1			SETQIIPGKGQEKPLQNIEPDLVHHLTFQAREE
ł					i	YDPSDCAVPISTSLIKQIATKVHPGGTVNQILD
ı			į			EFYGPEKSLQPIWPYNKKDSDRNEQLSQWDS
ļ		-				PMRVKLSIWKPYVRTLLIELLPWALLINESKW
1	Į	ł	i	1		DLWLFEGEKIVLQVPAGKIIIPPNFQEAFQIGIY
ŀ		- 1		1		WANTNTVHKSVAIKLVHNLTSPKWKDGGNG
		1		-		EVVTLDEEAFVDTEIRLGAFPGHQKLCQFCIS
				1		SMVQQGIQIIQIEDKTTIINNTPYQIFYKPQLSV
						CNPHSGKEYFRVPDSATFSICPGGEQPAMKSS
		1				SLPCWDLMPDISQSVLDASLLQKQIMLGFSPA
				1		PGADSSQCWSLPAIVRPEFPRQSVAVPLGNFR
		1		1		ENGFCTRAIVLTYQEHLGVTYLTLSEDPSPRV
		-				IIHNRCPVKMLIKENIKDIPKFEVYCKKIPSECS
		-	1			IHHELYHQISSYPDCKTKDLLPSLLLRVEPLDE
		1				VTTEWSDAIDINSQGTQVVFLTGFGYVYVDV
		j		}		VHQCGTVFITVAPEGKAGPILTNTNRAPEKIV
		-			İ	TF/KMPITQLSLAVFDDLTHHKASAELLRLTL
		1				DNIFLCVAPGAGPLPGEEPVAALFELYCVEIC
			Ī	[		CGDLQLDNQLYNKSNFHFAVLVCQGEKAEPI
1						OCSKMOSLLISNKELEEYKEKCFIKLCITLNEG
		1	]	ļ		KSILCDINEFSFELKPARLYVEDTFVYYIKTLF
	1	1				DTYLPNSRLAGHSTHLSGGKQVLPMQVTQH
						ARALVNPVKLRKLVIOPVNLLVSIHASLKLYI
						ASDHTPLSESVEERGPIFTTARQLVHALAMHY
				1		AAGALFRAGWVVGSLDILGSPASLVRSIGNG
		-		}	•	VADFFRLPYEGLTRGPGAFVSGVSRGTTSFVK
1		ĺ			ĺ	HISKGTLTSITNLATSLARNMDRLSLDEEHYN
	ł	1				ROFFWRROLPESLGEGLROGLSRLGISLLGAI
		-		1		AGIVDQPMQNFQKTSEAQASAGHKAKGVISG
1	1		l			1

			·	<b>7</b> 1: 1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	_	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	Ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, r=rioline,
	Learne	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ	Ì		ì		Sequence	/=possible nucleotide deletion, \=possible
	1	1	1	peptide		nucleotide insertion
		ļ		sequence	<u> </u>	VGKGIMGVFTKPIGGAAELVSQTGYGILHGA
						GLSQLPKQRHQPSD\VHADQAPNSHVKYVW
}		ł	ı			KMLQSLGRPEVHMALDVVLVRGSGQEHEGC
j	1	1	1	1	1	KWLQSLGRPEVHWALDVVLVKGSGQLIEGC
ŀ			1		1	LLLTSEVLFVVSVSEDTQQQAFPVTEIDCAQD
		1	1			SKQNNLLTVQLKQPRVACDVEVDGVRERLSE
1			ł		İ	QQYNRLVDYITKTSCHLAPSCSSMQIPCPVVA
Į	1	1	ļ	1		AEPPPSTVKTYHYLVDPHFAQVFLSKFTMVK
}	ł		1	(		NKALRKGFP
}					ļ. <u></u>	FVGAPRGNPFGSPGNPGRHQGPCHRPRGTK
827	2177	A	6748	2	1662	ASGVSPTLWRPQAAATGLEMPSSGRALLDSP
}			Ĭ			ASGVSPILWRPQAAATGLEWI SSGRAEDSI
1		}			1	LDSGSLTSLDSSVFCSEGEGEPLALGDCFTVN
		1				VGGSRFVLSQQALSCFPHTRLGKLAVVVASY
	1		1		1	RRPGALAAVPSPLELCDDANPVDNEYFFDRS
	1	1	1	}	1	SOAFRYVLHYYRTGRLHVMEQLCALSFLQEI
	1	1			ļ	OVWGIDELSIDSCCRDRYFRRKELSETLDFKK
1		1		1	1	DTEDQESQHESEQDFSQGPCPTVRQKLWNIL
				1	1	EKPGSSTAARIFGVISIIFVGVSIINMALMSAEL
1	1		]	}	1	SWLDLQLLEILEYVCISWFTGEFVLRFLCVRD
ı		1	1			RCRFLRKVPNIIDLLAILPFYITLLVESLSG\SQT
1		1	ľ			RCRFLRK VPNIIDLLAILFF III LE VESESO SQ I
			j	1	1	TQEL\ENVGAHCPGCLRLLRAL\RMLKAWGR
1	[	ĺ			1	HSTGLRSLGMTITQCYEEVGLLLLFLSVGISIF
i i	1	1	1			STVEYFAEQSIPDTTFTSVPCAWWWATTSMT
1	1		1		ł	TVGYGDIRPDTTTGKIVAFMCILSGILVLALPI
	1		1		1	AIDORESACYFTLKLKEAAVRQREALKKLTK
1		1	1			NIATDSYISVNLRDVYARSIMEMLRLKGRER
			1	ļ	Ì	ASTRSSGGDDFWF
		Ì			1260	GTHPASSGPVPLPPAAVSAATREELGEPVPFV
828	2178	A	6786	5672	1360	TASSGFQSMHSSNPKVRSSPSGNTQSSPKSKQ
		-	l l			EVMVRPPTVMSPSGNPQLDSKFSNQGKQGGS
ł	1 .	1		Į.	-	EVMVKPPT VMSPSGNPQLDSM SNQGNQGG
1	ŀ	1	l l			ASQSQPSPCDSKSGGHTPKALPGPGGSMGLK
1	j	1	ļ	j.	1	NGAGNGAKGKGKRERSISADSFDQRDPGTPN
ł			- [			DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT
1	l	1	1			APRSSTPPHGQTTATEPTPAQKTPAKVVYVFS
1	ı			1		TEMANKAAEAVLKGQVETIVSFHIQNISNNK
1	İ					TERSTAPLNTOISALRNDPKPLPQQPPAPANQ
1	1		Į.	1		DQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRE
				1	1	SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN
		1	1	1		NRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPT
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l						DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP
		- 1				FOIAWLKLOOEFYEEKRRKPEQVVVQQCSLQ
	Į			1		DMMVHOHGPRGVVRGPPPPYQMTPSEGWAP
	1		1	1		GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ
	1	,				MRLPGFAGMINSEMEGPNVPNPASRPGLSGV
		1			1	SWPDDVPKIPDGRNFPPGQGIFSGPGRGERFP
1	1					2MADDALVILDOVALLEGÓGILGOLGVORIGI
	1				1	NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR
				1		PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP
	1					LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM
	)	-	1			KGDVNLNVNMGSNSQMIPQKMREAGAGPEE
1						MLKLRPGGSDMLPAOOKMVPLPFGEHPQQE
	Ì	1			į	YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ
1	}	1	1	1	İ	RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG
1	1					LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ
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ì		I.	]	1		SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA
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1						SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS
						PEPPLOSPGIPPNHKAPLTMASPAMLGNVESG
						PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASOPASVNIPG\SLPSSTPYTMPPEPTL
				5		SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPPTASQPASVNIPG\SLPSSTPYTMPPEPTL SONPLSIMMSR\MSKFAM\PS\SNPGYNHDAI

					To divided	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uchcc		}	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	1	i	peptide		/=possible nucleoude deletion, /-possible
	1	1	1	sequence		nucleotide insertion
ļ		<del></del>				KTVASSDDDSPPARSPNLPSMNNMPGMGINT
	1	1				QNPRISGPNPVVPMPTLSPMGMTQPLSHSNQ
ł		ľ	1			MPSPNAVGPNIPPHGVPMGPGLMSHNPIMGH
	l	1				GSQEPPMVPQGRMGFPQGFPPVQSPPQQVPFP
		1		1		HNGPSGGOGSFPGGMGFPGEGPLGRPSNLPQ
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İ		1	l	1	1	VEDRGEVPGRKOPOGPGPGFSHMQGMMGEQ
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\	1	1				CHNIDMRPPAFLOOGMMGPHHRMMSPAQST
1	1	1			İ	MPGQPTLMSNPAAAVGMIPGKDRGPAGLYT
	1	1		İ		HPGPVGSPGMMMSMQGMMGP\NRTS
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327		-				ASTCPPSPGGSGADRFGPSPPPPSREAAPTAG
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830	2180	1	0000			DREPRAPGPWLCPSRAGTAQDPARIRERRGR
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		1	İ			DEIDIDAT\RA\FVAAR\SFVOGLGVAS\DVVK
		}	]			KVAOVPLG\PEC\SRAVIEAGSYC/ALHCVGVP
-	İ					GARPCPDYCRNVLKGCLANQADLDAEWKNL
		1		Į.		I DSMVLITDKFWGTSGVESVIGSVHTWLAEA
-		ł	1		1	INAL ODNROTLTAKVIOGCGNPKVNPQGPGP
		1	i			FEV D D D CKLAPRER PPSGTLEKLVSEAKAQL
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		1	- 1			GMARGRYLPEVMGDGLANQINNPEVEVDIT
	ł		l			KPDMTIRQQIMQLKIMTNRLRSAYNGNDVDF
l	1					QDASDDGSGSGSGDGCLDDLCGRKVSRKSSS
	1					SRTPLTHALPGLSEQEGQKTSAASCPQPPTFL
1						LPLLLFLALTVARPRWR
			1			ASRHGMTPGALLMLLGALGPPLAPGVRGSEA
831	2181	A	6808	2	1522	EGRLREKLFSGYDSSVRPAREVGDRVRVSVG
031	1					LILAQLISLNEKDEEMSTKVYLDLEWTDYRLS
						WDPAEHDGIDSLRITAESVWLPDVVLLNND
	1					WDLAFHDOIDOPKI WESA MPLDA AFFILIATO
		-				GNFDVALDISVVVSSDGSVRWQPPGIYRSSCS
						IQVTYFPFDWQNCTMVFSSYSYDSSEVSLQT
		-				GLGPDGQGHQEIHIHEGTFIENGQWENIHKPS
			1			RLIQPPGDPRGGREGQRQEVIFYLIRRKPLFY
		1				LVNVIAPCILITLLAIFVFYLPPDAGEKMGLSIF
		ł		1		ALLTLTVFLLLLADKVPETSLSVPIIIKYLMFT
			İ			LANT VTESVILSVVVLNLHHRSPHTHQMPLWV
		1				POTETHKLPLYLRLKRPKPERDLMPEPPHCSSP
		- 1				GSGWGRGTDFYFIRKPPSDFLFPKPNKFQFEL
				1	1	CADDI PRETOGPNRAVALLPELREVVSSISYIA
	1	1		1		ROLOFOEDHDALKEDWOFVAMVVDRLFLW
	1	1				TEUETSVGTL\VIFLDATYHLPPPDPFP
						ETMAKNPPENCEDCHILNAEAFKSKKICKSLK
832	2182	A	6824	71	1079	ICGLVFGILALTLIVLFWGSKHFWPEVPKKAY
1 332		1				DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGN
		-				DWEHIT ISHUERANI IMEDI VIRIBIRON
		J	Į	İ	1	GTDETLEVHDFKNGYTGIYFVGLQKCFIKTQI
						KVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAE
		-				KPIENROFLKNSKILEICONVTMYWINPTLIS
1	1	i	1			

SEQ ID SEQ ID Met SEQ Predicted Predicted end nucleotide NO: of NO: of hod ID NO: beginning nucleotide of nucleotide eotide seq-  SEQ ID SEQ ID Met SEQ Predicted Predicted end nucleotide location corresponding of nucleotide peptide in nucleotide location corresponding to last amino M-Methionine, N-Asparagine, Predicted end nucleotide publication corresponding to last amino M-Methionine, N-Asparagine, Predicted end nucleotide publication corresponding to last amino M-Methionine, N-Asparagine, Predicted end nucleotide publication corresponding to last amino makes a sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid sequence (A=Alanine acid s	cid, -Histidine,
nucl- eotide seq-  NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO: of NO:	Histidine,
eotide seq- USSN location corresponding I=Isoleucine, K=Lysine, L=Leuci	
coude Seq. N-Asparagine P	ine.
	Proline.
CO- I HEILE   OVITION COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE COLLEGE   TO THE C	erine.
Uence   Marian Walling Walling Walling Walling Walling Walling	ptophan.
1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	op codon.
103100001	possible
Popular to at the formation	
sequence nucleotide insertion  GTFAKQLHHNFAFIILVSELQ	DFEEEGEDLHFP
ANEKKGIEQNEQWVVPQVK'	VEKTRHARQAS
EEELPINDYTENGIEFDPMLD	ERGYCCIYCRR
GNRYCRRVCEPLLGYYPYPY	CYOGGRVICRV
IMPCNWWVARMLGRV	
FAEGEOVCGAKCCGDAPHV	ENREEETARIGP
833 2183 A 6846 116 602 EAEGEQVCUARCCODAINY	OENDEKDEKE
QVANKGEPLALPLNVSEYCV	PRGNRRRFRVR
QPILQYRWDIMHRLGEPQAR	MREENMERIGE
EVRQLMEKLREKQLSHSLRA	VSTDPPHHDHH
DEFCLMP	
PNGVALLHLPGAAVIPNTNY	MFQDALGGRSR
GSREESPAPSRAPASASLWRI	rlvvveakmaa
HAAAAOAAAAOAAHAEA	ADSWYLALLGF
AEHFRTSSPPKIRLCVHCLQA	VFPFKPPQRIEA
RTHLOLGSVLYHHTKNSEQA	ARSHLEKAWLIS
OOIPOFEDVKFEAASLLSELY	/CQENSVDAAKP
LLRKAIOISOOTPYWHCRLLI	FQLAQLHTLEKD
LVSACDLLGVGAEYARVVG	SEYTRALFLLSK
GMLLLMERKLQEVHPLLTLC	CGQIVENWQGN
PIQKESLRVFFLVLQVTHYLI	DAGQVKSVKPC
LKQLQQCIQTISTLHDDEILP	SNPADLFHWLP
KEHMCVLVYLVTVMHSMQ	AGYLEKAQKYT
DKALMQLEKLKMLDCSPILS	SSFQVILLEHIIM
CRLVTGHKATALQEISQVCQ	LCQQSPRLFSN
HAAQLHTLLGLYCVSVNCM	UNAEAQFIIAL
RLTNHQELWAFIVTNLASVY	(IREGNRHQEVV)
LYSLLERINPDHSFPVSSHCL	RAAAFY VRGLF
SFFQGRYNEAKRFLRETLKM	ASNAEDLNKLIA
CSLVLLGHIFYVLGNHRESN	NMIVYPAMQLAS
KIPDMSVQLWSSALLRDLNF	CONAMDATE
AAQMHQNFSQQLLQDHIEA  POPPPLYOFO A ON CRAFTSLAS	CSELEIIIVEXX WI
DGPPPVQFQAQNGPNTSLAS  1268 PTRRPILPLTSPKAISVPSPLQ  1268 PTRRPILPLTSPKAISVPSPLQ	CKUHTI VKSCI
835 2185 A 6855 334 1268 PTRRPILPLTSPKAISVPSPLQ SVSGIGGFLVSLSSRMKLQTI	AVSVTALKEWS
AYVPCQTQDRDALRLTLEQI	IDI IRRMCASYSE
LELVTSAKALNDTQKLACLI	GVEGGHSLDNS
LSILRTFYMLGVRYLTLTHT	CNTPWAESSAK
GVHSFYNNISGLTDFGEKVV	AEMNRLGMMV
DLSHVSDAVARRALEVSQA	PVIFSHSAARGV
CNSARNVPDDILQLLEEERW	AFVMVSLFHGE
LIQWQPIRPMCSTVADHFDH	IIKAV\IGSKFIGI
GGDYDGAGKYRKKTTCKAI	PWRTSSRMSS
PPRSRPSCWRKKVGPGRPW	WWGGTGPPGQG
836 2186 A 6862 315 II PPRSRPSCWRRXVOPORTW RPEIRLLPLPMTGACGAVAA	SRTGSSGPG/SSL
PNGHGGKGSGLANGLAGNE	<b>AGHLGLGSSFGT</b>
GPGSGRPPP	
VI DGODGBAGGI AFFRRIG	RNEWRIHDVTT
837 2187 A 6863 2 1615 VLRGQRGFAGGLAEERRRG APFPGLVQRRSRLLIVSQVR	YFLKNKVSPDLC
NEDGLTALHQCCIDNFEEIV	KLLLSHGANVN
AKDNELWTPLHAAATCGHI	NLVKILVQYGA
DLLAVNSDGNMPYDLCEDE	EPTLDVIETCMAY
OGITOEKINEMRVAPEOOM	<u>IADIHCMIAAGQ</u>
DLDWIDAQGATLLHIAGAN	GYLRAAELLLDH
GVRVDVKDWDGWEPLHAA	LAFWGQMQMAE
LLVSHGANLNARTSMDEM	PIDLCEEEFKVL
LLELK\HKHDVIMKSQLRHK	SSLSRRTSHRQA
S/SVGKVVRRTQPVGTGPNL	YRKEYE/GEEAL
LWQRSA\AEDQRTSTYNGDI	RET\RTDQENKD

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	Í		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}		peptide		/=possible nucleotide deletion, \=possible
		1	l	sequence	i	nucleotide insertion PNPRLEK\PVLLSEFPTKIPRGELDMPVENGLR
	+					APVSAYQYALANGDVWKVHEVPDYSMAYG
ļ					1	NPGVADATPPWSSYKEQSPQTLLELKRQRAA
			1			AKLLSHPFLSTHLGSSMARTGESSSEGKAPLI
	1					GGRTSPYSSNGTSVYYTVTSGDPPLLKFKAPI
	ł	1			}	FEMEEK VHGCCRIS
	2100	A	6865	6291	739	AGPLEPRVOGAMALOLWALTLLGLLGAGAS
838	2188	}^	0005	0251	1	LRPRKLDFFRSEKELNHLAVDEASGVVYLGA
		ì	1			VNALYQLDAKLQLEQQVATGPVLDNKKCTP
Ì		1	1			PIEASQCHEAEMTDNVNQLLLVDPPRKRLVE CGQLLKGNCALRALSNISLRLFYEDGSGEKSF
1	ļ	1				VASNDEGVATVGLVSSTGPGGDRVLFVGKG
		İ				NGPHDNGIIVSTRLLDRTDSREAFEAYTDHAT
1		1	1			VKAGYLSTNTOOFVAAFEDGPYVFFVFNQQD
İ		1	1		1	KHPARNRTILLARMCREDPNYYSYLEMDLQC
1						RDPDTHAAAFGTCLAASVAAPGSGRVLYAVF
		į				SRDSRSSGGPGAGLCLFPLDEVHAKMEANRN
İ			Ì		}	ACYTGTREARDIFYKPFHGDIQCGGHAPGSSK
		[			ļ	SFPCGSEHLPYPLGSRDGLRGTAVLQRGGLN LTAVTVAAENNHTVAFLGTSDGRILKVYLTP
		1				DGTSSEYDSILVEINKRVKRDLVLSGDLGSLY
İ		1		1	1	AMTODKVFRLPVOECLSYPTCTQCRDSQDPY
1		1		1	{	CGWCVVEGRCTRKAECPRAEEASHWLWSRS
		ļ				KSCVAVTSAOPONMSRRAQGEVQLTVSPLPA
ļ	ļ					LSEEDELLCLFGESPPHPARVEGEAVICNSPSS
					1	IPVTPPGQDHVAVTIQLLLRRGNIFLTSYQYPF
1						YDCRQAMSLEENLPCISCVSNRWTCQWDLR YHECREASPNPEDGIVRAHMEDSCPQFLGPSP
1						LVIPMNHETDVNFQGKNLDTVKGSSLHVGSD
		- 1		1		LIKEMEPVTMOESGTFAFRTPKLSHDANEIL
		i				PLHLYVKSYGKNIDSKLHVTLYDCSFGRSDC
		1		į		SLCRAANPDYRCAWCGGOSRCVYEALCNII
		1			1	SECPPPVITRIQPETGPLGGGIRITILGSNLGVQ
		ļ		}	1	AGDIQRISVAGRNCSFQPERYSVSTRIVCVIEA
}	İ					AETPFTGGVEVDVFGKLGRSPPNVQFTFQQP KPLSVEPQQGPQAGGTTLTIHGTHLDTGSQED
		- 1				VRVTLNGVPCKVTKFGAQLQCVTGPQATRG
				i	}	OMILEVSYGGSPVPNPGIFFTYRENPVLRAFE
		-		1	Į.	PLRSEASGGRSINVTGOGFSLIQRFAMVVIAEP
		- 1	1			LOSWOPPREAESLOPMTVVGTDYVFHNDTK
		1				VIVEL SPANDEEPEAYNLTVLIEMDGHRALLKI
					1	EAGAFEYVPDPTFENFTGGVKKQVNKLIRAR
Ì				}	}	GTNLNKAMTLQEAEAFVGAERCTMKTLTET DLYCEPPEVQPPPKRRQKRDTTHNLPEFIVKF
1	1	- {				GSREWVLGRVEYDTRVSDVPLSLILPLVIVPM
	1				1	VVVIAVSVYCYWRKSOQAEREYEKIKSQLEG
İ		- 1				I FESVRORCKKEFTDLMIEMEDQTNDVHEAG
				1		IPVI DYKTYTDRVFFLPSKDGDKDVMITGKL
]		- 1				DIPEPRRPVVEOALYOFSNLLNSKSFLINFIHT
	100			1		LIFNOPEFSARAKVYFASLLTVALHGKLEYYI
		-		ì		DIMHTLFLELLEQYVVAKNPKLMLRRSETVV
						ERMLSNWMSICLYQYLKDSAGEPLYKLFKAI KHQVEKGPVDAVQKKAKYTLNDTGLLGDD
	1	1		1		VEYAPLTVSVIVQDEGVDAIPVKVLNCDTISQ
						VEYAPLIVSVIVQDEGVDAIFVKVLNCDIISQ VKEKIIDQVYRGQPCSCWPRPDSVVLEWRPG
		1		1		STAOII SDLDLTSOREGRWKRVNTLMHYNVR
						DGATLIL SKVGVSOOPEDSOQDLPGERHALL
		1		1		FFFNR VWHI. VRPTDEVDEGKSKRGSVKEKE
1	- 1					PTK ATTELYLTRILLSVKGTLQQFVDNFFQSVL
	- 1	1				APGHAVPPAVKYFFDFLDEQAEKHNIQDEDTI

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NO. of non-circle could septide could be sequence of the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding t	SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	1 D-Aspartic Acid E=Glutamic Acid,
nucle curicle sequence    Sequence   14		NO: of	hod		beginning		F=Phenylalanine, G=Glycine, H=Histidine,
eorde uence 914 914 914 915 correspond; 10 sal ammo aid residue of repide signation acid residue of repide signation acid residues of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature of repide signature	nucl-	peptide					I=Isoleucine K=Lvsine, L=Leucine,
sequence    914	eotide	seq-				to last amino	M=Methionine, N=Asparagine, P=Proline,
uence   914   Samino acid reside sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequence   915   Sequenc	seq-	uence				acid residue	O-Glutamine R=Arginine, S=Serine,
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D-A martic Acid F=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O-Glutamine R=Arginine, S=Serine,
uence	1	ļ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
	ļ	ļ		sequence		nucleotide insertion
	ļ					KGLVQVTKHRLCRLPPSRAHLPTKEASSLHA
		Ì				VRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLS LPSWRARRLSLSRSLVLNRLRPVASGGGKAQ
	İ	1	1	1		PGSPWWRSKGYRCIGGVLYKVSANKLSKTSG
	1	1			1	QPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
		Į.		l .		RSLAIIRQARQRREKRKEYCMYYNRFGRCNR
	1			1	}	GERCPYIHDPEKVAVCTRFVRGTCKKTDGTC
	1			}	1	PFSHHVSKEKMPVCSYFLKGICSNSNCPYSHV
	1					VVCDKAEVCSDFLKGYCPLGAKCKKKHTLLC
		ł				DDEADDGACPRGACCOLLHRTOKRHSKKAAI
		1	ļ			1 CDADCDSDATARSRVSASHGPRKPSASQRPIR
	İ	1	-	,	Į.	LOTES AT TA A AVAAPPHCPGGSASPSSSNAS
		1	i	1	*	LCCCCCCDDASI DHE\APSLOEAALAAACSNK
		}	Ì			LCKLPSFISLQSSPSPGAQPRVRAPRAPLTKDS
	1	1		1		CVDI UTVPRI
		<del> </del>	6898	506	2071	WPDLVHTWSSEEAMGSCCSCPDKDTVPDNH
842	2192	A	0070	300		RNKFKVINVDDDGNELGSGIMELTDTELILYT
		1		· I	1	RKRDSVKWHYLCLRRYGYDSNLFSFESGRRC
						QTGQGIFAFKCARAEELFNMLQEIMQNNSIN
				ļ.		VVEEPVVERNNHQTELEVPRTPRTPTTPGFAA QNLPNGYPRYPSFGDASSHPSSRHPSVGSARL
	-	Ì	1			PSVGEESTHPLLVAEEQVHTYVNTTGVQEER
		Ì				KNRTSVHVPLEARVSNAESSTPKEEPSSIEDR
	1	1			ì	DPQILLEPEGVKFVLGPTPVQKQLMEKEKLE
ĺ			Ì	İ	· ·	OLGPDOVSGSGANNTEWDTGYDSDERKDAP
	ì		}	}	}	L CONIKI VYENINGI SIPSASGVRRGRL 151515D
ł			1			TONININGAORRTALLNYENLPSLPPVWEARK
1		ļ				I SPITEDDNI GPKTPSLNGYHNNLDPMHN I V
ļ		ĺ				NUTENTATIVEASAHKIEYSRRRDCTPIVENEDIK
		[				DDGI EUROI MVIOVDI EGGSDSDNPQIPKIPI
	Į	- 1		İ	İ	TPLPOTPTRRTELYAVIDIERTAAMSNLQKAL
1	]	1		}		PRDDGTSR\KTRHNST\DLPL
	2102	$\frac{1}{A}$	6919	2	663	AGRPGTTHASGKMAYQSLRLEYLQIPPVSRA
843	2193	^	10,17	-		YTTACVLTTAAVQLELITPFQLYFNPELIFKHF
		l				QIWRLITNFLFFGPVGFNFLFNMIFLYRYCRM LEEGSFRGRTADFVFMFLFGGFLMTLFGLFVS
1		İ	1		Ì	LVFLGPGLYNN/GSSMCGAE\EPLCPHELLRP
i						SQLPGPLSALGAHGIFLVVGELNHCGPFGYCS
	ĺ	1				WTHIFFLGRCISQSTWWNKNSENTIYFESYF
				1		HRLCMPIQGACGERME/FSLLLPGLECNGVIL
844	2194	A	6928	902	366	AUCNI RI PGSSNSPASASOVAGITGVCHHAR
		İ				I IEVESVETGELHAGOAGLELLISGDPPASAS
1		}	1			QSAGITGKSQHTRPGYEFIIPYSAAQEDALKA
		1	1			1 M
ļ				1	317	I VDENI GESI EPII I I PPPWPDGGRPCCVEMS
845	2195	A	6939	1660	317	TOAKKI PRIWRILEEKESVAGAVQTLLLRSQI
1	l			ļ	j	COMPS A A STI SEPPRRIUESKIKI KALULFI
1	1					T DATE LE A A STEPOGPR PVLGRES VQ VPUDQU
		1			}	EDGEDGECEAFVGWNLTYSRAGVSVWVQAV
1		ļ				EMDRTI HKIKCRMECCDVPAETLYDVLHDIE
1				1		VDKKWDSNVIETFDIARLTVNADVGYYSWK
		1		1		CDKDI KNRDVITLRSWLPMGADYIIMNYSVK
	1	ĺ				IDV VDDDK DI VRAVSIOTGYLIOSTGPKSCVI
		Į.	ļ			VI A OVDPK GSLPK WVVNKSSQFLAPKAMKK
				1		AVEACI KYPEWKOKHL\PHFKPWL\HPEQSP
	Ì				İ	I DSLAI SYFLSVOHADS/LENIDESAV/AESKEE
					- 1	DIMGGAGGEGISDDDTSLYAEAPHRERETET
1						PGAGRALGAAAAPALSPLHPPGTWWHRARP
						RRVLQPGWTEPQ

			CEO	Deadistad	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
пенсе		Ì	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1		į.	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
İ	1	1		peptide	5042551	/=possible nucleotide deletion, \=possible
	j	1	}	sequence	1	nucleotide insertion
		<del>                                     </del>	6044	42	2672	RRKMAGCRGSLCCCCRWCCCCGERETRTPE
846	2196	Α	6944	42	2072	ELTILGETQEEEDEILPRKDYESLDYDRCINDP
1	1	1				YLEVLETMONKKGRRYEAVKWMVVFAIGV
	1	1				CTGLVGLFVDFFVRLFTQLKFGVVQTSVEECS
1	İ	1				QKGCLALSLLELLGFNLTFVFLESLLGLIEPVE
	}	1		-		AGSGITEGKCYLYAROVPGLVRLPTLLWKAL
}		1			1	GVILTVAAMLLI\GLGSPMIHSGSVVGAGLPQ
					ì	FQSISLRKIQFNFPYFRSDRYGK\DKRDFVSAG
		}	1			AAAGVAAAFGAPIGGTLFSLEEGSSFWNQGL
1					}	TWKVLFCSMSATFTLNFFRSGIQFGSWGSFQL
	1	}		1		PGLLNFGEFKCSDSDKKCHLWTAMDLGFFV
	Į.	l			}	VMGVIGGLLGATFNCLNKRLAKYRMRNVHP
		1		1	1	KPKLVRVLESLLVSLVTTVVVFVASMVLGEC
	1	Ì				RQMSSSSQIGNDSFQLQVTEDVNSSIKTFFCP
	}	1			}	NDTYNDMATLFFNPQESAILQLFHQDGTFSPV
		1	1			TLALFFVLYFLLACWTYGISVPSGLFVPSLLC
	1	1	1			GAAFGRLVANVLKSYIGLGHIYSGTFALIGAA
1		1				AFLGGVVRMTISLTVILIEST\NEITYGLPIMVT LMVGKWTGDFFNKGI\YDIHVGLRGVPLLEW
- [	1	ļ				ETEVEMDKLRASDIMEPNLTYVYPHTRIQSLV
1		[				SILRTTVHHAFPVVTENRGNEKEFMKGNQLIS
1	Ì	1			ļ	NNIKFKKSSILTRAGEQRKRSQSMKSYPSSEL
}	ł	l	1			RNMCDEHIASEPAEKEDLLQQMLERRYTPY
	l l	ļ		}	}	PNLYPDQSPSEDWTMEERFRPLTFHGLILRSQ
-	i	1		1		LVTLLVRGVCYSESQSSASQPRLSYAEMAED
	ì	1			1	YPRYPDIHDLDLTLLNPRMIVDVTPYMNPSPF
	1	İ	ì	i	1	TVSPNTHVSQVFNLFRTMGLRHLPVVNAVGE
			1			IVGIITRHNLTYEFLQARLRQHYQTI
ļ <u>.</u>				<del>+</del>	1994	NTNSSSVTNSAAGVEDLNIVOVTVPDNEKER
847	2197	Α	6951	3	1334	LSSIEKIKOLREOVNDLFSRKFGEAIGVDFPVK
		1			1	VPYRKITENPGCVVIDGMPPGVVFKAPGYLLI
1.		-			}	SSMRRILEAAEFIKFTVIRPLPGLELSNGEYST
			ì			VGKRKIDOEGRVFOEKWERAYFFVEVQNIST
	į.	- 1				CLICKRSMSVSKEYNLRRHYQTNHSKHYDQY
	ļ					MERMRDEKLHELKKOLRKYLLGLSDTECPE
					}	QKQVFANPSPTQKSPVQPVEDLAGNLWEKLR
	1					EKIRSFVAYSIAIDEITDINNTTQLAIFIRGVDE
1		[		Ì		NFDVSEELLDTVPMTGTKSGNEIFSRVEKSLK
ļ	1	1	İ	ļ.	ļ	NFCINWSKLVSVASTGTPPMVDANNGLVTKL
		İ	}			KSRVATFCKGAELKSICCIIHPESLCAQ\KLKM
						DHVMDVVVKSVNWICSRGLNHSEFTTLLYEL DSQYGSLLYYTEIKWLSRGLVLKRFFESLEEI
		1		1	ļ	DSQYGSLLYY TEIK WLSKGLVLARFFESLEDI DSFMSSRGKPLPQLSSIDWIRDLAFLVDMTM
1		1				DSFMSSRGKPLPQLSSIDWIRDLATE VDMTM HLNALNISLQGHSQIVTQMYDLIRAFLAKLCL
					1	WETHLTRNNLAHFPTLKLVSRNESDGLNYIP
1	}					KIAELKTEFQKRLSDFKLYESELTLFSSPFSTKI
						DSVHEELQMEVIDLQCNTVLKTKYDKVGIPE
ľ		}		}	1	FYKYLWGSYPKYKHHCAKILSMFGSTYICEQ
1	1					LFSIMKLSKTKYCSQLKDSQWDSVLHIAT
	1				1.00	SVQYLPGRPTRTHASTDAPLMLKFTPLPSKTK
848	2198	A	6985	3	289	ASAPVQCLLLMAATFSPQGLAKPHSGTIPIT\C
					1	CFNAINTKIPIQRLESYTRITNIQCPKEAVM
1		1	1			LDFLCHRDMGDNITSITEFLLLGFPVGPRIQM
849	2199	A	6999	963	5	LLFGLFSLFYVFTLLGNGTILGLISLDSRLHAP
1						MYFFLSHL\AVVDIAYACNTVPRMLVNLLHP
						AKPISFAGRMMQTFLFSTFAVTECLLLVVMS
	]					YDLYVAICHPLRYLAIMTWRVCITLAVTSWT
1						TGVLLSLIHLVLLLPLPFCRPQKIYHFFCEILA
	}	j	1	1		VI KI ACADTHINENMVLAGAISGLVGPLSTIV
						VSYMCILCAILQIQSREVQRKAFCTCFSHLCVI
1	l	ı	l l	1	1	1011/0000105 4-4

CEO ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	"	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
1	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			Ì	1	sequence	/=possible nucleotide deletion, \=possible
İ		1		peptide		nucleotide insertion
			<b></b>	sequence		GLFYGTAIIMYVGPRYGNPKEQKKYLLLFHS
ļ	ļ					LFNPMLNPLICSLRNSEVKNTLKRVLGVERAL
L						MGNDSVSYEYGDYSDLSDRPVDCLDGACLAI
850	2200	Α	7001	1	1011	1
		1	1			DPLRVAPLPLYAAIFLVGVPGNAMVAWVAG
}						KVARRRVGATWLLHLAVADLLCCLSLPILAV
		1			!	PIARGGHWPYGAVGCRALPSIILLTMYASVLL
1	ĺ	1	1	1		LAALSADLCFLALGPAW\CLRFS/GACGVQVA
}	ļ	j	)	j	ļ	CGAAWTLALLLTVPSAIYRRLHQEHFPARLQ
1	l .	1			1	CVVDYGGSSSTENAVTAIRFLFGFLGPLVAVA
		1		1		SCHSALLCWAARRCRPLGTAIVVGFFVCWAP
		1			i .	YHLLGLVLTVAAPNSALLARALRAEPLIVGL
				Ì		ALAHSCLNPMLFLYFGRAQLRRSLPAACHW
1	1	1	1		1	ALRESQGQDESVDSKKSTSHDLVSEMEV
851	2201	A	7011	1	2310	AAASPLRMSRKGPRAEVCADCSAPDPGWASI
05.		1	1			SRGVLVCDECCSVHRSLGRHISIVKHLRHSA
1	ļ	}	}	1	}	WPPTLLQMVHTLASNGANSIWEHSLLDPAQV
		ł		1		QSGPALKQTPKDKV\HPIKSEFIRAKYQMLAF
						VHKLPCRDDDGVTAKDLSKQLHSSVRTGNLE
1	1	1	l			TCLRLLSLGAQANFFHPEKGTTPLHVAAKAG
i	1	}	}			QTLQAELLVVYGADPGSPDVNGRTPIDYARQ
	1	}	1		}	AGHHELAERLVECQYELTDRLAFYLCGRKPD
	1		l	1		HKNGHYIIPQMADSLDLSELAKAAKKKLQAL
†				1		SNRLFEELAMDVYDEVDRRENDAVWLATQN
	1	1			Į.	HSTLVTERSAVPFLPVNPEYSATRNQGRQKL
			1			ARFNAREFATLIIDILSEAKRRQQGKSLSSPTD
1	Į.	1	ł	1	{	NLELSLRSQSDLDDQHDYDSVASDEDTDQEP
1			Į			LRSTGATRSNRARSMDSSDLSDGAVTLQEYL
1	1		İ		1	
		İ				ELKKALATSEAKVQQLMKVNSSLSDELRRLQ
ì		1	1			REIHKLQAENLQLRQPPGPVPTPPLPSERAEH
ł	ł	1	1		ì	TPMAPGGSTHRRDRQAFSMYEPGSALKPFGG
1		1	1			PPGDELTTRLQPFHSTELEDDAIYSVHVPAGL
	ļ					YRIRKGVSASAVPFTPSSPLLSCSQEGSRHTSK
j		1	1	ļ	l	LSRHGSGADSDYENTQSGDPLLGLEGKRFLE
1			1	}		LGKEEDFHPELESLDGDLDPGLPSTEDVILKT
			1		j	EQVTKNIQELLRAAQEFKHDSFVPCSEKIHLA
	1				1	VTEMASLFPKRPALEPVRSSLRLLNASAYRLQ
	}		1		1	SECRKTVPPEPGAPVDFQLLTQQVIQCAYDIA
1				Ĭ .	1	KAAKQLVTITTREKKQ
852	2202	A	7016	484	1777	RISKIQVYYSTGYSSRKMNPTLGLAIFLAVLL
	1					TVKGLLKPSFSPRNYKALSEVQGWKQRMAA
1					}	KELARQNMDLGFKLLKKLAFYNPGRNIFLSP
			1		}	LSISTAFSMLCLGAQDSTLDEIKQGFNFRKMP
1		1				EKDLHEGFHYIIHELTOKTODLKLSIGNTLFID
			1			QRLQPQRKFLEDAKNFYSAETILTNFQNLEM
		}	1			AOKOINDFI/ESKTHGKINNLIENIDPGTVMLL
1		]	1	1		ANYIFFRARWKHEFDPNVTKEEDFFLEKNSS
		1		}		VKVPMMFRSGIYQVGYDDKLSCTILEIPYQK
		1	Į.	1		NITAIFILPDEGKLKHLEKGLQVDTFSRWKTL
						LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVS
					1	KIFEEHGDLTKIAPHRSLKVGEAVNKAELKM
			1	1		DERGTEGAAGTGAQTLPMETPLVVKIDKPYL
		1				DEPOTE DAY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
						LLIYSEKIPSVLFLGKIVNPIGK
853	2203	A	7017	1	3293	MTHACNPSTLGGQGRRITRSHGRRRSSRGPV
					1	ARHVAAGAGHENKHGGSRRFPAGVAPRRAM
		1	1	}	!	ANVSKKVSWSGRDRDDEEAAPLLRRTARPG
						GGTPLLNGAGPGAARQSPRSALFRVGHMSSV
		1				ELDDELLEP\DMDPPHPFPKEIPHNEKLLSLKY
						ESLDYDNSENQLFLEEERRINHTAFRTVEIKR
						WVICALIGILTGLVACFIDIVVENLAGLKYRVI
1		1	1	1		KGSILPNIDKFTEKGGLSFSLLLWATLNAAFV
	<u> </u>		ــــــــــــــــــــــــــــــــــــــ	L	L	

			000	Desidiated	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in	nucleotide	location	F=Phenylalamine, 0=Olychic, 11=Thistianic,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		i	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
derice	1	1	{	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		ŀ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ.		İ		peptide	304255	/=possible nucleotide deletion, \=possible
1		i	l		İ	nucleotide insertion
	ļ	<u> </u>		sequence		LVGSVIVAFIEPVAAGSGIPQIKCFLNGVKIPH
	1					LYGSVIVAPIEP VAAGSGIPQIKCE ENGVIRITI
]			1	ļ		VVRLKTLVIKVSGVILSVVGGLAVGKEGPMI
]	1	1	ì	İ	ì	HSGSVIAAGISQGRSTSLKRDFKIFEYFRRDTE
1					1	KRDFVSAGAAAGVSAAFGAPVGGVLFSLEEG
1	}		1			ASFWNQFLTWRIFFASMISTFTLNFVLSIYHG
Ì	1	i			İ	NMWDLSSPGLINFGRFDSEKMAYTIHEIPVFI
1		ļ			]	AMGVVGGVLGAVFNALNYWLTMFRIRYTHR
t	í	1		1		PCLQVIEAVLVAAVTATVAFVLIYSSRDCQPL
Ì	1	Į.			}	QGGSMSYPLQLFCADGEYNSMAAAFFNTPEK
	1	1		1		SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWT
1			ŀ			SVVSLTHDPPOSTNFLTLODFTLYTTTLACUT
1	ì		1			YGLTVSAGVFIPSLLIGAAWGRLFGISLSYLTG
	1	i		1		AAIWADPGKYALMGAAAQLGGIVRMTLSLT
		1	1	1		VIMMEATSNVTYGFPIMLVLMTAKIVGDVFIE
1	1	1		1		GLYDMHIQLQSVPFLHWEAPVTSHSLTAREV
1		1		1		MSTPVTCLRRREKVGVIVDVLSDTASNHNGF
			1	1	1	PVVEHADDTQPARLQGLILRSQLIVLLKHKVF
	ļ	i	i	1	1	VERSNLGLVQRRLRLKDFRDAYPRFPPIQSIH
	1	1	1	1	1	VSQDERECTMDLSEFMNPSPYTVPQEASLPR
Į		ł	1			VFKLFRALGLRHLVVVDNRNQVVGLVTRKD
l			1			LARYRLGKRGLEELSLAQTGPKAQATAEGRV
İ	ì	1	ł		i	AGAAQQPCQLRAVTLEDLGLLLAGGLASPEP
1	ľ	1	Į.		1	LSLEELSERYESSHPTSTASVPEQDTAKHWNQ
	ł				}	LSLEELSEK TESSHITISTASVIEQUITATITATIV
	1			1		LEQWVVELQAEVACLREHKQRCERATRSLL
1	Ì	ļ			1	RELLQVRARVQLQGSELRQLQQEARPAAQAP
ĺ	1	1		1		EKEAPEFSGLQNQMQALDKRLVEVREALTRL
			,	I .	I	EKEM BI BOBQI QIII QI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI III DI I
1		1				RRROVOOEAERRGAEQEAGLRLAKLTDLLQ
						RRROVOOEAERRGAEQEAGLRLAKLTDLLQ
						RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M
			7027	120	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M AGTWEPRPYDOAKETGAPGSQPPVPPMELRP
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EOOVAKRRTKRDVYQEPTDPKFPQQWYL\SG
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTORDLMVKAAWAQGYTGHGIVVSILDDGI
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TOMNDNRHGTRCAGEVAAVANNGVCGVGV
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSOGRGGLGSIFVWASGNGGREHDSCNCD
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRTKRDVYQEPTDPKFPQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRTKRDVYQEPTDPKFPQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNONEKOIVTTDLRQKCTESHTGTSAS
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAONWTTVAPQRKCIIDILTEPKDI
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQRDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSOACVVCEEGFSLHQKSCVQHCPP
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPOVLDTHYSTENDVETIRASVCAPCHAS
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPOVLDTHYSTENDVETIRASVCAPCHAS
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHYSASWGPEDDGKTVDGPARLAEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCOGPALTDCLSCPSHASLDPVEQTCSRQS
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS OSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS
854	2204	A	7037	139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHYSASWGPEDDGKTVDGPARLAEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS
854	2204	A	7037	139	2604	RRRQVQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HHHYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD
854	2204	A	7037	139	2604	RRRQVQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVLQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SFEDEGRGERTAFIKDQSAL
				139	2604	RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQPPRLPPEVEAGQRLRAGLLP HLPEVVAGLSCAFIVLVFVTVFLVQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL
854	2204	A	7037			RRRQVQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL  QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF
						RRRQVQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFTVFLVQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL  QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELLNVTPEDWDFCCKGLALDL
						RRRQVQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFTVFLVQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL  QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF LVKEKGYDKELLNVTPEDWDFCCKGLALDL
						RRRQVQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR M  AGTWEPRPYDQAKETGAPGSQPPVPPMELRP WLLWVVAATGTLVLLAADAQGQKVFTNTW AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI EKNHPDLAGNYDPGASFDVNDQDPDPQPRY TQMNDNRHGTRCAGEVAAVANNGVCGVGV AYNARIGGVRMLDGEVTDAVEARSLGLNPN HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD GYTNSIYTLSISSATQFGNVPWYSEACSSTLA TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS APLAAGIIALTLEANKNLTWRDMQHLVVQTS KPAHLNANDWATNGVGRKVSHSYGYGLLD AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAQARLT LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY SADGFNDWAFMTTHSWDEDPSGEWVLEIEN TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP GFAPQVLDTHYSTENDVETIRASVCAPCHAS CATCQGPALTDCLSCPSHASLDPVEQTCSRQS QSSRESPPQQQPPRLPPEVEAGQRLRAGLLPS HLPEVVAGLSCAFIVLVFVTVFLVQLRSGFS FRGVKVYTMDRGLISYKGLPPEAWQEECPSD SEEDEGRGERTAFIKDQSAL  QRPASQLLAPFAAEALPGAPRAAMAQHFSLA ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF

				S	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D-Aspartic Acid F=Cilutamic Acid,
O: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
q-	uence		09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence			914	amino acid	of peptide	T-Threonine V=Valine W=Tryptophan,
	1	1		residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
	1	1	1	peptide	Sequence	/=possible nucleotide deletion, \=possible
		1	1	sequence		nucleotide insertion
				sequence		YFDLPGALLCARVVDYLTKLNNGQKTFDFW
		ļ		t I	}	PDIVALIOHNYKMSAFKENCGIYFPEIKROPG
	[	1		1		DVI USBPESVKKWLROLKNAGKILLLII SSRS
	1	1	1	ļ		DVCRI I CALVILGNDFTDLFDIVITNALKPGFF
		1	1	•		SUIT PSORPERTLENDEEOEALPSLUKPUW ISQ
		}	1	}		CNAVHI VELLKKMTGKPEPKVVYFGDSMINS
				1		DIFPARHYSNWETVLILEELRGDEGTRSQRPE
		1	1		l .	ESEPLEKKGKYEGPKAKPLNTSSKKWGSFF\I
		1	1			DSVLGLENTEDSLVYTWSCKRISTYSTIAIPSI
			1			EAIAELPLDYKFIRFSSSNSKTAGYYPNPPLV
	Į.	1	1			LSSDETLISK
	0000		7082	396	1635	CODEVEREHAVOPVETMEFLKTCVLRRNACI
856	2206	Α	1002	3,50	1	AVCEWRSKVVOKPSVRRISTTSPRSTVMPAW
		1				VIDENCENEVERETONMMMPHHYPNEVIVE
	1	1	1			VHAASVNPIDVNMRSGYGATALNMKRDPLH
		1		l		VKIKGEEFPLTLGRDVSGVVMECGLDVKYFK
		1	1	1 '		PGDEVWAAVPPWKQGTLSEFVVVSGNEVSH
	ļ	1	<b>\</b>		1	KPKSLTHTQAASLPYVALTAWSAINKVGGLN
						DKNCTGKRVLILGASGGVGTFAIQVMKAWD
	- 1		1			AHVTAVCSQDASELVRKLGADDVIDYKSGSV
	1	1		1		EEQLKSLKPFDFILDNVGGSTETWAPDFLKK
		-		Ì	ļ.	WSGATYVTLVTPFLLNMDRLGIADGMLQTG
		1	ł	1	<b> </b>	VTVGSKALKHFWKGVHYRWAFFMASGPCL
	1				ļ	DDIAELVDAGKIRPV\IEQTFPFSKVPEAFLKV
	1	l	l			ERGHARGKTVINVV
0.57	2207	A	7088	320	2417	LRRKMTPQSLLQTTLFLLSLLFLVQGAHGR
857	2207	1	1			GHREDFRFCSQRNQTHRSSLHYKPTPDLRISH NSEEALTVHAPFPAAHPASRSFPDPRGLYHFC
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	1		l l			QHQEESLAQGPPLLATSVTSWWSPQNISLPSA
	ł	1	(	ĺ		ASFTFSFHSPPHTGAHNASVDMCELKRDLQL
	1		1	1		LSQFLKHPQKASRRPSAAPASQQLQSLESKL
	1		1			SVRFMGDMGSFEEDRINATVWKLQPTAGLQ
	1		1	1	l l	DLHIHSRQEEEQSEIMEYSVLLPRTLFQRTKG
	Į.					RSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
	1	Ì	- }			KVLGIVVQNTKVANLTEPVVLTFQHQLQPKI
	1					VTLQCVFWVEDPTLSSPGHWSSAGCETVRR
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		1		1		TO VEL VAL VOVDNYGPIILAVHRTPEGVIYP
				j	}	MCWIRDSLVSYITNLGLFSLVFLFNMAMLA
		1		1	1	LAWOU DI RPHTOKWSHVLILLCLSLVLUL
		1	-			WAI TEESEASGIFOL VVI.YLFSIIISFUGILLIN
			1	- {		WYWSMRLQARGGPSPLKSNSDSARLPISSG
1				1	1	TCCCRI
					415	DAGAVK SSDTNIWERGMCDDKKGHRCPS*(
858	2208	A	7091	185	415	QPQHFHVAFHTEAEGAMFYFRLHVIHRVMC
						OCOL EPSTI ESWILE
1						FEETUPOSI ALL PRI ECSGATGAHCNLHFPGS
859	2209	A	7136	3	302	DCDTGAG*IAGITGACYHAWLLFVFLAEIGF
					1	HVGQGGLELLTSSDPSGSASQSAGITGVSHC
1			1	1		WDI
						ALSTETRTPDMRRLLLVTSLVVVLLWEAGA
860	2210	A	7156	23	591	PAPKVPIKMQVKHWPSEQDPEKAWGARVV
1 000	1210	'.		1		PPEKDDQLVVLFPVQKPKLLTTEEKPRGQGI
	l.			1	1	I DDFK DECEA APEL ACKLETTE LEGISLACK
	İ					GPILPGTKAWMETEDTLGRVLSPEPDHDSL'

_				TO allowed	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D-Aspartic Acid F=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	<u> </u>	ţ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ì	1	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł	1	peptide	Joquin	/=possible nucleotide deletion, \=possible
		i	1	sequence		nucleotide insertion
		↓	<b></b>	sequence	<del> </del>	HPPPEEDQGEERPRLWVMPNHQVLLGPEEDQ
		1	1			DHIYHPQ*GSRGHHCPRPVPRPRLLGLGPSLP
	ĺ	1		}	1	CDC
		ļ	7161	1220	1003	NYVCTIAF*EKKMGF*LSLSCLVLLFVLFLDCI
861	2211	A	/101	1220	1.005	LTTTTRIMFHCTYLFASVCLSLLNTLLSPNCL
		1		}	1	KSAMIO
		<del>  </del>	7211	665	847	LKYYHITMGIYKTGKKVIL*KSSMSNRFSVIF
862	2212	A	/211	003	047	VENTORI SESNYVYHONYVESSDWSYDF
		<del> </del>	7212	924	1273	HGSSCALGDLAPG*LPSGPVLSSPAVKL*KKP
863	2213	A	1212	924	1275	T VWDSPSCLPATGPT*GLVLVLGGPDC1*WA
		1	1		1	RGOHEHKRMRAP*SCRVTVNLAKKKKKTDQ
		1		İ	l	CTKPNYOSPPKECDYNILANSVA
			7214	845	1619	CDVCCVKADRKNHLRHAFPLLPHRVREKLH
864	2214	Α	/214	047	1.0.0	DPKVPVDADHVOGODPGRAAHDIHGEDVIE
		1			1	KVCKUDI APDEVGDTDEGHDRHGHREVOUR
	1	1	1	1	1	HGHDOFEVAYEERACEGGKFATVEVIDKPV
	1	1				DEALBEAMPKVAKYAGGTNDKGIGMGMIV
		1				PISFAVFPNEDGSLQKKLKVWFRIPNQFQSDP
	1	1			1	PAPSDKSVKIEEREGITVYSMQFGGYAKEAD
		- 1		1		YVAQATRLRAALEGTATYRGDIYFCTGYDPP
	1	}			}	MKPYGRRNEIWLLKT
	2215	A	7246	559	682	RRLGAVAHAYTSSTLGGRGGWIT*GQELQTS
865	2213	1^	1240	1 023		LANMAKPRLY
066	2216	- A	7257	641	1310	TCTYKYLMGWIRGRRSRHSWEMSEFHNYNL
866	2210	1	, 23.			DLKKSDFSTRWQKQRCPVVKSKCRENASPFF
1		1		1		FCCFIAVAMGIRFIIMVAIWSAVFLNSLFNQEV
1		1			1	QIPLTESYCGPCPKNWICYKNNCYQFFDESKN
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		1	}	ļ		IEMQKGDCALYASSFKGYIENCSTPNTYICM
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ļ	1.	-				QRTV SIKIIEAFGSNGPDFWFFRYWSP*LFRQQVVFI
867	2217	A	7288	151	396	MPFFQTLWLMNANRFCSIFTTTNVANNCWW
807					i	TPYHCWLSVVVCRCESHGI
1		- }	1	_		PDTVIGGRGSGGKEFGRWVLW*VFE*RLGTP
868	2218	A	7298	3	272	KGSCPAGGSRMVSESD*EGRGC*ASYPCAC*
000			l l			AGS*WR*GSRPAGRGTPPRSLSHARPP
1		1	1			PRRDAEDRDESCLNPAFPIGLLHPNSVNSMAR
869	2219	A	7332	1223	332 .	PREDAEDRIESCENPAPFICEEIT NO VICTOR STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF
809	2217	1		Ì	}	YRLVRPADINFLACVMECEGKLPSLKIWETC
ì		- {	1			KELLQLSKPELPQDGTSTLRENSKPEESHLLA
1		1	1	1		KRYGGFMKRYGGFMKKMDELYPMEPEEEA
1		- 1	1	l		NGSEILAKRYGGFMKKDAEEDDSLANSSDLL
					1	NGSEILAKRYGGFMKKDAEEDDSLAIGSDIE KELLETGDNRERSHHQDGSDNEEEVSKRYGG
ł	ì	- 1		1		FMRGLKRSPQLKEKAKELQKRYGGFMRRVG
1			1			POKW*MTSPQNRYGGFLKRFAEALPSDEEGE
1		1	1	1		FOR MAM 12 SAUK I GOLF VALUE OF FROM
1		1	1			SYSKEVPEMEKRYGGFMRF EIHQRLTERTQFLDESRKNPNS*QANLLRGGC
870	2220	A	7382	216	1018	AGQGRGREGAESGGSRGEGPGSDGRLPATGI
3,0	2220	1 ' '				FWSPRSQRRGCCGRRAPRPEAMENGAVYSP
	1	1	1			TEEDPGPARGPRSGLAAYFFMGRLPLLRRVL
1	1					TEEDPGPAKGPKSGLAATFFMGKLI LEKKYL
1		1				KGLQLLLSLLAFICEEVVSQCTLCGGLYFFEF
ĺ						VSCSAFLLSLLILIVYCTPFYERVDTTKVKSSI
					1	FYITLGTGCVFLLASIIFVSTHDRTSAEIAAIVF
1		1	ĺ	1		GFIASFMFLLDFITMLYEKRQESQLRKPENTT
i						RAEALTEPLNA
871	2221	-	7403	3	393	SCAMCSGLL*LLLPIWLSWTLGTRGSEPRSVI
10/1	2221	1	1 / .55			DPGNMSFVKETVDKLLTGFRCFREREAAPRF ALRGAALPGESEAGDPESLRSSVNADWIQYS
1	i				1	THE RESERVE AND PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH

			1 000	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D-A sportic Acid F=Glutamic Acid,
IO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	į	in	location	corresponding	I-Icoleucine K=Lysine L=Leucine,
otide	seq-	]	USSN		to last amino	M=Methionine, N=Asparagine, P=Proline,
:q-	uence	Į.	09/496	correspondi	acid residue	Calutamine R=Arginine, S=Serine,
ence	1	ļ	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Ì	1	1	amino acid		V=Tyrosine X=Unknown, *=Stop codon,
	)	ł	}	residue of	sequence	/=possible nucleotide deletion, \=possible
	į	ł	1	peptide	1	avalentide insertion
	1	1		sequence		DLWEAEVSTPRCEAGFCQECFRTPGNQEKDG
	-				1	
	)	}	1			PFIC FVDIVSVVEFPHCPEARFPAQHGQDSKRLTLC
72	2222	A	7413	1061	359	PGGS*PQATLHLDRMRVSASPTKEIQVKKYK
14	22.2.2	1			\	PGGS*PQATLHLDKMKVSASFTKEIQ*IMCFED
		1		i		CGLIKPCPANYFAFKICSGAANVVGPTMCFED
	}	1	}		l .	RMIMSPVKNNVGRGLNIALVNGTTGAVLGQ
	į.	1	1			KAFDMYSGDVMHLVKFLKEIPGGALVLVAS
		1	1	}		YDDPGTKMNDESRKLFSDLGSSYAKQLGFRD
	1	1				SWVFIGAKDLRGKSPFEQFLKEQPQTQNKYE
		1	ł		ì	CWPELLEMEGCMPPKPF
				<del> </del>	2394	ILKCAGHGGSCL*SQHFGRLRWEDRLRLGVQ
873	2223	Α	7429	2242	2394	L DUDGOHCETPSLLKIERKLF
		}		<u> </u>		T DOTOGY WATE HI PASTRKAPOALCOMISITE
874	2224	A	7468	146	894	WQKIGVGITGFGIFFILFGTLLYFDSVLLAFGN
•.		1				LLFLTGLSLIIGLRKTFWFFFQRHKLKGTSFLL
	1	1	1		1	GGVVIVLLRWPLLGMFLETYGFFSLFKGFFPV
	1	1	ı			AFGFLGNVCNIPFLGALFRRLQGTSSMV*KTE
	Į	1	1		[	MSSLNLDHWLKGAKREEWEPPPQSPALTHSP
	1	-	1			MSSLNLDHWLKGARREEWEFF QSFAETHOL
	Ì	l l	] .		)	TYPGPPQVQKERNGAEQLTSNPQVDSRGCQE
	1	- [	1			AEMQTPRRLGWGWYHTLTLYLWEEK
		A	7498	91	251	GEKPVPTWLQDEAGQWLLGFVAQPWGWPG
875	2225	^	7470	1		SERHEP*HGGVLFRLGPSAPPGKL
			7544	403	587	YSCLCFLFKHITSFKNSVHIWLGTVVHAYNPN
876	2226	Α	/344	403	1 20,	II GGOGGWIA*GOEFKTSLGNTVRPCLYK
			<del></del>	2	940	CCAPOTREEVPEPGGRGAAPWVALVARGGC
877	2227	A	7566	2	1 340	TEKDKVI VA ARRNASAVVLYNEERY GNITLP
	}	1	,	1	1	MSHAGTGNIVVIMISYPKGREILELVQKGIPV
						TMTIGVGTRHVOEFISGOSVVFVAIAFILMMI
		1	1		<b>\</b>	et AMI TEVYTORFI YTGSOIGSOSHRKETKKV
		1	1	1		GQLLLHTVKHGEKGIDVDAENCAVCIENFKV
		ł		ì	ì	KDIIRILPCKHIFHRICIDPWLLDHRTCPMCKL
		- (		1	1	DVIKALGYWGEPGDVQEMPAPESPPGRDPAA
	l	-	-	1		NLSLALPDDDGSDESSPPSASPAESEPQCDPSI
	. }	i i	ì			KGDAGENTALLEAGRSDSRHGGPIS
	1	1	1			ERSLLCKVDVRWIYVSEGTKTQRRHRQGSLF
878	2228	A	7586	315	1232	RGRMQAACWYVLFLLQPTVYLVTCANLTNC
0/0	2226	1	1		1	RGRMQAACWYVLFLLQFIVILVICANDING
Ì		1		]		GKSELLKSGSSKSTLKHIWTESSKDLSISRLLS
}		ļ	1			QTFRGKENDTDLDLRYDTPEPYSEQDLWDW
l		1	1		ļ	LRNSTDLQEPRPRAKRRPIVKTGKFKKMFGV
				ļ		COFHSNIKTVKLNLLITGKIVDHGNG1FSV11
		Ì		1		PUNCTGOGNVSVSLVPPTKIVEFDLAQQIVII
)						A V DOV CENCRIEVEK VDKATKNIL CNYDPSI
l		l				TCYOEOTOSHVSWLCSKPFKVICIYISFYSID
		1		1	l'	VKI VOKVCPDYNYHSDTPYFPSG
ļ						TESWKI KWWSPTCLDOLNGSAPGNVFIHG
879	2229	A	7605	479	391	DAAVAMTAQGGLVANRGRRFKWAIELSGP
880	2230	Ā	7612	93	659	GGSRGRSDRGSGQGDSLYPVGYLDKQVPDT
300		1		1	1	VOETDRILVEKRCWDIALGPLKQIPMNLFIM
1		1			- 1	VQETDRILVERRCWDIALOTERQITATION IN
1		- 1		İ	İ	MAGNTISIFPTMMVCMMAWRPIQALMAISA MAGNTISIFPTMMVCMMAWRPIQALMAISA
1				1	1	FKMLESSSQKFLQGLVYLIGNLMGLALAVY
	1	1			l l	CQSMGLLPTHASDWLAFIEPPERMEFSGGGI
1		1				137
<u></u>					1452	SPOKTMRSHTITMTTTSVSSWPYSSHRMRFI
881	2231	A	7615	291	1434	NUSDOPPONESATPNVTTCPMDEKLLSIVLI
{						Leventervoi vonital YVFLGIHRKKNSIQIY
	1	1			1	LATUATA DI LI IECL PERIMYHINONKWILGV
	1	}	}		1	CKVVGTLFYMNMYISILLGFISLDRYIKINR
1		l	Ì	1		QQRKAITTKQSIYVCCIVWMLALGGFLTMII
	1	- 1				QQRKAITTKQSIYVCCIVWMLALGGFFTMIL TLKKGGHNSTMCFHYRDKHNAKGEAIFNFI
				1	1	The same of the torm (OPP1370) DV (TALK V (LA ALEX L)

						// Unit of Courtains
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-	l	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l		amino acid residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1	1	}		Sequence	/-possible nucleotide deletion, \-possible
	}	İ	i	peptide sequence		nucleotide insertion
		<b></b>	<del> </del>	sequence	<del> </del>	VVMEWLIELLIILSYIKIGKNLLRISKRRSKFPN
		1		1		SCKYATTARNSFIVLIFTICFVPYHAFRFIYISS
		1	}	}		QLNVSSCYWKEIVHKTNEIMLVLSSFNSCLDP
		1		1		VMYFLMSSNIRKIMCQLLFRRFQGEPSRSEST
	1				1	SEFKPGYSLHDTSVAVKIQSSSKST
000	2232	A	7617	67	379	RQMALLKANKDLISAGLKEFSVLLNQQVFND
882	2232	1	1,01,	,		PLVSEEDMVTVVEDWMNFYINYYRQQVTGE
				i		PQERDKALQELRQELNTLANPFLAKYRDFLK
	1		1			SHELPSHPPPSS
883	2233	A	7622	400	215	KVKTCRYNPKYSAANDTGFVDIPSREKDLAK
883	2233	1	1,022			AVATVGPISVAVGASHVFFQFYKKGKHLSS
884	2234	HA	7638	2640	2861	APVLILQMVKLSIVLTPQFLSHDQGQLTKELQ QHVKSVTCPCEYLRKVSECRQMGPGALEQFP
804	2234	15		}		QHVKSVTCPCE YLRK VSECRQIVIOF GALLEYI
				1		GLSCHTSHSG PSRGKMELEAMSRYTSPVNPAVFPHLTVVLL
885	2235	A	7642	201	455	AIGMFFTAWFFVYEVTSTKYTRDIYKELLISL
803	2233					VASLFMGFGVLFLLLWVGIYV
Ì	1	Į.				APENPFSRQHFNSETKVKLSLKTGTWLGNHA
886	2236	A	7692	61	569	HLGEHFSTHHELGLSGKVVGFLVKNILEVIRN
000		l		1	1	GGMETRHPGKVSSWFHRWDSRAEQHNHAE
ļ		j		1		HHEDVPQGDEDSKVSEAQQEFPDVVTCAGLP
l	}			}		GLLPKALRVLLFQLKVQHRPGIHQQRPEQQD
	Ì			1		VSDHRYGRSVRQNRK
		1				NPGCCLPVAMRTSYLLLFTLCLLLSEMASGG
887	2237	A	7693	85	315	NFLTGLGHRSDHYNCVSSGGQCLYSACPIFTK
1	Ì	1				IQGTCYRGKAKCCK
\		1 .			1208	APSHRRYLSPSRSAGQLGNMALERLCSVLK
888	2238	A	7702	242	1298	VITTIVI VVEGIAVAOKTODGONIGIKHIPAT
		- 1		}		OCCIWURTSNGGHFASPNYPDSYPPNKECIYI
		1				I FAAPRORIELTFDEHYYTEPSFECRFDHLEVK
1		ł	Į.			DGPEGESPI IDRYCGVKSPPLIRSTGREMWIKE
		- 1				SSDEELEGLGFRAKYSFIPDPDFTYLGGILNPIF
}	{	1	ľ	1		DOOFFI SGADGIVRSSOVEOEEKTKPGQAVD
	ļ	- 1				CIWTIK ATPKAKIYLRFLDYQMEHSNECKKNI
		Į				VAVVDGSSSIENI KAKFCSTVANDVMUKI GI
		j		]		GVIRMWADEGSRLNRFRMLFTSFGGASPAQA
1	1	l	- 1			ALSFCHSNMCINNSLVCNGVQNCAYPWDEN
1	1	i				HC CE CE CE CE CE CE CE CE CE CE CE CE CE
000	2239	A	7707	185	2911	CHYIMNPSTHHPASAGGSILGLFDFFGLGLGE
889	2239	^	1 ' ' '	1		MTMDALLARLKLLNPDDLREEIVKAGLKCGI
		}	}	}	-	ITSTTRFIFEKKLAQALLEQGGRLSSFYHHEA
1		Ì		- 1		GVTALSQDPQRILKPAEGNPTDQAGFSEDRDI
1		- 1		1		GYSVGLNPPEEEAVTSKTCSVPPSDTDTYRAC
	1	ĺ			}	ATASKEPPLYYGVCPVYEDVPARNERIYVYE
1		1				NKKEALQAVKMIKGSRFKAFSTREDAEKFAF
1		1		- {		GICDYFPSPSKTSLPLSPYKTAPLFSNDRLKDC LCLSESETVNKERANSYKNPRTQDLTAKLRK
1		1				LCLSESET VINERANS I ANTRI QUETTALERA
1			-			AVEKGEEDTFSDLIWSNPRYLIGSGDNPTIVQ
		i				EGCRYNVMHVAAKENQASICQLTLDVLENP DFMRLMYPDDDEAMLQKRIRYVVDLYLNTF
1		1				DKMGYDTPLHFACKFGNADVVNVLSSHHLI
1		}				VKNSRNKYDKTPEDVICERSKNKSVELKERII
1	1	İ	1	1		EYLKGHYYVPLLRAEETSSPVIGELWSPDQT
	l l	- 1	l l	1		EASHVSRYGGSPRDPVLTLRAFAGPLSPAKA
					1	EVZHAZKA OROZLYDLA PITEVAR VOL POLVIGE
			}		1	DEDKI WILEDDER VOEL RANKKODEB GEER
						DERKI WKTPPREKAGFLHHVKKSDPERGFER
						DFRKLWKTPPREKAGFLHHVKKSDPERGFER VGBELAHELGYPWVEYWEFLGCFVDLSSQE
					÷	DFRKLWKTPPREKAGFLHHVKKSDPERGFER VGRELAHELGYPWVEYWEFLGCFVDLSSQE
						DFRKLWKTPPREKAGFLHHVKKSDPERGFER VGBELAHELGYPWVEYWEFLGCFVDLSSQE

				D 1:4-1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
O; of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	s <b>e</b> q-		USSN	location		M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		Ì	ļ	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
i			}	residue of	sequence	Y=1 yrosine, X=Unknowii, '-Stop codon,
[		ļ	1	peptide		/=possible nucleotide deletion, \=possible
		1	1	sequence		nucleotide insertion
		<del> </del>	<del></del>	sequence	<del>                                     </del>	EPGGPHSSRNGLCHPLNHSRTLAGKRPKAPR
-	1	{		{		GEFAHI PPVSDLTVEFDKLNLQNIGRSVSKTP
	<b> </b>	ļ.	1	l .		DESTRIKTEDOILTSRINAVERDLLEPSPADQLG
	ł	1	ł	ļ		NGHRRTESEMSARIAKMSLSPSSPRHEDQLEV
			ł		į	TREPARRLFLFGEEPSKLDQDVLAALECADV
	1	1	1	1	[	DPHQFPAVHRWKSAVLCYSPSDRQSWPSPAV
	1	-	İ	1	1	DPHQFPAVHKWKSAVLCISPSDKQSWISHAVP
	1	1	1		1	KGRFKSQLPDLSGPHSYSPGRNSVAGSNPAKP
	ł	1	ĺ		ì	GLGSPGRYSPVHGSQLRRMARLAELAAL
		<del> </del>		360	269	RHMPVIPALWEAEVGGLLEPRSSRSAWATE
890	2240	Α	7711			KI PWEPSELIKMOIIRHSEOTLKTALISKNPVL
891	2241	Α	7721	61	1175	VSQYEKLDAGEQRLMNEAFQPASDLFGPITL
		1		1		HSPSDWITSHPEAPQDFEQFFSDPYRKTPSPN
	1	1	1	1		KRSIYIQSIGSLGNTRIISEEYIKWLTGYCKAYF
	1	1		1		KKSI I IQSIQSEQINI KIISEETIK WETO TOKATI
				1	1	YGLRVKLLEPVPVSVTRCSFRVNENTHNLQIH
	1	1		1	1	AGDILKFLKKKKPEDAFCVVGITMIDLYPRDS
		1		l .		WNFVFGQASLTDGVGIFSFARYGSDFYSMHY
	1		1		1	KGKVKKLKKTSSSDYSIFDNYYIPEITSVLLLK
		1	l l	]	Į.	SCKTLTHEIGHIFGLRHCQWLACLMQGSNHL
			1		į	FEADRREI NI CPICLHKLOCAVGFSIVERYKA
	1	Į.	Į.			LVRWIDDESSDTPGATPEHSHEDNGNLPKPV
	1	ł		j	1	FAFKEWKEWIIKCLAVLOK
		[			1660	SAPTAPARPCRAERGSGGGMLALLAASVALA
892	2242	A	7723	2	1650	VAAGAQDSPAPGSRFVCTALPPEAVHAGCPL
0,2	1		i	1		PAMPMQGGAQSPEELRAAVLQLRETVVQQ
	}	1	1	1		KETLASARAIRELTGKLARCEGLAGGKARGA
	İ		İ	1		KETLASARAIRELTGREARCEGEAGGIOTIKOT
	ļ	Ì	1	ì	<b>\</b>	GATGKDTMGDLPRDPGHVVEQLSRSLQTLK
		- 1	<b>\</b>	Ì	l	DRLESLEPLPAMPMQGGAQSPEEELRAAVLQ
		1				LRETVVQQKETLASARAIRELTGKLARCEGL
	1			1		AGGK ARGAGATGKDTMGDLPRDPGHVVEQ
	1	1		ļ	}	I SRSI OTLK DRLESLEHOLRANVSNAGLPGD
	1	ĺ			Į.	FREVLOORLGELEROLLRKGAELEDEKSLLH
1	1		1			METSAHROKTESTINALLORVTELERGNSAF
1		1	i	į.	ì	KSPNAFKVSLPLRTNYLYGKIKKTLPELYAFT
	ł	-	1	1	Ì	ICLWLRSSASPGMGTPFSYAVPGQANEIVLIE
	- 1	- }	1	ļ		WGNNPIELLINDKVAQLPLFVSDGKWHHICV
	1		1			WGNNPIELLINDK VAQLELI VSDOK WILLIO
1	1	- 1		l	1	TWTTRDGMWEAFQDGKKLGTGENLAPWHPI
1	1	i	-	1	<b>\</b>	KPGGVLILGQEQDTVGGRFDATQAFVGELSQ
	}	1			1	FNIWDRVLRAQEIVNIANCSTNMPGNIPWVD
	1	1		1		NNVDVFGGASKWPVETCEERLLDL
				2554	2419	LTAGTAMNYPLTLEMDLENLEDLFWELDRL
893	2243	Α	7729	3554	4717	DNVNDTSLVENHLCPATEGPLMASFKAVFVP
1						VAYSLIFLLGVIGNVLVLVILERHRQTRSSTET
1			1		1	FLFHLAVADLLLVFILPFAVAEGSVGWVLGTF
		-				FLITTLA VADILLE VILLE PAVALOGIO VILLE
}	1	1		]		LCKTVIALHKVNFYCSSLLLACIAVDRYLAIV
		1				HAVHAYRHRRLLSIHITCGTIWLVGFLLALPEI
			1		1	I FAK VSOGHHNNSLPRCTFSQENQAETHAWF
}			Į			TSRFLYHVAGFLLPMLVMGWCYVGVVHRLR
			1		i	OAORRPOROKAVRVAILVTSIFFLCWSPYHIV
1			1	1	}	IFLDTLARLKAVDNTCKLNGSLPVAITMCEFL
1		1			}	GLAHCCLNPMLYTFAGVKFRSDLSRLLTKLG
1		i	ļ	1	Ī	CTGPASLCQLFPSWRRSSLSESENATSLTTF
1		1_			L	CIGPASLCULFFSWKKSSLSESLIKKISETTI
904	2244	A	7738	670	287	FVTRAGRWGAGARVRGGAGGMASGAARWL
894	2244	^	'''			VLAPVRSGALRSGPSLRKDGDVSAAWSGSGR
					1	ST VPSRSVIVTRSGAILPKPVKMSFGLLRVFSI
1						VIPFLYVGTLISKNFAALLEEHDIFVPEDDDDD
		}			}	D
1					1270	APYAHSQVHCLDKVCGLLPFLNPEVPDQFYR
1		A	7753	119	278	AT IMISO THOUSE COURT IN
895	2245					I I WILL OF CLUATOR FAPPH PRIKEL
895	2245	^			372	LWLSLFLHAGKEAPHCPRTRPL SPAWWNSQQRVVSPFLALLTLEPTFHHLLPIM

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uenœ	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine V=Valine, W=Tryptophan,
				amino acid	of peptide sequence	V=Turnsine, X=Unknown, *=Stop codon,
	}	}	}	residue of	sequence	/=possible nucleotide deletion, \=possible
	1	ì		peptide		nucleotide insertion
		<u> </u>		sequence	<u> </u>	OVSTAALAVILCIMALCNOVLSAPLAADIPI
						ACCESYTSROIPONFIADYFETSSQCSKPSVIFL
			1	ļ	1	TKRGROVCADPSEEWVOKYVSDLELSA
	<u> </u>	ļ		1725	445	PPRRGTHHESCYLGSFRVSAMFPRVSTFLPL
897	2247	A	7761	1723	443	RPI SRHPLSSGSPETSAAAIMLLTVRHGTVKY
	1	}		}		DSSALI ARTKNNIORYFGTNSVICSKKDKQSV
		1		1		PTETSKETSESODSEKENTKKDLLGIIKGMK
	1	1			1	VELCTVNVRTTKPPKRRPLKSLEATLGRLRRA
		1				TEVADER PIEPI SPELVAAASAVADSLPFDKQ
		Ì	ŀ	1	1	TTK SELL SOLOOHEEESRAORDAKRPKISESNI
	1	1	1	1	1	I ISDNOVVARSATARVRSRPELRIUFDEGYDNYR
	ł	1	1	ĺ		GOEKTDDLKKRKNIFTGKRLNIFDMMAVIKE
		-				A DET DTSPSI WDVEFAKOLAT VNEQPLQNOF
	1			}		EELIQWTKEGKLWEFPINNEAGFDDDGSEFH
	1	1		1		EHIFLEKHLESFPKQGPIRHFMELVTCGLSKNI
		1		1		YLSVKQKVEHIEWFRNYFNEKKDILKESNIQF
		}	1			KLRPWKFLFRNN
000	2248	+A	7775	• 85	496	SCOTTOPPAQSCSTGTMRIMLLFTAILAFSLA
898	2248	^	1 '''	"		QSFGAVCKEPQEEVVPGGGRSKRDPDLYQLL
						QRLFKSHSSLEGLLKALSQASTDPKESTSPEK
				]		RDMHDFFVGLMGKRSVQPDSPTDVNQENVP
		1		]		SFGILKYPPRAE
900	2249	A	7785	179	703	PFHLGASSNTFRLQVQTQESKAQKEVKMGFI
899	2249	1 ^	1,703			FSKSMNESMKNQKEFMLMNARLQLERQLIM
		1	ł		1	QSEMRERQMAMQIAWSREFLKYFGTFFGLA
			i .			AISLTAGAIKKKKPAFLVPIVPLSFILTYQYDL
		}	1	1		GYGTLLERMKGEAEDILETEKSKLQLPRGMI
		1				FESIEKARKEQSRFFIDK VWLPLKSYKIRSPSLHCQCEIFREEFLFSSLQE
900	2250	A	7789	1465	300	GRDKDTFSKMAMVSEFLKQAWFIENEEQEY
300	2230					VQTVKSSKGGPGSAVSPYPTFNPSSDVAALH
		ļ		ľ	1	KAIMVKGVDEATIIDILTKRNNAQRQQIKAA
		l l		j	1	LQETGKPLDETLKKALTGHLEEVVLALLKTP
		ļ		ł	1	AQFDADELRAAMKGLGTDEDTLIEILASRTN
		ļ	Ì		1	KEIRDINRVYREELKRDLAKDITSDTSGDFRN
				1		ALLSLAKGDRSEDFGVNEDLADSDARALYE.
		- 1	1			GERRKGTDVNVFNTILTTRSYPQLRRVFQKY
	1	İ	1			TKYSKHDMNKVLDLELKGDIEKCLTAIVKC
	1	1	}			TCKDAFFAFKI HOAMKGVGTRHKALIRIMV
		j				RSEIDMNDIKAFYQKMYGISLCQAILDETKG
	1	l i				VEKTI VAT CGGN
		i	l		007	VEELDOR AR AGAR APSMGVLLTORTLLSLV
901	2251	A	7796	72	807	LATTEDOMA SMA AIGSCSKEYRVLLGOLQKQ
	1					DI MODTSRI I DPYTRIOGLDVPKLREHCKER
		-	1			GAEDSEETT RGLGRRCFLOTLNATLGCVLHK
1	1	-				ADI FORI PK AODLERSGLNIEDLEKLUMARI
1	Ì	-				NILGERNNIYCMAOLLDNSDTAEPIKAGROZ
1	- {					SOPPTPTPASDAFORKLEGCRFLHGYHREME
1						SVGRVFSKWGESPNRSRRHSPHQALRKGVR
]					1	TD DCD K GKRI MTRGOLPR
						TAARROKGTAARRLOKGTAARRROKGIA
902	2252	A	7802	2	721	DDDOKGTAARRPOKGTAARRRQKG AARR
	}	}				LOVGTA ARRROKGTA ARRPOKGTAARKKUK
İ			- {			TAARROKGTAARROKGLAIASRGCPCAS
		1				AGGVRGAGSRLRAMAPKVFRQYWDIPDGT
	}	1	1	}	<u>}</u>	CUDY AVSTTSIASVAGLTAAAYRVTLNPPG
1	1		1			LEGVAKVGQYTFTAAAVGAVFGLTTCISAH
	1	j				REKPDDPLNYFLGGCAGGLTLGARTHNYGI
	1	1	1	ı	1	KENTUDI LITTI DOGCAGGETES
1	- 1	ĺ	j			AAACVYFGIAASLVKMGRLEGWEVFAKPK

			1.000	Deadlead	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	!	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	{	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	l i		714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}		peptide		/=possible nucleotide deletion, \=possible
		1	j	sequence	1	nucleotide insertion
903	2253	A	7807	1	584	PWLPWSDGRAARSSRKCPRSRFPVQVGKMA
903	22.33	^	1,00,	•		VSTVFSTSSLMLALSRHSLLSPLLSVTSFRRFY
			İ		1	RGDSPTDSQKDMIEIPLPPWQERTDESIETKR
		1	1	1		ARLLYESRKRGMLENCILLSLFAKEHLQHMT
		1			1	EKQLNLYDRLINEPSNDWDIYYWATEAKPAP
		1				EIFENEVMALLRDFAKNKNKEQRLRAPDLEY
		1		1		LFEKPR
904	2254	+A	7813	40	821	GAGRALGHLETGAGDVAAALPARKFPRSLLG
704		1				AGARLTGWTMNVFRILGDLSHLLAMILLLGK
		-	1		ļ	IWRSKCCKGISGKSQILFALVFTTRYLDLFTNF
				ļ	}	ISIYNTVMKVVFLLCAYVTVYMIYGKFRKTF
		1				DSENDTFRLEFLLVPVIGLSFLENYSFTLLEIL
•		1			1	WTFSIYLESVAILPQLFMISKTGEAETITTHYL
		l l		1		FFLGLYRALYLANWIRRYQTENFYDQIAVVS GVVQTIFYCDFFYLYVTKGRSWDDSNADTGL
					}	
•					-	RSYSSI LSNKDVLSPQLKDENSKLRRKLNEVQSFSEA
905	2255	Α	7817	1399	881	QTEMVRTLERKLEAKMIKEESDYHDLESVVQ
				1		QVEQNLELMTKRAVKAENHVVKLKQEISLL
				<b>\</b>		QAQVSNFQRENEALRCGQGASLTVVKQNAD
	{		1		1	VALQNLRVVMNSAQASIEQLVSGAETLNLVA
	Ì					EILKSIDRISEVKDEEEDS
		<u> </u>	7000	3	1462	DSPRNRFEILGRPTRTPTRPGPRPAMEDLDAL
906	2256	Α	7822	3	1402	1 SDLETTTSHMPRSGAPKERPAEPLTPPPSYG
				Į.		HOPOTGSGESSGASGDKDHLYSTVCKPRSPK
		1				PAAPAAPPFSSSSGVLGTGLCELDRLLQELNA
		1		ļ		TOFNITDEIMSOFPSSKVASGEQKEDQSEDKK
,		1	-		1	RPSLPSSPSPGLPKASATSATLELDRLMASLSD
			1	1		FRVQNHLPASGPTQPPVVSSTNEGSPSPPEPTG
		1		1	1	KGSLDTMLGLLQSDLSRRGVPTQAKGLCGSC
	1	- }				NKPIAGQVVTALGRAWHPEHFVCGGCSTAL
ĺ	1			[		GGSSFFEKDGAPFCPECYFERFSPRCGFCNQPI
		1		İ	1	RHKMVTALGTHWHPEHFCCVSCGEPFGDEG
1		1				FHEREGRPYCRRDFLQLFAPRCQGCQGPILDN
		1		1		YISALSALWHPDCFVCRECFAPFSGGSFFEHE GRPLCENHFHARRGSLCATCGLPVTGRCVSA
	Į.					LGRRFHPDHFTCTFCLRPLTKGSFQERAGKPY
İ						
						CQPCFLKLFG FIYVNQSFAPSPDQEVGTLYECFGSDGKLVLH
907	2257	A	7828	1792	1671	YCKSOAWG
L				<del>                                      </del>	1170	KLSCPCSHGTRVTAVRGPRLKAGVQWHDLG
908	2258	Α	7842	110	1172	SI OPPPSGLKOSSHLSLSSSWDFRHAPTHPET
		1		1		YTCPKMIEMEQAEAQLAELDLLASMFPGENE
[	1					LIVNDOLAVAELKDCIEKKTMEGRSSKVYFII
1	-	- 1	1			ADMILI DVSDEKMAMESLACILPEKYPAVLPEI
1		1				TVRSVLLSRSOOTOLNTDLTAFLQKHCHGDV
			1			CII NATEWVREHASGYVSRDTSSSPI IGSI VQ
1			1			SVDLIFTRLWIYSHHIYNKCKRKNILEWAKEL
i			1			SLSGFSMPGKPGVVCVEGPQSACEEFWARLR
	ŧ		l			KINWKRILIRHREDIPFDGTNDETERQRKFSIF
	4			]		EEKVFSVNGARGNHMDFGQLYQFLNTKGCG
	Ì	1	1	1		DVFOMFLWV
			1			EGICVYTFIYVHMYTRTCMHTYPYMYMNSV
000	7250		7970	3067	2923	EGICV I IFIT VIIIVITI IKI CIVILITI I I I I I I I I I I I I I I I I I
909	2259	A	7870	3067	2923	LISSEILLIPSKYLFESK
					2923 4874	LISSEILLIPSKYLFESK  GALTWSHPLLAVCPOGVWLGSTPSGSPALLP
909	2259 2260	A	7870 7884	3067		LISSEILLIPSKYLFESK  GALTWSHPLLAVCPQGVWLGSTPSGSPALLP PSHRVNAEPGCVVTNACASGPCPPHANCRDL
						LISSEILLIPSKYLFESK  GALTWSHPLLAVCPQGVWLGSTPSGSPALLP PSHRVNAEPGCVVTNACASGPCPPHANCRDL WOTESCTCOPGYYGPGCVDACLLNPCQNQG
						LISSEILLIPSKYLFESK  GALTWSHPLLAVCPQGVWLGSTPSGSPALLP PSHRVNAEPGCVVTNACASGPCPPHANCRDL

NO. of nucleotide peptide coulded sequence where the control of the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulded sequence where the coulde				·	<del></del>	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl- cotide seq- uence    Seq- uence	SEQ ID	SEQ ID	Met	SEQ	Predicted		Millio acid Sequence (11 7 Edition C - Systems)
cortesponding sequence  ### USSN   09/496     914     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     19     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10     10	NO: of	NO: of	hod	ID NO:		-	P. Di autologico Geologico Hellictidine
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	nucl-	peptide	1	in	nucleotide		replication, o-diverse, remaine,
uence    09/496   correspondi   foliat amino acid residue of peptide residue of peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide sequence   peptide s		• •		USSN	location		I=Isoleucine, K=Lysine, L=Leucine,
uence  ### amino acid residue of peptide sequence eptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide				09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
amino acid of peptide residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide		donoc		914		acid residue	Q=Glutamine, R=Arginine, S=Serine,
residue of sequence periode detection, "possible nucleotide detection," persosible nucleotide detection, "possible nucleotide insertion TNGQCIGCKERFHYRPRGSDSCLPCDCYPVGS SRSCAPHSQQCPCRPGALGRQCNSCDSPAAT ASGCRVLYDACPKSLRSGVWWPQTKFGVV ATVPCPGGALGRAVRLCDEAQGWL PDLFNCTSPAFRELSLLLDGLENKTALDTM AKKLAQRLREVTGHTDHYTSQDVRVTARLUM AKLAJARLREVTGHTDHYTSQDVRVTARLUM AKLAJARLREVTGHTDHYTSQDVRVTARLUM GSALLAPETGDLWAALGGAPGSPGSAGI RHLEEVAATLARNMELTVINPMGLVTPIN SIDRAMEHPSSPGARRYRYHSNLFRGQDAD DPHTHVLLPSQSPRPSPSEVLPTSSSEINSTTS VVPPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTS VVPPAPPEPEPGISIILLVYTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTSISSEINSTTPPRPRRTSIDLSISSESSEINGRTRG QRPLCRAAGSERLLTHPKDVPONDLSYWLGCEAAPACALOTWGSERALGHAVAPAYAGAPTALGHAVAPAYAGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGALTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGAPTALGA	uence		}	· · ·	_	of peptide	T=Threonine, V=Valine, W=Tryptophan,
pepide sequence nucleotide deletion, v-possible nucleotide insertion nucleotide insertion TNGQCHCKEFHYRPGSDSCLPCDCYPVGS SRSCAPHSQCPCRPGALGRQCNSCDSPLAT ASGCRVLYDACPKSI.RSGVWWPQTKFGV ATVPCPRGALGRQCAQWILDGLENKTALDTW AKLAQRI.REVTGHTDHYFSQDVRVTARLI AHLAPESHQQFGLTATQDAHFNENLLW, GSALLAPETGDLWAALGQRAPGGSPGSAGI RHLEEYAATLARNMELTYLNFMGLVTPNIN SIDRMEHPSSPRGARR YRYHSNLFRQQDA DPHTHVLLPSQSPRSPSESVLYTSSSENSTIT VVPPRAPPEPPGISIIILLVTRITLGGLLPAQF AERGARLQNPVMNSPVVSVAVHIGRNFGILSEPSILEFRLLQTHANKSKLCVQWDPPGI EQHGVWTARDCELVHRNGSHARCRCSRTC FGVLMDASPRERLEGDLEAVTHVVAVA VAALVLTAAILLSLRSLKSNVRGHIANNAA LGVAELLFILLGHRYTHVVAV VAALVLTAAILLSLRSLKSNVRGHIANNAA LGVAELLFILLGHRYTHVQUFRNVDRGAM FYHALGWGVPAVLIGLAVGLDPEGVORFT CWISVHEPLIWSFAGPVVJVIVMNGTMFLLL ARTSCSTGQREAKKTSALTLRSSFLLLLVSSWLFGLLAVHSILAFFLYHLAGLGGQAA SWLFGLLAVHSILAFFLYHLAGLGGQAA DSDSDSDLSLEERSLSJPSSEDINGRTGG QRPLCRAAQSERLLTHKQDVGDNULSYW LGCCAAPGAAPTAAAAAHTDHSLQAHAGFTGLDDVAMFHAAAAHTDHSLQAHAGFTGLDVAMFAAAAHTDHSLQAHAGFTGLDRAAPTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	i	}	1	}			Y=Tyrosine, X=Unknown, *=Stop codon,
nucleotide insertion  TNGCGHCKEFHYRRGSDSCLPCDCYPVGS SRSCAPHSQQPCRPGALGRQCNSCDSPAAT TASGCRVLYDACPKSLRSGVWWPQTKFGVV ATYPCPRGALGLRGAGAVRLCDEAQGWL PDLFNCTSPAFRELSLLLDGLENKTALDTM AKKLAGRLREVTGHTDHYFSQDVRVTARLI AHLLAFESHQQGFGLTATQDAHFNENLLW. GSALLAFETGDLWAALGQRAFGGSFGSAG RHLEFYAATLARNMELTYLNPMGLVTPIN SIDRNEHPSSFGARRYPKYSNLFRGQDA DPHTHYLLPSQSPRPSFSEVLPTSSEINSTTS VVPPPAPPEPPGISIIILLVRTIGGLLPAGF AERGARLPQNFVMNSPVSVAVFHGRNF- GILESPISLEFRLQTANRSKAICVQWDPGI EQHGVWTARDCELVHRNGSHARCRGSRT- FGVLMDASPRERLEGDLELLAVTHYVVAA LGVAELLFLLGHRTHNQLVCTAVVLLHYI LSTFAWLFVQGHLYRMPGSPRVPNDRGAA LGVAELLFLLGHRTHNQLVCTAVVLLHYI LSTFAWLFVQGHLYRMPACLGRKAAPEA- PAFGLGPGAYNNTALFEESGLIRTLGASTV VSSARSGRTQDQDSQGRGSVLRDNVLVHH AADHTDHSQAHAGPTDLDVAMFHRDAG. DSDSDSLSLEERESLSPSESSEDNGRTRGF QRPLCRAAQSERLLTHPKDVDONDLSYW LGEGEAAPGACLOTWGSERLGLDTSKDAA NQPPLATTSGDETSLGRAQAGRKGILKN QYPLVPQTRGAPELSWCRAATLGHRAVPA YGRYAGGGTGSLSQPASRYSSREQLDLLL QLSRERLEEAPAPVLRLESRGQECMDAA RLEPKDRGSTLFRRQPRDGGCMCMAA RLEPKDRGSTLFRRQPRRDGGCMCMAA RLEPKDRGSTLFRRQPRDTPGAMAGRFG DALDLGAPERWLTDFPRRTRDLDDPPP LSPQRQLSGDPLTLSRRDLDSLSSRSSNSREQL VPSRHPSREALGPLPQLLRAREDSVGSPH STEQLDLISSLASFNSSRSLSLSPDSE DTQALLSATQAMDLRRRQYMERPLLDQPPP LSPQRQLSGDPLTLSRRDLDSLSSRSSNSREQL VPSRHPSREALGPLPQLLRAREDSVGSPH STEQLDLUSLASFNSSRSLSSVGSSSTPLGPP TATFSATASVLGFSTPRSATSHISSLSESDE DTQALLSATQAMDLRRRQYMERPLLDQ LEELGRWGSAPRTHQWRTWLQCSRRAY LLQHLPVLVWLPPYPVRDWLLGOLLSGLS IMQLPQGLAYALLAGLPVFGLYSSFYPVF FLGTTSRHISVESLCVPGPVDT  1VSCLRAQGGACVOFOALKGQEFAPSHQO LFSCLRARASSRAWALTCCLVLLPTLAGLTT LVSCLRAQGGACVOFOALKGQEFAPSHQO LVSCRARASSRAWALTCCLVLLPTLAGLTT LVSCLRAQGGACVOFOALKGQEFAPSHQO LVSCRARASSRAWALTCCLVLLPTLAGLTT LVSCLRAQGGACVOFOALKGQEFAPSHQO LVSCRARASSRAWALTCCLVLLPTLAGLTT LVSCLRAQGGACVOFOALKGQEFAPSHQO LVSCRARASSRAWALTCCLVLLPTLAGLTT LVSCLRAQGGACVOFOALKGQEFAPSHQO LVSCRARASSRAWALTCCLVLLPTLAGLTT LVSCLRAQGGACVOFOALKGQEFAPSHQO LVSCRARASSRAWALTCCLVLLPTLAGLTT LVSCLRAQGGACVOFOALKGQEFAPSHQO LVSCLRARGSCACAFGALKGQEFAPSHQOP LVSCLRAGGACVOFOALKGQEFAPSHQO LVSCLRAGGACVOFOALKGQEFAPSHQO			1 1	1		Soqueilor	/=nossible nucleotide deletion. \=possible
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LSPQRQLSRDPLLPSRPLDSLSRSSNSREQLI VPSRHPSREALGPLPQLLRAREDSVSGPSH( STEQLDILSSILASFNSSALSSVQSSSTPLGPI TATPSATASVLGPSTPRSATSHSISELSPDSE DTQALLSATQAMDLRRRDYHMERPLLNQI LEELGRWGSAPRTHQWRTWLQCSRARAY. LLQHLPVLVWLPRYPVRDWLLGDLLSGLS IMQLPQGLAYALLAGLPPVFGLYSSFYPVF FLFGTSRHISVESLCVPGPVDT  911 2261 A 7890 21 806 EFGTSRSSRSMAEDLGLSFGETASVEMLPE SCRPKARSSSARWALTCCLVLLPFLAGLTT LVSOLRAOGEACVOFQALKGQEFAPSHQQ		1		j	İ		RLEPKDROSTLPRRQFFRDTT DROPPPI P
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TATPSATASVLGPSTPRSATSHSISELSPDSE DTQALLSATQAMDLRRRDYHMERPLLNQI LEELGRWGSAPRTHQWRTWLQCSRARAY. LLQHLPVLVWLPRYPVRDWLLGDLLSGLS IMQLPQGLAYALLAGLPPVFGLYSSFYPVF FLFGTSRHISVESLCVPGPVDT  911 2261 A 7890 21 806 EFGTSRSSRSMAEDLGLSFGETASVEMLPE SCRPKARSSSARWALTCCLVLLPFLAGLTT LVSOLRAOGEACVOFQALKGQEFAPSHQQ	1	1	1			1	STEQLDILSSILASFNSSALSSVQSSSTPLGPHT
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911 2261 A 7890 21 806 EFGTSRSSSSMAEDLGLSFGETASVEMLPE SCRPKARSSSARWALTCCLVLLPFLAGLTT LVSOLRAOGEACVOFQALKGQEFAPSHQQ			1	1		)	LLOHLPVLVWLPRYPVRDWLLGDLLSGLSVA
911 2261 A 7890 21 806 EFGTSRSSSSMAEDLGLSFGETASVEMLPE SCRPKARSSSARWALTCCLVLLPFLAGLTT LVSOLRAOGEACVOFQALKGQEFAPSHQQ	1		1	1	1	•	IMOL POGLAYALLAGI PPVFGLYSSFYPVFIY
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LVSQLRAQGEACVQFQALKGQEFAPSHQQ	1				1	1	SCRPKARSSSARWALTCCLVLLPFLAGLTTTL
				1	1		LVSQLRAQGEACVQFQALKGQEFAPSHQQV
YAPLRADGDKPRAHLTVVRQTPTQHFKNQ			1		1		YAPI RADGDKPRAHLTVVRQTPTQHFKNQFP
ALHWEHELGLAFTKNRMNYTNKFLLIPES(		1		1	1		ALHWEHELGLAFTKNRMNYTNKFLLIPESGD
YFIYSOVTFRGMTSECSEIRQAGRPNKPDSI				1	1		YFIYSOVTFRGMTSECSEIRQAGRPNKPDSITV
VITKVTDSYPEPTOLLMGTKSVCEVGSNW				}			VITKVTDSYPEPTQLLMGTKSVCEVGSNWFQ
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			1				PVPYILKKIFQDREAAATTGVSRDLCYVKELG
VRGNVLRFLPDOGFFLYPKKISQASSCLQK			1	}			VRGNVLRFLPDQGFFLYPKKISQASSCLQKLL
YFNLSAIKEREOLTLAQLGLDLGPNSYYNI					1	ł	YFNLSAIKEREQLTLAQLGLDLGPNSYYNLGF
FI FI AI FLVOEPHVWGOTTPKPGKMFVLR					J	1	ELELALFLVQEPHVWGQTTPKPGKMFVLRSV
						L	

	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Institute, I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
donoc		l		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		residue of	sequence	/=possible nucleotide deletion, \=possible
		}		peptide		-volectide insertion
			J	sequence		DWPOGAVHENLLDVAKDWNDNPRKNFGLFL
				1	1	ET VKEDRDSGVNFOPEDTCARLRCSLHASLL
		1		1		A TOTAL NIPLOCHPSRKRRAAIPVPKLSCKNLCH
		1	1			PUOI FINERDI GWHKWIIAPKGFMANYCHGE
			i	İ		CDEST TIST NSSNYAFMOALMHAVDPEIPUAY
						CIPTKLSPISMLYQDNNDNVILRHYEDMVVD
		ļ				ECGCG
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913	2263	Α	7892	13	""	VI I STRI PRGRRLGSTEEAGGRSLWFPSDLAE
		1				T DET CEVT DEVRKEHOAY VELLECGAYLYNG
		1				GFAIPGSSFLNVLAGALFGPWLGLLLCCVLTS
		1				VGATCCYLLSSIFGKQLVVSYFPDKVALLQR
		1		Į.	}	KVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPI
	ł	1	1			LNIPIVQFFFSVLIGLIPYNFICVQTGSILSTLTS
						LDALFSWDTVFKLLAIAMVALIPGTLIKKFSQ
			1			KHLQLNETSTANHIHSRKDT
914	2264	A	7893	815	959	KSGWVWWLTPLIPALWEAQTEGSLRPEVKN
914	2204	1.	1			RLSNITRPFFSKKKKILV HASGPGGLLRRRRGSGANMPVARSWVCRKT
915	2265	A	7909	3	641	YVTPRRPFEKSRLDQELKLIGEYGLRNKREV
913	7203	1				WRVKFTLAKIRKAARELLTLDEKDPRRLFEG
			1		Ì	NALLRRLVRIGVLDEGKMKLDYILGLKIEDFL
		1	l		1	ERRLQTQVFKLGLAKSIHHAHVLIQQCHIRVR
				ļ		EQVVNILFFTVRLDSQKHIDFSLCFPIGVANPS
		ļ.				INVERNASKGOGGAGARDDEEEE
		·			967	- LVAUTOWUTCORI SOLTHRSILKYLLIDIHAC
916	2266	A	7914	3	967	OUT IT KUTHASI SI PSCUEUFPSSIFSASIIM VS
		1				UDUDDDSDRWGOTPEGLPAASPCGPGPKSCFS
					}	en prodewgmlaci.ctvlwhlpavpalnki
		1				CDBCBCBCIOKTYDLTRYLEHOLKSLAGI YLN
1		- 1				VI CODENIEDDENPPRI GAETLPRATVULEV W
		Į	1	1		RSLNDKLRLTQNYEAYSHLLCYLRGLNRQAA
1		-	1	1		TART DRST AHECTSLOGLIGSLAGYMAALGI
ł				1		PLPQPLPGTEPTWTPGPAHSDFLQKMDDFWL
ļ						LKELQTWLWRSAKDFNRLKKKMQPPAAAVI
ŀ	1					LHLGAHGF
017	2267	A	7921	2	1166	RPRRGQGLVQEVQTENVTVAEGGVAETTCRL HQYDGSIVVIQNPARQTLFFNGTRALKDERFO
917	2207	\ \frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\fir}}}}}}}{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac}\fir}}}}}}{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac	1,7=1			LEEFSPRRVRIRLSDARLEDEGGYFCQLYTED
l		1	ļ	1		THHQIATLTVLVAPENPVVEVREQAVEGGEV
ì		1	1			ELSCLVPRSRPAATLRWYRDRKELKGVSSSQ
1	1	1	1			ELSCLVPRSRPAATLKWTRDRKLDRGUICEAQN ENGKVWSVASTVRFRVDRKDDGGIICEAQN
1		1				QALPSGHSKQTQYVLDVQYSPTARIHASQAV
			}	1		VREGDTLVLTCAVTGNPRPNQIRWNRGNESI
1					1	PERAEAVGETLTLPGLVSADNGTYTCEASNK
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}						CAVVE A OTSVPYATVGGILALLVILLICVLVU
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1		1			l	LNGSDGHKRKEEFFI
		1				PPDI PPASPPSSSVSSSLSPSAVVMACRWSTK
918	2268	A	7938	3	2653	PCDD WD SALLIEFI AGVYGNGALAEHSENVI
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						A A TO PETA A A FOPCAYNOFOCL SREEK Y Y I CLE
						ANPPTAAAFQPCAYNQFQCLSRFIKVYICLE
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<del></del>	050 55	1.1.	L CEC	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	}	09/496	correspondi	ř .	Q=Glutamine, R=Arginine, S=Serine,
uence		ļ	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
				amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
i		l	ł	residue of	sequence	/=possible nucleotide deletion, \=possible
ì	ì	1	1	peptide		/=possible nucleotide defendit, /-possible
	ļ		1	sequence	<u></u>	nucleotide insertion
	-					VILRFTDFKLDGTGYGDYVKIYDGLEENPHK
l	1	1	1	1	į	LLRVLTAFDSHAPLTVVSSSGQIRVHFCADKV
\			ł		İ	NAARGFNATYQVDGFCLPWEIPCGGNWGCY
1	1	1		1	1	TEQQRCDGYWHCPNGRDETNCTMCQKEEFP
İ	l .	ì				CSRNGVCYPRSDRCNYQNHCPNGSDEKNCFF
ļ	1	1	}	}		CQPGNFHCKNNRCVFESWVCDSQDDCGDGS
	Į.		-	İ		DEENCPVIVPTRVITAAVIGSLICGLLLVIALG
	1		1	1		CTCKLYSLRMFERRSFETQLSRVEAELLRREA
1		1	1			PPSYGOLIAOGLIPPVEDFPVCSPNQASVLENL
1			1		1	RLAVRSQLGFTSVRLPMAGRSSNIWNRIFNFA
1	1	ļ	}	ł		RSRHSGSLALVSADGDEVVPSQSTSREPERNH
j	}	1	1	}		THRSLFSVESDDTDTENERRDMAGASGGVAA
1	1					PLPQKVPPTTAVEATVGACASSSTQSTRGGH
1						ADNGRDVTSVEPPSVSPARHQLTSALSRMTQ
1	1					GLRWVRFTLGRSSSLSQNQSPLRQLDNGVSG
}	1	Ì	j	1		REDDDDVEMLIPISDGSSDFDVNDCSRPLLDL
1	1	1	· I	1		ASDQGQGLRQPYNATNPGVRPSNRDGPCERC
1	1	1	1	1		GIVHTAQIPDTCLEVTLKNETSDDEALLLC
ļ			l		1000	VVRVTCCPPARSTTERTNAYDEEDCVEMVAS
919	2269	Α	7951	1674	1839	GGWNDVACHTTMYFMCEFDKKNM
ł				<u> </u>		GGRASWPEQAKEPRREGHTDKQQTEDVLAA
920	2270	A	7953	47	572	GLRCLPHLPAICARRMSPAFRAMDVEPRAKG
	ĺ	i	}		İ	VLLEPFVHQVGGHSCVLRFNETTLCKPLVPRE
	1	ł	1	1	1	VLLEPFVHQVGGHSCVLRINETTECKTEVTTC
1	ŀ	Ì	i	1		HQFYETLPAEMRKFTPQYKGKSQLLEGLPHW
	1	1	ļ	1		RGDVRDRGHGRPWQPSLEPSLPPTLCFPSLSS
1			1			FSSSWPSAQHLTPSVFNPW
921	2271	A	7957	612	812	RSGRTVVTGIGYSKALQSSNRNTKSLLQNEF
, , ,	1					MMVYSFRALSFKESTWATFQHGGEATKSRSL
ļ						SSTQ
922	2272	Ā	7967	1443	1660	ENITEKWKEIWMCRGNKKSCCWTFIKDRHLT
1 322	22.2	' '				VSCCKSKSGETLLICIFCSNLVGFFFFGIRGFSN
ļ						WELVKPN
923	2273	HA-	7981	1	3023	GSAPRAATAMARARPPPPPSPPPGLLPLLPPLL
923	22/3	1	,,,,,,	1		LLPLLLLPAGCRALEETLMDTKWVTSELAWT
1	İ	i	1	}		SHPESGWEEVSGYDEAMNPIRTYQVCNVRES
1	1					SONNWLRTGFIWRRDVQRVYVELKFTVRDC
		1		Ì		NSIPNIPGSCKETFNLFYYEADSDVASASSPFW
1	1	ľ	-	1		MENPYVKVDTIAPDESFSRLDAGRVNTKVRS
1	1		1	1		FGPLSKAGFYLAFODOGACMSLISVRAFYKK
1	{	1	1	1		CASTTAGFALFPETLTGAEPTSLVIAPGTCIPN
	ŀ	1	ì			AVEVSVPLKLYCNGDGEWMVPVGACTCATG
			1	1	1	HEPAAKESOCRPCPPGSYKAKQGEGPCLPCPP
1	1					NSRTTSPAASICTCHNNFYRADSDSADSACTT
1			1	1		VPSPPRGVISNVNETSLILEWSEPRDLGVRDD
1				1		LLYNVICKKCHGAGGASACSRCDDNVEFVPR
				1		QLGLSEPRVHTSHLLAHTRYTFEVQAVNGVS
				1	1	GKSPLPPRYAAVNITTNQAAPSEVPTLRLHSS
1	1	1		1		SGSSLTLSWAPPERPNGVILDYEMKYFEKSEG
	1	1	]	1		IASTVTSQMNSVQLDGLRPDARYVVQVRART
1	1	l	1			VAGYGQYSRPAEFETTSERGSGAQQLQEQLP
1	ļ	ļ	1		1	VAUTUUTSKLAETETTSEKUSUAUQUUGUUT
	1	1			i	LIVGSATAGLVFVVAVVVIAIVCLRKQRHGS
						DSEYTEKLQQYIAPGMKVYIDPFTYEDPNEA
		1		}		VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRL
		1		1		KQPGRREVFVAIKTLKVGYTERQRRDFLSEA
1						SIMGQFDHPNIRLEGVVTKSRPVMILTEFME
					1	NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM
						KYLSEMNYVHRDLAARNILVNSNLVCKVSDF
				1	ļ	GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPEAI
			-	Į.	1	AYRKFTSASDVWSYGIVMWEVMSYGERPY
L						

770 TD	CEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of		i noa	in	nucleotide	location	F-Phenylalanine, G-Glycine, H-Histidine,
aucl-	peptide	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence			ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ience	1	ì	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	[	1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	residue of	Sequence	/=possible nucleotide deletion, \=possible
	1	1	1	peptide		nucleotide insertion
	1	Į.	J	sequence		WDMSNQDVINAVEQDYRLPPPMDCPTALHQ
			1		1	LMLDCWVRDRNLRPKFSQIVNTLDKLIRNAA
		1		]	İ	SLKVIASAQSGMSQPLLDRTVPDYTTFTTVGD
	1	1	Į.	1		SLKVIASAQSGMSQPLLDRI VIDITITIVOD
	1	ł	1			WLDAIKMGRYKESFVSAGFASFDLVAQMTA
	1	ì	i	l		EDLLRIGVTLAGHQKKILSSIQDMRLQMNQT
	-	1	1	1		LPVQV
024	2274	A	7985	1	503	FRPRTKKATAMYLEHYLDSIENLPCELQRNF
924	22/4	^	1700	1.		QLMRELDQRTEDKKAEIDILAAEYISTVKTLS
	1		ì			PDORVERI OKIONAYSKCKEYSDUKVQLAM
		1	1	1	}	OTYEMVDKHIRRLDADLARFEADLKDKMEG
	1	1	1			SDFESSGGRGLKKGRGQKEKRGSRGRGRRTS
		-	-	ŀ		FEINTPKKKKHKGG
				1.00	589	LPCSFCAQCMSSFERVWLQQSHFHNPRWNSR
925	2275	A	7994	447	589	SPIRCYCQHWPHCVHC
	}		1	l		GPCKVCCITLAIMLQCHSFYRKDVQVEHPKS
926	2276	A	7996	925	582	LNPKYSQIENFLSADMALKRKCLLSISDLDFW
	1			· I		IWDAQPVGIMQTLQNLKKIPNPGCFWSQAFQ
	1	}	1			IWDAQPYGIMQTEQNEARING GET WOOTH Q
		1				RDTQPILPLGGRYYTTIRQ
927	2277	A	7998	2	353	RIQRPLNSRSPNHSLFVKAELTAKQATMKLSV
921	2211	1 **	1			CLLLVTLALCCYQANAEFCPALVSELLDFFFI
	1	1	1	}		SEPLFKLSLAKFDAPPEAVAAKLGVKRCTDQ
	1		ł	Į.		MSLQKRSLIAEVLVKILKKCSV
	2220	A	8004	130	588	LAPLRCQPGTRTQPRSHPAANDPSAAMSAAG
928	2278	A	8004	130	300	ARGURATYHRLLDKVELMLPEKLRPLYNHPA
	-	į.	<b>\</b>	ĺ		GPRTVFFWAPIMKWGLVCAGLADMARPAEK
	1	1	1	1		LSTAOSAVLMATGFIWSRYSLVIIPKNWSLFA
	<b>\</b>			1	ļ	VNFFVGAAGASOLFRIWRYNQELKAKAHK
				<del></del>	1016	FEARRVEIAAREMSLLRSLRVFLVARTGSYF
929	2279	A	8007	2	1010	AGSLLRQSPQPRHTFYAGPRLSASASSKELLM
	1		1			KLRRKTGYSFVNCKKALETCGGDLKQAEIWI
}			l l			HKEAQKEGWSKAAKLQGRKTKEGLIGLLQE
		1			,	GNTTVLVEVNCETDFVSRNLKFQLLVQQVAL
	1	.	l	į.	1	GTMMHCQTLKDQPSAYSKGFLNSSELSGLPA
	ł		l	1	Į.	GPDREGSLKDQLALAIGKLGENMILKRAAW
Ì	i	1		-		GPDREGSEKDQLALAIOKEGELIVILIGIGUT
1		ì	l l	i		KVPSGFYVGSYVHGAMQSPSLHKLVLGKYG
į	1			1	]	ALVICETSEQKTNLEDVGRRLGQHVVGMAPI
ł		- 1	1			SVGSLDDEPGGEAETKMLSQPYLLDPSITLGC
						YVQPQGVSVVDFVRFECGEGEEAAETE
	2200	+	8008	3	1679	NSDVWGPWTEPSAGSLRPMARKONRNSKEL
930	2280	A	0000	1		GI VPI TDDTSHAGPPGPGRALLECDHLRSGV
}		}	1	1		PGGRRRKDWSCSLLVASLAGAFGSSFLYGY
					•	LSVVNAPTPYIKAFYNESWERRHGRPIDPDII
		1		1		TILWSVTVSIFAIGGLVGTLIVKMIGKVLGRK
1				1		HTLLANNGFAISAALLMACSLQAGAFEMLIV
	1		İ			GRFIMGIDGGVALSVLPMYLSEISPKEIRGSLO
}	1		l l	1		QVTAIFICIGVFTGQLLGLPELLGKESTWPYL
			1			GVIVVPAVVQLLSLPFLPDSPRYLLLEKHNEA
1		1				GAIAALACALI ON A DAGO EAGEAU A EGDAODE
1						RAVKAFQTFLGKADVSQEVEEVLAESRVQR
İ		- 1	1	1		IRLVSVLELLRAPYVRWQVVTVIVTMACYQI
}		1	ĺ			CGLNAIWFYTNSIFGKAGIPPAKIPYVTLSTG
1		1	1			IETLAAVFSGLVIEHLGRRPLLIGGFGLMGLF
[	1	}		1	1	GTLTITLTLODHAPWVPYLSIVGILAIIASFCS
1		1	1			PGGIPFILTGEFFOOSORPAAFIIAGTVNWLSN
						FAVGLLFPFIQKSLDTYCFLVFATICITGAIYL
1			1		1	YFVLPETKNRTYAEISQAFSKRNKAYPPEEKI
I	į					DSAVTDGKINGRP
1		1				AAGAVVSAMPKAKGKTRRQKFGYSVNRKR
3	2201	A	8009	861	300	NRNARRKAAPRIECSHIRHAWDHAKSVRQN
931	1 //٨1			1		
931	2281	1	]	}	1	AEMGLAVDPNRAVPLRKRKVKAMEVDIEER

000 ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID NO: of	NO: of	hod	ID NO:		nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	,,,,,,	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	delice	l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uchec		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		1	peptide		/=possible nucleotide deletion, \-possible
	1			sequence	<b>\</b>	nucleotide insertion
	<del> </del>		+	344		PKELVRKPYVLNDLEAEASLPEKKGNTLSRD
	1			]		LIDYVRYMVENHGEDYKAMARDEKNYYQD
		ł		1		TPKQIRSKINVYKRFYPAEWQDFLDSLQKRK
	Ì	ì	İ			MEVE
	0000	<del> </del>	8011	412	1	SNLCLGNSWRWRWAKSRHHCIPTVTLSKRSG
932	2282	A	.0011	412	,	DIRGSHFSSPQRQRSQRVPGKETARVLRAGK
			ł	-	1	OGRGOIPIPCPWPPPPPPPPPPGSPGPGCRQFHQ
	ŀ			li .	1	SLEAKARHPASVREMRGKVKMRRALRRAPA
		1	1	}		STRASSROPNPK
		↓	<del> </del>	1.15	1077	PPVPPASRSDMAQNLKDLAGRLPAGPRGMGT
933	2283	A	8012	147	10//	ALKLLLGAGAVAYGVRESVFTVEGGHRAIFF
		1	Ì			NRIGGVQQDTILAEGLHFRIPWFQYPIIYDIRA
			ł		1	RPRKISSPTGSKDLQMVNISLRVLSRPNAQEL
	1	1			1	PSMYQRLGLDYEERVLPSIVNEVLKSVVAKF
	1		1			NASQLITQRAQVSLLIRRELTERAKDFSLILDD
	1	1	ļ			VAITELSFSREYTAAVEAKQVAQQEAQRAQF
	ł	1		ļ		LVEKAKQEQRQKIVQAEGEAEAAKMLGEAL
		1				SKNPGYIKLRKIRAAQNISKTIATSQNRIYLTA
	1	1				DNLVLNLQDESFTRGSDSLIKGKK
	i					SQFSLSQVLVDSAEEGSLAAAAELAAQKREQ
934	2284	Α	8023	255 .	982	RLRKFRELHLMRNEARKLNHQEVVEEDKRL
		1				KLPANWEAKKARLEWELKEEEKKKECAARG
	1	1	1		1	EDYEKVKLLEISAEDAERWERKKKRKNPDLG
		1				FSDYAAAQLRQYHRLTKQIKPDMETYERLRE
		Į	ì			KHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLE
	1	1	ļ		}	KHGEEFFFISNSLLHGIAVFSIEEDRAVIDEL
		l l	1			KQIEKRDKYSRRRPYNDDADIDYINERNAKF
	1					NKKAERFYGKYTAEIKQNLERGTAV LVSSTVNLLTEKAPWNSLAWTVTSYVFLKFL
935	2285	A	8027	59	310	OGGGTGSTGMRDSALTLLGIGPSHRHSLSIRL
	i	İ	İ		1	QGGGTGSTGMRDSALTLLGIGFSHRTISLSILCE
	Ì		1			SQHSSPAPMYSQTFHILVLG
936	2286	A	8032	1	639	SGRECHMAKTYDYLFKLLLIGDSGVGKTCVL
100			,	1	Į	FRESEDAFNSTFISTIGIDFKIRTIELDGKRIKLQ
[		1				IWDTAGQERFRTITTAYYRGAMGIMLVYDIT
1		Į.				NEKSFONIRNWIRNIEEHASADVEKMILGNKC
						DVNDKRQVSKERGEKLALDYGIKFMETSAK
		1	l	1		ANINVENAFFTLARDIKAKMDKKLEGNSPQG
	].	1				SNQGVKITPDQQKRSSFFRCVLL
937	2287	A	8039	393	311	EETIHSENSYILEKYIPISANLTLTIA
938	2288	<del>   </del>	8052	675	-1334	LHPAATSTAWLHVPPGLSMALSWVLTVLSLL
930	2200	1 '	1 5032			PLLEAQIPLCANLVPVPITNATLDRITGKWFYI
ļ	l		1		1	ASAFRNEEYNKSVQEIQATFFYFTPNKTEDTIF
{						LREYQTRQDQCIYNTTYLNVQRENGTISRYV
ł	1					GGOEHFAHLLILRDTKTYMLAFDVNDEKNW
İ	-	Ì	1			GLSVYADKPETTKEQLGEFYEALDCLRIPKSD
Į	1	-	ł	i	i	VVYTDWKKDKCEPLEKQHEKERKQEEGES
		+	- 0055	12	1039	SSVAEFPERVOLSOPONWNFSGAGGAWSLDF
939	2289	A	8055	12	1039	AEQLKWSAELARLGESIMDGKQGGMDGSKP
1						AGPRDFPGIRLLSNPLMGDAVSDWSPMHEAA
ł	i			ļ		IHGHQLSLRNLISQGWAVNIITADHVSPLHEA
						CLGGHLSCVKILLKHGAQVNGVTADWHTPL
					1	FNACVSGSWDCVNLLLQHGASVQPESDLASP
1					1	IHEAARRGHVECVNSLIAYGGNIDHKISHLGT
1					1	INTERPORTATION A CANANT I ESCAPANIO CACO
		}			1	PLYLACENQQRACVKKLLESGADVNQGKGQ
		1	}			DSPLHAVARTASEELACLLMDFGADTQAKN
J			-			AEGKRPVELVPPESPLAQLFLEREGPPSLMQL
	ļ	1			1	CRLRIRKCFGIQQHHKITKLVLPEDLKQFLLH
		1	1	1	1	L
	İ	- 1			1	
940	2290	A	8058	2	1203	KVLSIREPAHSTARKASEPSQPSQPSQPGGHLI ARLRTMDLHLFDYSEPGNFSDISWPCNSSDCI

	CEPC 1P	1 1/24	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid,
NO: of	NO: of	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence			ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	1	Ì	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		1		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	{	residue of	sequence	/=possible nucleotide deletion, \=possible
		1	ļ	peptide		nucleotide insertion
	ì	ł		sequence		VVDTVMCPNMPNKSVLLYTLSFIYIFIFVIGMI
		1			Ì	ANSVVVWVNIQAKTTGYDTHCYILNLAIADL
	]	j	1	1		ANSVVV WVNIQAKI I O I DI I O I DI CEL TOVVTU
	1	1	ì	1		WVVLTIPVWVVSLVQHNQWPMGELTCKVTH
	\	1			1	LIFSINLFGSIFFLTCMSVDRYLSITYFTNTPSS
	ļ	Į.				RKKMVRRVVCILVWLLAFCVSLPDTYYLKT
	ļ	1		•		VTSASNNETYCRSFYPEHSIKEWLIGMELVSV
	ì					VLGFAVPFSIIAVFYFLLARAISASSDQEKHSS
			ļ	į.	l .	RKIIFSYVVVFLVCWLPYHVAVLLDIFSILHYI
		1	ĺ		į	PFTCRLEHALFTALHVTQCLSLVHCCVNPVL
	1.		}	1	1	YSFINRNYRYELMKAFIFKYSAKTGLTKLIDA
	1	1		1	}	SRVSETEYSALEOSTK
			2050		432	DMAGLMTIVTSLLFLGVCAHHIIPTGSVVLPS
941	2291	A	8059	73	732	PCCMFFVSKRIPENRVVSYQLSSRSTCLKAGV
	1	1				IFTTKKGQQFCGDPKQEWVQRYMKNLDAKQ
		1				KKASPRARAVAVKGPVORYPGNQTTC
		L			1,000	GGIGEIKQRPSCLGRCLDPSLSVLMNISLGLGS
942	2292	A	8067	278	1262	VFSAVISQKPSRDICQRGTSLTIQCQVDSQVT
		1				MMFWYRQQPGQSLTLIATANQGSEATYESGF
			1			VIDKFPISRPNLTFSTLTVSNMSPEDSSIYLCSA
	į	ļ	}	1	ł	GROGTYEQYFGPGTRLTVTEDLKNVFPPEVA
	1		i	İ		VFEPSEAEISHTQKATLVCLATGFYPDHVELS
	ł	İ	1	1		WWVNGKEVHSGVSTDPQPLKEQPALNDSRY
	1					WWYNGKEYHSUVSIDPQIERCOVOEYGI SE
	1		1	1		CLSSRLRYSATFWQNPRNHFRCQVQFYGLSE
	l l		1			NDEWTQDRAKPVTQIVSAEAWGRADCGFTS
		1				ESYQQGVLSATILYEILLGKATLYAVLVSALV
			1		İ	LMAMVKRKDSRG
943	2293	A	8070	1	879	MVKVVPATRGNLPRSQLTGTHQHCQPREPKI
743		1.				TASERLRRPRATARLRAHAAPPEPPLAVFAP
	1	l	ĺ			PSDRKELLALPVACDPVIASVMSWVQAASLI
	ì	1	1	ŀ		QGPGDKGDVFDEEADESLLAQREWQSNMQR
}	}	- }	- 1	1		RVKEGYRDGIDAGKAVTLQQGFNQGYKKGA
ŀ						EVILNYGRLRGTLSALLSWCHLHNNNSTLINK
			İ	1		INNLLDAVGQCEEYVLKHLKSITPPSHVVDLL
	i				,	DSIEDMDLCHVVPAEKKIDEAKDERLCENNA
	1	1				EFNKNCSKSHSGIDCSYVECCRTQEHAHSGK
	1	- 1	ŀ			PKPHMDFGTDSQF
	10004	<del> </del>	8073	1	797	ESARWSRQLRRTLIRLSFPISCGRSHAFGGCK
944	2294	A	00/3	1	1	MAATSGTDEPVSGELVSVAHALSLPAESYGN
I	1					DPDIEMAWAMRAMOHAEVYYKLISSVDPQF
	1					I KI TKVDDOLYSEFRKNFETLRIDVLDPEELK
		1				SESAKEKWRPFCLKFNGIVEDFNYGTLLRLD
ł				}		CSOGYTEENTIFAPRIOFFAIEIARNREGYNKA
	[	1				VYISVQDKEGEKGVNNGGEKRADSGEEENT
				1		KNGGEKGADSGEEKEEGINREDKTDKGGEK
		-			1	GKEADKEINKSGEKAM
1						GAATLLRSASSAARKAAEAEQVWLHLHRYL
945	2295	A	8074	2	505	GAAILLKSASSAARRAAEAEQ WEILLINGE
					1	SADRRVLGLREWGRPASERECSLCQRLKREL
1		1			}	NMGDVEKGKKIFIMKCSQCHTVEKGGKHKT
1	1	}			1	GPNLHGLFGRKTGQAPGYSYTAANKNKGIIW
1					ļ	GEDTLMEYLENPKKYIPGTKMIFVGIKKKEER
1	ł		1	ì		ADLIAYLKKATNE
1000			8081	42	590	FGRRGKFGGKLCNFLFYFHSNSAESRMDVLF
946	2296	A	6061	172	1 370	VAIFAVPLILGOEYEDEERLGEDEYYQVVYY
[					1	VTVTPSYDDFSADFTIDYSIFESEDRLNRLDK
						DITEATETTISLETARADHPKPVTVKPVTTEPQ
				1		SPRSEAMPCPVLRSPIPLPPVRVPLFRWGCISC
}	1				1	KKVGRRLLMTLWMGVWQEEIGR
1	1				549	GGGSSPRELAGAAGLTVTSQAVAARRQQPSF
947	2297	A	8084	322	349	SRARAPAHSLRAALSLASSARSWGAVSRDRG

SEQ ID				<b>*</b>	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
aru w	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding	I=Isolcucine, K=Lysine, L=Loucine,
-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	delice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		İ	/ / / /	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ì	}		residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
	1	1			Jeque	/=possible nucleotide deletion, \=possible
	1	ł		peptide	ļ	nucleotide insertion
	1	ļ		sequence		
	1					PCPPAIMYQSSNKC
948	2298	В	8093	3905	846	MEPGEVKDRILENISLSVKKLQSYFAACEDEI
948	2296	1 5	0072			PAIRNHDKVLQRLCEHLDHALLYGLQDLSSG
	1	l	1	i	1	YWVLVVHFTRREAIKQIEVLQHVATNLGRSR
	1	Į.	1	1	j	AWI VI AI NENSLESYLRLFOENLGLLHKYYV
	1	1	ì			KNALVCSHDHLTLFLTLVSGLEFIRFELDLDA
	1	1		İ	1	DVI DI APYMPDYYKPOYLLDFEDRLPSSVHG
	1	l	1	1		SDSLSLNSFNSVTSTNLEWDDSAIAPSSEDYD
	}	1	ì	1		FGDVFPAVPSVPSTDWEDGDLTDTVSGPRST
	1	1	1			FGDVFPAVPSVPSTDWEDODDID: VSGV
	Į.	}	1			ASDLTSSKASTRSPTQRQNPFNEEPAETVSSS
	}	1	1	į.		DTTPVHTTSQEKEEAQALDPPDACTELEVIRV
		1				TKKKKIGKKKKSRSDEEASPLHPACSQKKCA
		1				KOGDGDSRNGSPSLGRDSPDTMLASPQEEGE
	1	1			1	CDSSTTESSERSEPGLLIPEMKDTSMERLGQPL
	1	1		1	1	SEVUIDOL NGOL DPSTWCSRAEPPDQSFRTGSP
		1			1	GDAPERPPLCDFSEGLSAPMDFYRFTVESPST
	1				1	VTSGGGHHDPAGLGQPLHVPSSPEAAGQEEE
	1	1	1	1	1	VISGGGHHDPAULOQPLITVI SSI LITTOQUEL
	l l	1	1	]	1	GGGGGGTPRPLEDTTREAQELEAQLSLVRE
	1		1	1	1	GPVSEPEPGTQEVLCQLKRDQPSPCLSSAEDS
	1	1	1	1	1	GVDEGQGSPSEMVHSSEFRVDNNHLLLLMIH
	1	4	1	İ		VERENEEOLEKMIRMSTGHMEGNLQLLYVLL
	Į.	ĺ	1			TDCYVYLLRKGATEKPYLVEEAVSYNELDY
		1		j	}	VSVGLDQQTVKLVCTNRRKQFLLDTADVAL
i	(	Į	1	Ì	ľ	AEFFLASLKSAMIKGCREPPYPSILTDATMEK
	l l			ļ		LALAKFVAQESKCEASAVTVRFYGLVHWED
ł	- {				ļ	PIDESLGPTPCHCSPPEGTITKEGMLHYKAGT
	1		I	1	i	PIDESLGPIPCHCSPPEGITIKEGWEITTGUS
	1	1		ì		SYLGKEHWKTCFVVLSNGILYQYPDRTDVIP
	1		- 1	Ì		LLSVNMGGEQCGGCRRANTTDRPHAFQVILS
)	1		ì			DPPCLELSAESEAEMAEWMQHLCQAVSKGVI
1	1		Ì	1		POGVAPSPCIPCCLVLTDDRLFTCHEDCQTSF
	į	1		1		EDGL GTAKL GDISAVSTEPGKEYCVLEFSQUS
l		]	1	}		OOLI PPWVIYI SCTSELDRLLSALNSGWKIIY
1	1	ı	1	ł		QVDLPHTAIQEASNKKKFEDALSLIHSAWQR
1	l l	1	1	}		SDSLCRGRASRDPWC*
1	1	- }	}			ARRADTVLLESPSMLQGLLPVSLLLSVAVSAI
949	2299	A	8095	9	2374	ARRADIVILLES POMIL QUELL VOLLES VILVOIT
747	2277	1				KELPGVKKYEVVYPIRLHPLHKREAKEPEQQ
1		- 1	1		1	EQFETELKYKMTINGKLAVLYLKKNKNLLAP
1	1	1	1		}	CVTETVVNSTGKEITTSPOIMDDCYYQGHUN
1	1		- 1	1	ı	
	L	1		<b>I</b>	1	EKVSDASISTCRGLRGYFSOGDORYFIEPLSPI
1			1			EKVSDASISTCRGLRGYFSQGDQRYFIEPLSPI
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSPI
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLOONIALPATKLVKLKDRKVQEHEKY
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IFYYI VI DNGFFKRYNENODEIRKRVFEMAN
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTI ENFSKWRGSVLSRKKHDIAQLITA
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRKKHDIAQLITA TFI AGTTVGLAFMSTMCSPYSVGVVQDHSD
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NJ I RVAGTMAHEMGHNFGMFHDDYSCKCP
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCP TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCP: TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCP: TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCP. TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSFFCTNICCDAKTCKIKATFOCALGECCER
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCP: TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCP; TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNG
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCP; TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNG PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCPICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLRVAGTMAHEMGHNFGMFHDDYSCKCP TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCER CQFKKAGMVCRPAKDECDLPEMCNGKSGNO PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLRVAGTMAHEMGHNFGMFHDDYSCKCP: TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNG PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLRVAGTMAHEMGHNFGMFHDDYSCKCP: TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNG PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLRVAGTMAHEMGHNFGMFHDDYSCKCP TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCER CQFKKAGMVCRPAKDECDLPEMCNGKSGNO PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC DNKVCINAECVDIEKAYKSTNCSSKCKGHAV
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLRVAGTMAHEMGHNFGMFHDDYSCKCP TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCER CQFKKAGMVCRPAKDECDLPEMCNGKSGNOPDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVV
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLRVAGTMAHEMGHNFGMFHDDYSCKCP TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCC DNKVCINAECVDIEKAYKSTNCSSKCKGHAN CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVV VLFPMAVIFVVVAMVIRHQSSREKQKKDQRI
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSFI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLRVAGTMAHEMGHNFGMFHDDYSCKCPS TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKI SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCC DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVC VLFPMAVIFVVVAMVIRHQSSREKQKKDQRI LSTTGTRPHKQKRKPQMVKAVQPQEMSQMI PHVYDLPVEGNEPPASFHKDTNALPPTVFKD
						EKVSDASISTCRGLRGYFSQGDQRYFIEPLSP. HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKRHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLRVAGTMAHEMGHNFGMFHDDYSCKCP TICVMDKALSFYIPTDFSSCSRLSYDKFFEDK SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEI CQFKKAGMVCRPAKDECDLPEMCNGKSGNI PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCF RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKC DNKVCINAECVDIEKAYKSTNCSSKCKGHAN CDHELQCQCEEGWIPPDCDDSSVVFHFSIVV

<del></del>	CEC TO	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D=A spartic Acid. E=Glutamic Acid.
NO: of	peptide	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl- eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
- 1	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	dence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uciicc		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	į	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
950	2300	A	8100	1	1251	MGLLLMILASAVLGSFLTLLAQFFLLYRRQPE
750	2000	1				PPADEAARAGEGFRYIKPVPGLLLREYLYGG
	1		ĺ	(		GRDEEPSGAAPEGGATPTAAPETPAPPTRETC
					1	YFLNATILFLFRELRDTALTRRWYTKKIKVEF
	1				1	EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI
		1			1	RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS
	1	ł				RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV
				Į		RSQFEGRPMPQLTSIIVNQLKKIIKRKHTLPNY
				į	1	KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE
		1	ĺ			GRLKVTLLECSRLLIFGSYDREANVHCTLELS
		}	1	ļ		SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE
		1	1			AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ
		1				CPG
				1.610	839	FVALECEEMAAGMYLEHYLDSIENLPFELQR
951	2301	A	8108	1612	039	NEOLMRDLDORTEDLKAEIDKLATEYMSSAR
						SUSSEEKLALLKOIOEAYGKCKEFGDDKVQL
		1			ĺ	AMOTYEMVDKHIRRLDTDLARFEADLKEKQI
			İ		1	FSSDYDSSSSKGKKKGRTOKEKKAARARSKG
			ļ		. 9	KNSDEEAPKTAOKKLKLVRTSPEYGMPSVTF
		1	Ì			GOVERNOVI DMPVDPNEPTYCLCHOVSYGE
	j	1	}		1	MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC
	1				_	PRCSQERKKK
952	2302	TA.	8112	595	291	PSVASLARRFSGRAL WPPSHSVPGNRALCPRL
752	2502	1				LHGTTLPGGNQRELARQKNMKKQSDSVKGK
		[	[	1		RRDDGLSAAARKQRDSTPRDSEIMQQKQKK
			-			ANEKKEEPK VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG
953	2303	Α	8118	1	669	LETNILKMTTPNKTPPGADPKQLERTGTVREI
1		1		Ì		GSQAVWSLSSCKPGFGVDQLRDDNLETYWQ
		1				SDGSQPHLVNIQFRRKTTVKTLCIYADYKSDE
1		İ	l l			SYTPSKISVRVGNNFHNLQEIRQLELVEPSGW
} .						IHVPLTDNHKKPTRTFMIQIAVLANHQNGRD
	İ		İ			THMRQIKIYTPVEESSIGKFPRCTTIDFMMYRS
ļ		1	1			TR
		٠	0133	66	1015	PPI PPRSFPNLFSRPEPLPEPGRRGCNRSREPA
954	2304	Α	8133	00	1015	ARAPSPPPPFEGAPGRAMVKVTFNSALAQKE
				i		AKKDEPKSGEEALIIPPDAVAVDCKDPDDVV
1						PVGORRAWCWCMCFGLAFMLAGVILGGAY
ļ		1		-		LYKYFALOPDDVYYCGIKYIKDDVILNEPSAD
		ļ	i			APAALYOTIEENIKIFEEEEVEFISVPVPEFADS
İ		ĺ				DPANIVHDFNKKLTAYLDLNLDKCYVIPLNT
1						SIVMPPRNLLELLINIKAGTYLPQSYLIHEHMV
	'	- 1	ļ	ļ		ITDRIENIDHLGFFIYRLCHDKETYKLQRRETI
1	1	1	}	1		KGIOKREASNCFAIRHFENKFAVETLICS
055	2305	-	8143	35	1171	VESRSAWHEGEDOIDRLDFIRNQMNLLTLDV
955	2303	^	0173	"		KKKIKEVTEEVANKVSCAMTDEICRLSVLVD
1						EFCSEFHPNPDVLKIYKSELNKHIEDGMGRNL
1			[	Į.		ADRCTDEVNALVLOTOOEIIENLKPLLPAGIQ
						DKLHTLIPCKKFDLSYNLNYHKLCSDFQEDIV
ļ						FRESLGWSSLVHRFLGPRNAQRVLLGLSEPIF
1				1	1	QLPRSLASTPTAPTTPATPDNASQEELMITLVT
		1		1	I .	GLASVTSRTSMGIIIVGGVIWKTIGWKLLSVS
				1	i	LTMYGALYLYERLSWTTHAKERAFKQQFVN
1	ı	- 1		J		YATEKLRMIVSSTSANCSHQVKQQIATTFARL
ı	1				1	THE PROPERTY OF PERSON DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
			ĺ	1		CQQVDITQKQLEEEIARLPKEIDQLEKIQNNS
						KLLRNKAVOLENELENFTKQFLPSSNEES
956	2306	A	8157	1854	798	CQQVDITQKQLEEEIARLPREIDQLERIQINIS KLLRNKAVQLENELENFTKQFLPSSNEES ASGSPAPSSSSAMAAACGPGAAGYCLLLGLH LFLLTAGPALGWNDPDRMLLRDVKALTLHY

						(A-Alonine C-Cysteine
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	Ì	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uenœ	1	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue of peptide	T=Threonine, V=Valine, W=Tryptophan,
		{	1	amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			İ	residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ	1		peptide		nucleotide insertion
		ļ	ļ	sequence	<del> </del>	DRYTTSRRLDPIPOLKCVGGTAGCDSYTPKVI
		<b>\</b>				OCONKGWDGYDVOWECKTDLDIAYKFGKT
		}				VVSCEGVESSEDOYVLRGSCGLEYNLDYTEL
		1				GLOKLKESGKOHGFASFSDYYYKWSSADSC
			}			MMSGLITIVVLLGIAFVVYKLFLSDGQYSPPP
				1	-	VSEYPPESHRYORFTNSAGPPPPGFKSEFTGPQ
	}	1		Ì		NTGHGATSGFGSAFTGQQGYENSGPGFWTGL
1	1		}			GTGGILGYLFGSNRAATPFSDSWYYPSYPPSY
			1			PGTWNRAYSPLHGGSGSYSVCSNSDTKTRTA
	}	1		1		SGYGGTRRR
957	2307	A	8159	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSL
957	2507	1	0.37			VYSMPSRNLSLRLEGLQEKDSGPYSCSVNVQ
		1				DKQGKSRGHSIKTLELNVLVPPAPPSCRLQGV
						PHVGANVTLSCQSPRSKPAVQYQWDRQLPSF
	1	į				OTFFAPALDVIRGSLSLTNLSSSMAGVYVCKA
	1	1				HNEVGTAQCNVTLEVSTGPGAAVVAGAVVG
		-	1			TLVGLGLLAGLVLLYHRRGKALEEPANDIKE DAIAPRTLPWPKSSDTISKNGTLSSVTSARAL
1	1	1		ì	ļ	RPPHGPPRPGALTPTPSLSSQALPSPRLPTTDG
	1	}				AHPQPISPIPGGVSSSGLSRMGAVPVMVPAQS
1	1.4					QAGSLV
					1100	ELARRPKQQSSEKSRNMIRNWLTIFILFPLKLV
958	2308	Α	8161	2340	1192	EKCESSVSLTVPPVVKLENGSSTNVSLTLRPP
		1	1	1		LNATLVITFEITFRSKNITILELPDEVVVPPGVT
		1				NSSFQVTSQNVGQLTVYLHGNHSNQTGPRIR
		1	}			FI VIRSSAISIINOVIGWIYFVAWSISFYPQVIM
ì		1	-		l	NWRRKSVIGLSFDFVALNLTGFVAYSVFNIGL
Ì		1				LWVPYIKEOFLLKYPNGVNPVNSNDVFFSLH
}		İ		}	1	AVVITLIIIVOCCLYERGGQRVSWPAIGFLVL
				ļ.		AWLEAFVTMIVAAVGVITWLQFLFCFSYIKL
	ì	ł	İ	1	1	AVTLVKYFPQAYMNFYYKSTEGWSIGNVLL
i		1		1		DFTGGSFSLLQMFLQSYNNDQWTLIFGDPTK
-		-	-	1		FGLGVFSIVFDVVFFIQHFCLYRKRPGYDQLN
959	2309	A	8163	521	1345	GERAGRRGRLGVWAQPQPLLPRPVGSRRE
1 737	2507					MQPPGPPPAYAPTNGDFTFVSSADAEDLSGSI
					j	ASPDVKLNLGGDFIKESTATTFLRQRGYGWL
İ				1		LEVEDDDPEDNKPLLEELDIDLKDIYYKIRCV LMPMPSLGFNRQVVRDNPDFWGPLAVVLFFS
1			1	1		MISLYGQFRVVSWIITIWIFGSLTIFLLARVLG
						GEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSF
						EVVSTLIKLFGVFWAAYSAASLLVGEEFKTK
		1			}	KPLLIYPIFLLYIYFLSLYTGV
				<del></del>	2921	MTCFKGQKGEQRSHAFEANKDHKAKVPSPN
960	2310	A	8167	1	2921	I VSOLNALOFTVDERSILWLNOFLLDLKQSL
j	1	1			-	NOFMAVYKLNDNSKSDEHVDVRVDGLMLK
						FVIPSEVKSECHODOPRAISIQSSEMIATNIRH
			1	1	1	CPNCRHSDLEALFQDFKDCDFFSKTYTSFPKS
j	)		}	1		CDNFNLLHPIFORHAHEQDTKMHEIYKGNITP
						OLNKNTLKTSAATDVWAVYFSQFWIDYEGM
						KSCKGRPISFVDSFPLSIWICOPTRYAESQKEP
	}		}			OTCNOVSLNTSOSESSDLAGRLKRKKLLKEY
	}					YSTESEPLTNGGOKPSSSDTFFRFSPSSSEADI
	1			1		HI I VHVHKHVSMOINHYQYLLLLFLHESLILL
						SENI.RKDVEAVTGSPASQTSICIGILLRSAELA
				1		LLLHPVDOANTLKSPVSESVSPVVPDYLPTEN
	}	1		1	1	GDFLSSKRKOISRDINRIRSVTVNHMSDNRSM
	-					SVDLSHIPLKDPLLFKSASDTNLQKGISFMDY
						LSDKHLGKISEDESSGLVYKSGSGEIGSETSD
			1			KKDSFYTDSSSVLNYREDSNILSFDSDGNQNI
						LSSTLTSKGNETIESIFKAEDLLPEAASLSENL
1	1					

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=A spartic Acid. E=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in USSN	location	corresponding	i=Isoleucine, K=Lysine, L=Leucine,
otide	seq- uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uaicc	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1		peptide		/=possible nucleotide deletion, \-possible
	}	İ		sequence		nucleotide insertion  DISKEETPPVRTLKSQSSLSGKPKERCPPNLAP
						LCVSYKNMKRSSSQMSLDTISLDSMILEEQLL
	1	1	1		l	ESDGSDSHMFLEKGNKKNSTTNYRGTAESVN
			1		l	AGANI ONYGETSPDAISTNSEGAQENHUULM
			1	Į.	1	CVVVEKITGVNGEIDIRGEDTEICLQVNQVTP
		1				DOLGNISLRHYLCNRPVGSDQKAVIHSKSSPE
	İ	}		1	ì	IST REESGPGAVIHSLLAEKNGFLQCHIENEST
					1	LEELTSSI MNIOHFLEDETVATVMPMKIQVSNI
	1			1		KINLKDDSPRSSTVSLEPAPVTVHIDHLVVER
		1	1			SDDGSFHIRDSHMLNTGNDLKENVKSDSVLL
		i	<b>\</b>		}	TSGKYDLKKQRSVTQATQTSPGVPWPSQSAN
		1				FPEFSFDFTREQLMEENESLKQELAKAKMAL
		1		l		AEAHLEKDALLHHIKKMTVE TAAMSIFTPTNQIRLTNVAVVRMKRAGKRFEI
961	2311	A	8172	1442	682	ACYKNKVVGWRSGVEKDLDEVLQTHSVFVN
	1	1				VSKGQVAKKEDLISAFGTDDQTEICKQILTKG
	1			1		EVOVSDKERHTOLEOMFRDIATIVADKCVNP
	1	ļ	l	1		FTKRPVTVILIERAMKDIHYSVKTNKSTKQQA
		1	-		1	LEVIKOLKEKMKIERAHMRLRFILPVNEGKKL
		1	-			KEKLKPLIKVIESEDYGOQLEIVCLIDPGCFRE
		}				DELIKKETKGKGSLEVLNLKDVEEGDEKFE
962	2312	+A	8175	286	587	NISNKAEVSSHPSVISHSMDSFGQPRPEDNQS
902	23.2	1.	1			VLRRMQKKYWKTKQVFIKATGKKEDEHLVA
			1		ĺ	SDAELDAKLEVFHSVQETCTELLKIEKYQLR
						LNGMKS AEGCAERRGTEPVVELSMSWESGAGPGLGSC
963	2313	A	8181	13	2215	GMDLVWSAWYGKCVKGKGSLPLSAHGIVV
		'		j		AWLSRAEWDOVTVYLFCDDHKLQRYALNKI
1		{			İ	TVWRSRSGNELPLAVASTADLIRCKLLDVIG
		1	ŀ			GI GTDELRLLYGMALVRFVNLISERKTKFAK
						VPLK CLAOEVNIPDWIVDLRHELTHKKMPHI
		1	ĺ			NDCRRGCYFVLDWLQKTYWCRQLENSLRET
				i	1	WELEEFREGIEEEDQEEDKNIVVDDITEQKPE
						PODDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYI
}			{			PKAIKAWNNPSPRVECVLAELKGVTCENREA
1		ļ.		[		VLDAFLDDGFLVPTFEQLAALQIEYEENVDL
l						NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE
				1		DMI SEI PALGISGIRPTYILRWTVELIVANIKI
)			1	ł	1	GRNARRESAGOWEARRGWRLFNCSASLDWI
l			1	İ	ļ	PANYESCI GSPCWASPOLLRIIFKAMGQGLPD
İ						EEQEKLLRICSTYTQSGENSLVQEGSEASPIGK
j	1			1		SPYTI DSI YWSVKPASSSFGSEAKAQQQEEQ
l					*	GSVNDVKEEEKEEKEVLPDQVEEEEENDDQI
					İ	EEEEDEDDEDDEEEDRMEVGPFSTGQESPTA
ŀ		- {	1			ENARLLAQKRGALQGSAWQVSSEDVRWDTI PLGRMPGQTEDPAELMLENYDTMYLLDQPV
	1	-	ł			LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS
1		1	1		1	NFEGLLWSQGQLHGLKTGLQLF
Į .						EPRRNFRDDSTRPRTRGRTRGRRRRACRSAE
964	2314	A	8184	6	1393	GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPF
	i				1	PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGL
	Ì	1				NVGKSTFFNVLTNSOASAENFPFCTIDPNESF
ĺ						VPVPDERFDFLCOYHKPASKIPAFLNVVDIAG
[		Ì				1 VKGAHNGOGLGNAFLSHISACDGIFHLTRA
1				ļ		FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEN
1	1	1	1			GPUDKI EKVAVRGGDKKLKPEYDIMCKVKS
						WVIDOKKPVRFYHDWNDKEIEVLNKHLFLT
1	1	1	1	I		THE COLUMN TENDVIOLENCE IN THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
ŀ		i	ľ		J	KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD KYDPGALVIPFSGALELKLQELSAEERQKYL

SEQ ID No. of nucleotide peptide entered to the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of						Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
mucleotide per per per per per per per per per pe	SEQ ID	SEQ ID	Met	SEQ	Predicted		D=A sportic Acid F=Glutamic Acid.
neutic sequence  1914  1914  1916  1915  1916  1916  1917  1917  1917  1918  1918  1918  1918  1918  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1919  1	NO: of	NO: of	hod				E-Phenylalanine G=Glycine H=Histidine.
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uence  amina acid recidue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence per solo codon, "Possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "Possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "Possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "Possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "Possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "possible aucleotide deletion, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possible nucleotide insertion and per solo codon, "possibl	seq-	uence	1	09/496			O Clusterine P-Arginine S-Serine
residue of peptide sequence per per per per per per per per per pe	uence	1	1	914			C Therein W-Voline W-Treatenhan
peptide sequence    Possible nucleotide diction, impossible nucleotide insertion		İ					
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MCAEGYALSRDRKYCEGNNEW YCEDVNEV AFWNHGCTL GCKNTPGSYYCTCPVGFVLLPD GKRCHQLVSCPRNVSECSHDCVLTSEGPLCF CPEGSVLERDGKTCSGCSSPDNGGCSQLCVPL SPVSWECDCFPGYDLQLDEKSCAASGPQPFL LFANSQDIRHMHFDGTDYGTLLSQQMGMVY ALDHDPVENKIYFAHTALK WIERANMDGSQ RERLIEGGVDYPEGLAVDWIGRFYWTDRGK SLIGRSDLNGKRSKIITIENISQPRGIAVHPMAK RLFWTDTGINPRIESSLQQUGRLVIASSDLIW PSGTIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGEMASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVWGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVLV MLLLSLWGAHYYRTQKLLSKNPKNPYBESS RDVRSRPADTEDGMSSCPQFFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVWERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMWGVQVTEQU ENADRTVQEADEDGDGAVSFVEFTKSLEKM		İ	1	1			KDWAKINFH221 ALCHCECTA AULTWOLVER
AFWNHGCTLGCKNTPGSYYCTCPVGFVLLPD GKRCHQLVSCPRNVSECSHDCVLTSEGPLCF CPEGSVLERDGKTCSGCSSPDNGGCSQLCVPL SPVSWECDCFPGYDLQLDEKSCAASGPQPFL LFANSQDIRHMHFDGTDYGTLLSQQMGMVY ALDHDPVENKIYFAHTALKWIERANMDGSQ RERLIEEGVDVPEGLAVDWIGRRFYWTDRGK SLIGRSDLNGKRSKIITIENISQPRGIAVIPMAK RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGGEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARGISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEFQ LCGMGTEQGCWIPVSSDKGSCPQVWERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYARQLY DLDRDGKISRHEMLQVLRLIMVGVQVTEQUL ENADRTVQEADEDGDGAVSFVEFTKSLEKM		1		1	1		DTWEPEQKLCKLRRGNCSSTVCGQDEQSITEC
GKRCHQLVSCPRNVSECSHDCVLTSEGPLCF CPEGSVLERDGKTCSGCSSPDNGGCSQLCVPL SPVSWECDCFFGYDLQLDEKSCAASGPQFFL LFANSQDRHMHFDGTDYGTLLSQQMGMVY ALDHDPVENKIYFAHTALK WIERANMDGSQ RERLIEEGVDVPEGLAVDWIGRRFYWTDRGK SLIGRSDLNGKRSKITTIENISQPRGIAVHPMAK RLFWTDTGRPRIESSSLQGLGRLVLASSDLIW PSGTIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTONDVGHPFAVAVFEDDYWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNOVTPLDILSKTRVSEDNITESOHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHLCDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HIDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVLV MLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQVBVVIKEHQD LKNGGQPVAGEDQQAADGSMQPTSWRQEFQ LCGMGTEQGCWPVSSDKGSCPQVMERSPH MPSGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV VPLGDRIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKFEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGQVTTEQL ENIADRIVQEADEDGDGAVSFVEFTKSLEKM	1	1		1	1	}	MCAEGYALSRDRRYCEGNDWRICEDVINEC
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SPVSWECDCFGYDLQLDERSCAASGPQFFL LFANSQDIRHMHFDGTDYGTLLSQQMGMVY ALDHDPVENKIYFAHTALKWIERANMDGSQ RERLIEEGVDVPEGLAVDWIGRRFYWTDRGK SLIGRSDLNGKRSKIITIENISQPRGIAVHPMAK RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHFFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSQDDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSSEQYQDDGHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVVLV MLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVWERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIESFFPDGSQRVDFPGFVRVLAHFRP VEOEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVURLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	1			· ·			GKRCHQLVSCPRNVSECSHDCVLTSEGFLCF
LFANSQDIRHMHFDGTDYGTLLSQQMGMVY ALDHDPVENKIYFAHTALKWIERANMDGSQ RERLIEEGVDVPEGLAVDWIGREFYWTDRGK SLIGRSDLNGKRSKIITIENISQPRGIAVHPMAK RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDPLITDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHICLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPHILREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVLV MLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIESFFPDGSQRVDFPGFVRVLAHFRP VEOEDTETQDPKKPEFLNSRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENJADRTVQEADEDGDGAVSFVEFTKSLEKM			ļ	1			CPEGSVLERDGKTCSGC55PDNGGC5QLCVFL
ALDHDPVENKIYFAHTALKWIERANMDGSQ RERLIEEGVDVPEGLAVDWIGRRFYWTDRGK SLIGRSDLINGKRSKITTIENISQPRGIAVHPMAK RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDCKLCSDIDECEMGYPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVGYIGERCQYR DLK WWELRHAGHGQQQK VIVVAVCVVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDFKKPPPLNSRNKLHYAFQLY DLDRDGKISRHEMUQVIRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	1	1		ì	1		SPVSWECDCFPGYDLQLDEKSCAASUPQFFL
RERLIEEGVDVPEGLAVDWIGRRFYWTDRGK SLIGRSDLNGKRSKIITIENISQPRGIAVHPMAK RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCCVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADCSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRNKLHYAFQLY DLDRDGKISRHEMLQVIRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	Ï	<b>.</b>	ĺ	Ì			LFANSQDIRHMHFDGTDYGTLLSQQMGMV1
SLIGRSDLNGKRSKIITIENISOPRGIAVHPMAK RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPYGCSMYARCISEGEDATCQLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHIDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDQQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	1			1		1	ALDHDPVENKIYFAHTALKWIERANMDGSQ
RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLITDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGENASCTINTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVVLV MLLLSLWGAHYYRTQKLLSKNPKNPYESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDPFGFFVXLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	1	į					RERLIEEGVDVPEGLAVDWIGRRFYWIDRGK
PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGIHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLKWWELRHAGHGQQQKVIVVAVCVVVLV MILLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM		1		1	1		SLIGRSDLNGKRSKIITIENISQPRGIAVHPMAK
RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYX DLKWWELRHAGHGQQQKVIVVAVCVVVLV MLLLISLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMOPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIESFFPDGSQRVDFPGFVVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM		ļ		1			RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW
SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGHICLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDK YACNCVVGYIGERCQYR DLK WWELRHAGHGQQQKVIVVAVCVVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	1	- [	1				PSGITIDFLTDKLYWCDAKQSVIEMANLDGSK
LAKPGADPCLYQNGGCEHICKKRLGTAWCS CREGFMKASDGKTCLALDGHQLLAGGEVDL KNQVTPLDILSKTRVSEDNITESQHMLVAEIM VSDQDDCAPVGCSMYARCISEGEDATCQCLK GFAGDGKLCSDIDECEMGVPVCPPASSKCINT EGGYVCRCSEGYQGDGIHCLDIDECQLGVHS CGENASCTNTEGGYTCMCAGRLSEPGLICPD STPPHLREDDHHYSVRNSDSECPLSHDGYCL HDGVCMYIEALDKYACNCVVGYIGERCQYR DLK WWELRHAGHGQQQKVIVVAVCVVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ  967 2317 A 8210 3 601 SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRNKLHYAFQLY DLDRDGKISRHEMILQVIRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM				1	ļ		RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP
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DLKWWELRHAGHGQQQKVIVVAVCVVLV MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ LCGMGTEQGCWIPVSSDKGSCPQVMERSFH MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL DPPHQMELTQ SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL RLHHRFRALDRNKKGYLSRMDLQQIGALAV NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY DLDRDGKISRHEMLQVLRLMVGVQVTEEQL ENIADRTVQEADEDGDGAVSFVEFTKSLEKM	[	1	(	1	}	1	HDGVCMYIEALDKYACNCVVGYIGERCQYR
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ENIADRTVQEADEDGDGAVSFVEFTKSLEKM						1	VEDEDTETQDPKKPEPLNSKKNKLHTAFQLT
	1						DLDRDGKISRHEMLQVLRLMVGVQVTEEQL
DVEHKMSIRILK	1					1	
		ĺ	Í				

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutarnine, R=Arginine, S=Scrine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}		amino acid	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			1	peptide	sequence	/=possible nucleotide deletion, \=possible
		Ì		sequence		nucleotide insertion
260	2210	-	8211	2	409	ISSCPHTAYEGSMSTLSNFTQTLEDVFRRIFIT
968	2318	A	0211	1		YMDNWRONTTAEOEALQAKVDAENFYYVIL
	]	}		1	1	YLMVMIGMFSFIIVAILVSTVKSKRREHSNDP
	1	}		<u> </u>		YHQYIVEDWQEKYKSQILNLEESKATIHENIG
		1		ł		AAGFKMSP
969	2319	A	8215	1	1938	GMPRSRGGRAAPGPPPPPPPPGQAPRWSRWR
707		}			1	VPGRLLLLLPALCCLPGAARAAAAAAGAGN
	i	}	Ì	]		RAAVAVAVARADEAEAPFAGQNWLKSYGY
	i	1				LLPYDSRASALHSAKALQSAVSTMQQFYGIP VTGVLDQTTIEWMKKPRCGVPDHPHLSRRRR
	[	1	1		ł	NKRYALTGQKWRQKHITYSIHNYTPKVGELD
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		1				VAVHELGHALGLEHSSDPSAIMAPFYQYMET
		1	1	1		HNFKLPODDLQGIQKIYGPPAEPLEPTRPLPTL
		1		1		PVRRIHSPSERKHEROPRPPRPPLGDRPSTPGT
	1					KPNICDGNFNTVALFRGEMFVFKDRWFWRL
	}	1		1		RNNRVQEGYPMQIEQFWKGLPARIDAAYER
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}		l	Ì	1		MYTINDVPGSVNAVAVVIPCILSLCILVLVYTI
	1	1	Ì			FQFKNKTGPQPVTYYKRPVQEWV
			8216	1235	2223	SRISLOFYVSFRRTGLFTCKLIVEIFFRNYMN
970	2320	Α	8210	1233	2223	DSLRTNVFVRFOPETIACACIYLAARALQIPLP
	1					TRPHWFLLFGTTEEEIQEICIETLRLYTRKKPN
		1				YELLEKEVEKRKVALQEAKLKAKGLNPDGTP
1	1	}	1			ALSTLGGFSPASKPSSPREVKAEEKSPISINVK
1		- [				TVKKEPEDRQQASKSPYNGVRKDSKRSRNSR
		-	1	}		SASRSRSRTRSRSRSHTPRRHYNNRRSRSGTY SSRSRSRSRSHSESPRRHHNHGSPHLKAKHTR
[	-			1		DDLKSSNRHGHKRKKSRSRSQSKSRDHSDAA
	ì		ļ	}		KKHRHERGHHRDRRERSRSFERSHKSKHHGG
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					3274	DCRLOAAMPTNFTVVPVEAHADGGGDETAE
971	2321	Α	8217	3	3214	RTEAPGTPEGPEPERPSPGDGNPRENSPFLNN
		1		1		VEVEOESFFEGKNMALFEEEMDSNPMVSSLL
1						NKLANYTNLSOGVVEHEEDEESRRREAKAPR
				1		MGTFIGVYLPCLONILGVILFLRLTWIVGVAG
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1	1	1		l l	l	A DEPLEIA MAIGCLE LIME LARGING 111
}						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLI GNRTLSRRSFDACVKAYGIHNNSATSAL
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSOPSAACDEYFIONNVTEIQGIPGA
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AFESRASTLPYVLTDIAASFTLLVGIYFPSVTG
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAOKSIPTGTILAIVTTSFIY
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLOTLTGAPRLL
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLOTLTGAPRLL
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL OAIARDGIVPFLOVFGHGKANGEPTWALLLT
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL QAIARDGIVPFLQVFGHGKANGEPTWALLLT VI.ICETGILIASLDSVAPILSMFFLMCYLFVNL
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL QAIARDGIVPFLQVFGHGKANGEPTWALLLT VLICETGILIASLDSVAPILSMFFLMCYLFVNL ACAVQTLLRTPNWRPRFKFYHWTLSFLGMSL CLALMFICSWYYALSAMLIAGCIYKYIEYRG
						AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA AMLHNMRVYGTCTLVLMALVVFVGVKYVN KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV, CLLGNRTLSRRSFDACVKAYGIHNNSATSAL WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL QAIARDGIVPFLQVFGHGKANGEPTWALLLT VI.ICETGILIASLDSVAPILSMFFLMCYLFVNL

				5 3:44	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D-Aspartic Acid F=Glutamic Acid,
10: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	i	in USSN	location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
otide	seq-	1	09/496	correspondi	to last amino	M=Methionine N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		Ì	717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	}	1		peptide	1	/=possible nucleotide deletion, \=possible
		1 .		sequence		nucleotide insertion
	<del> </del>	<del> </del>		<del>                                     </del>		LKAGKGLTIVGSVLEGTYLDKHMEAQRAEE NIRSLMSTEKTKGFCQLVVSSSLRDGMSHLIQ
						SAGLGGLKHNTVLMAWPASWKQEDNPFSW
	1	İ	ì	ì	)	KNFVDTVRDTTAAHQALLVAKNVDSFPQNQ
	}	1				ERFGGGHIDVWWIVHDGGMLMLLPFLLRQH
	1	}			}	KVWRKCRMRIFTVAQVDDNSIQMKKDLQMF
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	1			1		L VI NGVVI NKSODAOLVLLNMPGPPKNKQUD
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			8224	701	246	TEDDUTMKENPFUTSDRSKNRKRHENAPSHV
972	2322	Α	8224	1 /01		DDKIMSSPI SKELROKYNVRSMPIRKDDEVQ
	1	1				LANDCHYKGOOIGKVVOVYRKKYVIYIEKYV
			1			REKANGTTVHVGIHPSKVVITRLKLDKDRKKI
						LERKAKSRQVGKEKGKYKEELIEKMQE
973	2323	A	8237	873	4610	GCPHAGGKGRVPTGGLTGGRTWSPSAAPRSC PRPGPTPAPGAMDKLPPSMRKRLYSLPQQVG
913	2323	1.	-	,	1	AKAWIMDEEDAEEEGAGGRQDPSRRSIRLR
		1	1			PLPSPSPSAAAGGTESRSSALGAADSEGPARG
		1			ì	AGKSSTNGDCRRFRGSLASLGSRGGGSGGTG
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		1		1	}	CI A AEPERPGASAOPAASPPPPQQPPQPASAS
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		1		}		OAGEMOROFGAMLOPGVNKFSLRMFGSQKA
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		- 1				LI MOGNI HIPVGITFFKDENTTPWIVEN VOD
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			l	1	}	YLKSWFMVDFISSIPVDYIFLIVETRIDSEVYK
1		(	{			TARALRIVRFTKILSLLRLLRLSRLIRYIHQWE
1						EIFHMTYDLASAVVRIVNLIGMMLLLCHWDG CLQFLVPMLQDFPDDCWVSINNMVNNSWGK
İ		Ì		1.		QYSYALFKAMSHMLCIGYGRQAPVGMSDV
ł				İ	ļ	WLTMLSMIVGATCYAMFIGHATALIQSLDSS
Į.			l l	1		RRQYQEKYKQVEQYMSFHKLPPDTRQRIHD
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		- [		2	j	PODVIDECTICKKMYFIOHGVVSVLINGNAE
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			ļ			OWOUDDEMAHCAHRVOAAASAIPIPIPVIW
		1	}	1	Į.	TRI IOADI OAAAATTSVAIALIHHPKLPAALFA
	}	- 1	1	1		DDDCGCI GNI GAGOTPRHLKKLUSLIPSALUS
		ļ	1			A CDA CCPCOVDTPSSSSFHIOOLAGFSAFAULS
		- 1				DI I DOSSSSPPPGACGSPSAPIPSAGVAATIA
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						DCI VACASGGASPVGFTPRGGLSPPGHSPUFF
		1		}		DITEDS APPRASGSHGSLLLPPASSPPPPQVPQK
		}		1		P GTPPI TPGRLTODLKLISASQPALPQDGAQI
	1	1		1	1	T DD A SPHSSGESMAAFPLFPRAGGGSGGSGSS
		1				CCI CPPGRPYGAIPGOHVTLPRKTSSGSLPPP
1	}		}	}		LSLFGARATSSGGPPLTAGPQREPGARPEPVR
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074		<del>-   -</del>	8247	279	468	EYKQWERRFLSCQNRNDLGYGKPRKGGGLL
F 974	2324	A	0247	1		LVPVKDASRICSLTYLLGSHWNNLVVRSPVL
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					D. Jirand and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	De A enertic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide location	corresponding	I=Isoleucine K=Lysine, L=Leucine,
eotide	seq-	İ	USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine V=Valine, W=Tryptophan,
	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		(		peptide		/=possible nucleotide deletion, \=possible
		1		sequence	,	nucleotide insertion
	2325	A	8249	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYM
975	2323	1 ^	102.5	]	ł	MTKVLGMAPVLGPRPPQEQVGPLMVKVEEK
				1		EEKGKYLPSLEMFRQRFRQFGYHDTPGPREA LSQLRVLCCEWLRPEIHTKEQILELLVLEQFLT
		1	· I	l	1	ILPQELQAWVQEHCPESAFEAVTLLEDLEREL
					1	DEPGHQVSTPPNEQKPVWEKISSSGTAKESPS
	1	Ì		į		SMQPQPLETSHKYESWGPLYIQESGEEQEFAQ
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	1	1		ì	ļ	Direvitank PEASLEROCVNLENERGIAPPLQ
	į			1	1	FACSKKGRESVPTKPTPGERRYICAECGKAFS
		1	Ì			NISSNI TKHRRTHTGEKPYVCIKCGKAFSHSS
	1					NI TI LIVETHI VDRPYDCKCGKAFGQSSULLK
						HORMHTEFAPYOCKDCGKAFSGKGSLIKHIK
		i			1	TUTGERPYOCNECGKSFSOHAGLSSHQKLIT
	1		1	l .	1	GEVDVKCKECGKAFNHSSNFNKHHRIHIGEK
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0.77	2326	A	8257	298	7086	GNMACWPQLRLLLWKNLTFRRRQTCQLLLE
976	2320	1"		}	}	VAWPLFIFLILISVRLSYPPYEQHECHFPNKAM PSAGTLPWVQGIICNANNPCFRYPTPGEAPGV
			.	1		VGNFNKSIVARLFSDARRLLLYSQKDTSMKD
		1			ì	MRKVLRTLQQIKKSSSNLKLQDFLVDNETFS
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1		Ì	ļ			TFYDNSTTPYCNDLMKNLESSPLSRIIWKALK
1		1	l l	1		PLLVGKILYTPDTPATRQVMAEVNKTFQELA
1			ĺ			VFHDLEGMWEELSPKIWTFMENSQEMDLVR MLLDSRDNDHFWEQQLDGLDWTAQDIVAFL
İ					1	AKHPEDVQSSNGSVYTWREAFNETNQAIRTIS
1	ŀ	l	1		1	RFMECVNLNKLEPIATEVWLINKSMELLDER
1	1	}			1	VEWAGIVETGITPGSIELPHHVKYKIRMGIUN
	1	)	1	İ		VERTNKIKDGYWDPGPRADPFEDMRYVWGG
	1			1		FAVI ODVVEOAIRVLTGTEKKTGVYMQQMP
				1	1	VPCVVDDIFI RVMSRSMPLFM1LAWI1SYAY
1	1		1	1		TIK CIVVEK FARLKETMRIMGLDNSIL WESWEL
				1	ł	SCI IDI I VSAGLI VVILKLGNLLPYSDPSVVFV
						FI SVEAVVTILOCFLISTLFSRANLAAACGGIL
)				ì		VETT VI PVVI CVAWODYVGFTLKIFASLLSP
		1				VAFGFGCEYFALFEEQGIGVQWDNLFESPVE
		1		1	ĺ	EDGFNLTTSVSMMLFDTFLYGVMTWYIEAVF
.	1	1			1	PGQYGIPRPWYFPCTKSYWFGEESDEKSHPGS NQKRISEICMEEEPTHLKLGVSIQNLVKVYRD
1		(	ĺ		Ì	MOKRISEICMEEEPTHLACOVSIQUE VA VIOLE GMKVAVDGLALNFYEGQITSFLGHNGAGKT
		1	1	\	İ	TTMSILTGLFPPTSGTAYILGKDIRSEMSTIRQ
				\ \	1	NI CVCPOHNIVI FDMI TVEEHIWF YAKLKULS
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						GCMORKI SVALAFVGGSKVVILDEPTAGVDF
				1		Vede CIWELL KYROGRTIILSTHHMULAUYL
1	Ì					CDRIATISHICKI CCVGSSLFLKNOLGTGYYLL
1		1				I VENDUESSI SSCRNSSSTVSYLKKEDSVSQS
						SCDAGI GSDHESDTI.TIDVSAISNLIKKHVSEA
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1	ı	l l	1	)		DRLSDLGISSYGISETTLEEIFLKVAEESGVDA
	1	1		1	L	I DKESDEGISS I GISET I BEEN
						ETEDGTI PARRNRRAFGDKOSCLRPFTEDDA
						ETSDGTLPARRNRAFGDKQSCLRPFTEDDA ADPNDSDIDPESRETDLLSGMDGKGSYQVKG WKLTQQQFVALLWKRLLIARRSRKGFFAQIV

SEQ ID No. of nod-peptide colide sequence uence of the peptide colide sequence of the peptide colide sequence of the peptide of the peptide uence of the peptide colide sequence of the peptide of the peptide of the peptide of the peptide of the peptide of the peptide of the peptide of the peptide of the peptide sequence of the peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence of peptide sequence o						Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO. cit in contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the co	SEO ID	SEQ ID	Met	SEQ	Predicted		D-Amartic Acid F=Glutamic Acid,
nucle coide sequence 914  USSN 949  UENCE 914  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 917  UENCE 91	NO: of	NO: of	hod	ID NO:			F=Phenylalanine, G=Glycine, H=Histidine,
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HAISSELNYINNALIRANLUKGENSHATUAN NIPELNITKOOLSEVAMTISVOVUSICVIFA MSFVASFVVTLIQERVSKAHLIQFISGKEVI YWLSNFVWDMCNYVYPATLVIIIFICFOQKSY YWSTRILPVLALLLLLYGWSITPLMYPASFVYR PSTAYVVLTSVALFIGINSATFVLELFTDN KLANINDILKSVFLIPHFCLGRGLIDMYKNQ AMADALERFGERFKYPSLEWIDVGRNIFAM AVBOVVFFLITVLIQVRFFIRPRPVNAKLSFLN DEDEDVRERGRILDGGGODILEIKELTNY RRKKKPAVDRICVGIPPGECFGLLGVNGAGK SSTFKMLTGDITVTRODAFLNRNSLISHHEV HQNMGYCPFDAITELLTGRHVYEFFALLRG VPEKEVGKVGEWAIRKLGLVRYGEKYAGNY SGGNKRKLSTAMALIGGPFVVFLDEFTTOMD PKARRFLWNCALSVVKEGRSVALTRSMEEC EALCTRMAIMVNGRFRCLGSVQHLKNRFGD GYTIVVRIAGSNPDLKPVQDFFGLAFFGSVPK EKHNMG.YQLPSSISSLARIFSILSQSKKRLH IEDYSVSQTTLDQVFVNFAKDQSDDHLKDL LIHKNQTVVDAVLTSFLQBEVVKESYV PGSTISFSLCFIPPFCVFTMYRKFVVSTISKGG VLQGNVNGRLSIGNKEPGGEVYQLKRKV TLLRGVSIIIGTIIGAGFISPKGVLQNTGSVGM SLITWTVCQVLSLFGALSYAELGTTIKKSGGH YTYTLEVFGPLPAFVRVWVELLIRPAATAVIS LAFGRYLEPFFIQCEPELKLITALLITVPGV MOLIKGGTQNFKDAFSGRDSSITTLPLAFYYG MYAYAGWFVLNVTEEVENPEKTIPLACISM AIVTIGYVLTNVAYFTITNAEELLISNAAVT FSERLLGNRSLAYPFVALSCFGSMNGGVFAV SRLFYVASREGHLPELSMHTNKTHPLAFYYG VAGGIVVRTNVAYFTITNAEELLISNAAVT FSERLLGNRSLAYPFVALSCFGSMNGGVFAV SRLFYVASREGHLPELSMHTNKTHPLAFYYG LAPALSLYSDPFSTIGLGFVITLTOVAPAYYLFII WDKKPR WFRIMSEKITRTQJILEVYPEDKL VAGGIVLRYKCPDMHRFFKVPLFIPLAISFTC LEMVALSLYSDPFSTIGGFVITLTOVAPAYYLFII WDKKPR WFRIMSEKITRTQJILEVYPEDKL FRYDLENSLAGREPHLSSACEKQVHEVGLD GTETYLPLISNSQNLARLAQRIPSGSGSEE EEAAGTEGDAGEWPAGSSADQDDEGGVVK FOPSL WFRINSEKITRTQJILEVYPEDKL ROGSLCVIKSNGQNAPINGLGGISYPR AGSLEPTHERSSACEKQVHEVGLD GTETYLPLISNSQNLARLAQRIPSGSGSEE EEAAGTEGDAGEWPAGSSADQDDEGGVVK FOPSL WFRINSENALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPFKQNFQTIQLISK KKSLAGAAQILKGAGRALGGLSYPRS AGSLEPTHERSTFGTEVINTDLDLDKKREDDVCPL DVOJPSDLEGSAYKVSIQQAPDIGDLGTVN LFREPLENSKPSSPBWYLLEKAAQNVLLCKEI FAGLSREANDIKSSOKFATKSSIGACKGYHEVGLD LFREPLENSKPSSPBWYLLCKEI FAGLSREANDIKSSOKFATKNSIGQQAPDIGDLGTVN LFREPLENSKPSSPBWYLLCKEI FAGLSREANDIKSSOKFATKNSIGQCAPDIGDLGTVN LFREPLENSKPSSPBWYLGLEAAQNVLLCKEI FAGLSREANDIKSSOKFATKNSIGGRAPINGTGFFSVLC ROGSLECKNSSRDWSSOKFATKNSIGGRAPINGTGFFSL	1		1	1		1	NTQALPPSQEVNDAT KQWKKITEKE ACCOUNT
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AVEGVYFFLITVLIOYRPHER/RVNAKJ. IAN DEDEDVRERORILDGGGONDILEIKELTKIY RKRKRPAVDRICVGIPPGECFGLIGVNGAGK SSTFKMLTGDTTVTRDDAFLNKNSILSNIHEV HONMGYCPQFDAITELLTGREHVEFFALLRG VPEKEVGKVGEWAIRKLGLVKYGEKYAGNY SGGNKRLSTAMALIGGPPVYFLDEPTTGMD PKARRPLWNCALSVVKEGRSVVLTISIKSMEEC EALCTRMAIMVNGRFECLGSVOHLKNRFGD GYTIVVRIAGSNPDLKPVQDDFFGLAPPGSVYK EKHRNNLQVQLPSSLSSLARIFSILSGKKRLH IEDVSVSQTTLDQVFVNPAKDQSDDDHLKDL SLHKNQTVVDVAVLTSTQDBKVKESYV PGSTISFSLCPIPPCVPTMVRKPVVSTISKGG YLQGNNNGRLPSLGNKEPPGQEKVQLKRKV TILRGVSIIIGTIIGAGIPPKGVQLONTGSVGM SLTIWTVCQVLSLFGALSYASLGTTIKKSGGH YTYILEVFGPLPAFVRVWZLLIRPAATAVIS LAFGRYLEPFFTQCEIPELAIKLITAVGITVVM VLNSMSVSWSARIQIFLTFCKLTALLIIVPGV MQLIKGGTQNFKDAFSGRDSSITRLJAFYYG MYAYAGWFYLNVTTEEVENPEKTTPLAICISM AIVTIGVYLTNVAYFTTNAEELLSNAVAYT FSERLIGNISLAVPIVVALSCFGSMNGGVFAV SRLFYYASREGHLPELSSMIHVRKHTPLFAVIV LHPLTMIMLFSGDLSLNFLSFARWLFIGLA VAGLIYLRYKCPDMHRPFKVPLFIPALFSTFC LFMVALSLYSDPFSTCIGFVITLTQFVAYVLFII WDKKPRWFRINSEKITRTLQIILEVVPEEDKL RHGGGLLSSRLSGKPPLRTSFFGSWGVLPF LADAASMSGVRAVRISIESACKQVHEVGLD GTETYLPPLSMSQNLARLAQRIDFSGGSGSE EAAAGTEGDAQEWGAGSSADQDDEGVVK FQPSLWPWDSVRNILRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDPNSELLRLRQHWKLRVGDKLGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKJPEDVCPL DVQPSDLEGSAYIKVSQKQAPDIGDLGTVN LFKRPPLFKSKPGSSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVXNQOLSOPFPSLQ LEGG PLANSNING VGRATTKOCCPEDHLYVLE FAQLSREAVQIKSQVPHIVXNQOLSOPFPSLQ			- [		1		AMADALERFGENRFVSPLSWDLVGKNLFAM
DEDEDVRERQRILDGGGQNDILEISELTAT RKRKPAVDRICVGIPGECFGLLGVNGAGK SSTFKMLTGDTTVTRGDAFINNSILSNIHEV HQNMGYCPQFDAITELLTGREHVEFFALLRG VPEKEVGKVGEWAIRKLGLVKYGEKYAGNY SGGNKRKLSTAMALIGGPFVVFLDEPTTGMD PKARRFLWNCALSVVKEGRSVVLTSHSMEEC EALCTRMAIMVNGFFCLGSVOHLKNRFGD GYTIVVRIAGSNPDLYVLDSHSMEEC EALCTRMAIMVNGFFCLGSVOHLKNRFGD GYTIVVRIAGSNPDLYVLTSHSQSKKRLH IEDYSVSQTTLDQVFVNFAKDQSDDDHLKDL SHKNOTVDVDAVLTSFLQDEKYKESYV IPGSTISFSLCFIFPFCVFTWKFPVGSTSKGG YLQGNVNGRLPSLGNKEPFGGEKVLKRKV TLLRGVSIIGTIIGAGIFISPKGVLQNTGSVGM SLTIWTVCGVLSLFGALSYAELGTTIKKSGGH YTVILEVFGPLPAFVVWELLIIRPAATAVIS LAFGRYLLEPFFIQCEIPELAIKLITAVGITVVM VLNSMSVSWSARIQIFLTFCKLTALIILVPGV MQLKGGTQNFKDAFSGRDSSITRLPLAFYG MYAYAGWFYLNFVTEEVEPBEKTIPLAICISM AIVTIGVYLTNIVAYFTTINAEELLISNAVAVT FSERLLGNFSLAVPFVALSCFGSMNGGVFAV SRLFYVASREGHLPELSMHVKRHFLPAVIV LHHLTMIMLFSGDLDSLLNFLSFARWLFIGLA VAGLIVLRYKCPDMHRPFKVLFPALFSFTC LFMVALSLYSDPSTGIGFVITLTGVPAYYLFII WDKKPRWFRIMSEKITRTLQIILEVVPEEDKL RGGSLRCVLGKLLGQLCFGSERCVRFPGGLL CLFMVALSLYSDPSTGIGFVITLTGVPAYYLFII WDKKPRWFRIMSEKITRTLQIILEVVPEEDKL RGGSLRCVLGKLLGQLCFGSERCVRFPGGLL STRLSAGGRPPLRTSFFGSWGVLP LADAASMSGVRAVRISESACKQVHEVOLD GTETTYLPPLSMSQNLARLAQRIDFSQGSGSEE EAAGTEGDAQEWPGAGSSADQDDEGVVK FQPSLWPWDSVRNILRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPPKQPPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDPNSELLRLRQNMLRKYGDGLIGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQPSDLEGSAYTKVSQKQAPDIGDLGTVN LFKRPLPKSKPGSSPHWQTKLEAAQNVLLCKEI FAQLSREAVQKSQYPHVVKNQILSQFFPSLQ LEDG CHSNDLW KOKFATKOCGEDHLYVLE FAQLSREAVQKSQYPHTVKNQILGDLSYRS			1	1	ł	ļ	A VEGUVEELITYLIOYREEIRPRPYNANDSLUN
SSTFKMLTGDTTVTRGDAFLNRNSLISNHEV HQNMGYCPOFDAITELLTGREHVEFFALLRG VPEKEVGKVGEWAIRKLGLVKYGEKYAGNY SGGNKRKLSTAMALIGGPPVVPLDEPTTGMD PKARRFLWNCALSVVKEGRSVVLTSHSMEEC EALCTRMAIMYNGRFRCLGSVQHLKNRFGD GYTIVVRIAGSNPDLKPVQDFFGLAFPGSVPK EKHRNMLQYQLPSSLSSLARIFSILSOSKKRLH IEDYSVSQTTLDQVFVNFAKDQSDDHLKDL SLHKNQTVVDVAVLTSFLQDEKVKESYV  1605TISFSLCFIPPFCVPTNWRKPVSTISKGG YLQGNVNGRLPSSLGNKEPPGGEKVQLKRKV TLLRGVSIIIGTIIGAGIFISPKGVLQNTGSVGM SLTINTVCGVLSLFGALSYAELGTTIKKSGGH YTVILEVFGPLPAFVRVWVELLIIRPAATAVIS LAFGRYILEPFFIQCEIPELAIKLITAVGITVVM VLNSMSVSWARGIFLTFCKLTAILIIVPGV MQLIKGQTQNFKDAFSGROSSITRLPLAFYYG MYAYAGWFYLNFVTEEVENPEKTIPLAICISM AIVTIGYVLTNVAYFTITNAEELLLSNAVAVT FSERLIGNFSLAVPIFVALSCGSMNGQVFAV SRLFYVASREGHPELSMHVRKHTPLPAVIV LHPLTMIMLFSGDLDSLLNFLSFARWLFIGLA VAGLIYLRYKCPDMHRPKVPLFIPALFSFTC LFMVALSLYSDPFSTIGGFVITLTGVPAYYLFII WDKKPR WFRIMSEKITRTLQIILEVVPEEDKL RGGSLRCVLGKLIGQLLCFOSERCVRFPEGIL RHRGCGLLSSRLSAGKPPLRTSFFGSWGVLPP LADAASMSGVRAVRISISACEKQVHEVGLD GTETYLPPLSNSQNLARLAQRIDFSQCSGSEE EEAAGTEGDAQEWPGAGSSADQDDEEGVVK FQPSLWPWDSVRNLRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPFKQNPQTLQLISK KKSLAGAAQILLKGAETLKSVTENGENKLQ RDFNSELLRL RQHWKLRKVGDKRLIGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKPEDSPCYL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRFLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVYKNQIISGPPFSLQ LSTREYLCHSSNUKKSOKKFATEKOCFEDHLYVLE	1	1	Ì	- 1			DEDEDVERFRORILDGGGONDILEINELINI
HQNMGYCPGFDAITELLTRIKHNYFALLKU VPEKEVGKVGEWARKLGLVXYGEKYAGNY SGONKRKLSTAMALIGGPFVYFLDEPTTGMD PKARRFLWCALSVVKEGRSVVHLDEPTTGMD PKARRFLWCALSVVKEGRSVVHLNRFGD GYTIVVRIAGSNPDLKPVQDFFGLAFPGSVPK EKHRNMLQVQLSSLSIS.ARRISILSQSKKRLH IEDYSVSQTTLDQVFVNFAKDQSDDHLKDL SLHKNQTVVDVAVLTSFIJQBEKVKESYV PKEYSTIFPCVPTNWYRKPVVSTISKGG YLQGNVNGRLPSLGNKEPPGGEKVQLKRKV TLLRGVSIIIGTIIGAGIFISPKGVLQNTGSVGM SLTTUVLCGVLSLFGALSVAELGTTIKKSGGH YTVLEVFGPLPAFVRVWELLIRPAATAVIS LAFGRYLLEPFFQCEIPELAIKLIRVATGIVVVM VLNSMSVSWSARIQIFLTFCKLTAILIIVPGV MQLKKGQTQNFKDAFSGRDSSITRLPLAFYYG MYAYAGWFYLTVFTEEVENPEKTIPLAICISM AIVTIGVVLTNVAYFTTINAEELLLSNAVAVT FSERLLGNFSLAVPIFVALSCGSMNGGVPAV SRLFYVASREGHLPEILSMIHVRKHTPLPAVIV LHPLTMIMLFSGDLDSLLNFLSFARWLFIGLA VAGLIYLRYKCPDMHRPFKVPLFIPALFSFIC LFMVALSLYSDPFSTGIGFVITLTGVPAYYLFII WDKKPR WFRIMSSKITRTLQIILEVVPEEDKL WDKKPR WFRIMSSKITRTLQILLEVVPEEDKL RHRGCOLLSSRLSAGKPPLRTSFFGSWGVLPP LADAASMSVRAVRISIESACEKQVHEVGLD GTETYLPPLSMSQNLARLAQRIDFSQGSGSEE EEAAGTEGDAQEWFGAGSSADQDDEEGVVK FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPFKQNPOTLQLISK KKSLAGAQLILKGAERLTKSVTENQENKLQ RDFFNSELLRIR.GHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIFSDLEGSAYIKVSIGKQAPDIGDLGTVN LFKRFLPKSKFGSFHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSTELLCHSSNINK KSNKK SIGKQAPDIGDLGTVN LFKRFLFKSFROSFHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVFHIVVKNQIISGPFPSLQ LSTELLCHSSNINK KSNKK SIGKGAPPHIVYLE	1		1	1		1	RRKRKPAVDRICVGIPPGECFGLLGVNGAGK
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					D. disead and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
uci-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
ence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
icuc.		ļ	i	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		l	1	residue of	sequence	Y=1 yrosine, X=Unknown, -stop codon,
	ļ	ļ	1	peptide		/=possible nucleotide deletion, \=possible
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SEQ ID   SEQ ID   Mod   SEQ   Mode   Deginning in unclotted   Device   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Deginning   Degin							// Alaria C-Custaina
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			hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
USSN		1	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
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	i		i				M=Methionine, N=Asparagine, P=Proline,
### ### ### ### ### ### ### ### ### ##		uence	ļ	i			O=Glutamine, R=Arginine, S=Serine,
	uence	1	1	914			T=Threonine V=Valine W=Tryptophan.
Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Peptide   Pept	<b>\</b>						V=Turcoine Y=Unknown *=Ston codon
	l					sequence	1-Tyloshie, A-olikhown, Stop codon,
PEGDRTLFQWFVILDPGMSLTDRGVMSYLT	j	ļ	}	ļ	peptide	l	/=possible nucleotide deletion, /-possible
RRIVISCI.GGGI.ALI.WRAGGWI.WAQRI.GHOFT   TYWAYSELLI.PNSGIGPDGEVYENDKEGGWF   DI.GPPIVGSI.GPPDLIFFTEGGSRSPRYALWF   VICESWPQDQPWTKILMWYKVYFICLRALIVE   WARVGGASSLENTVDLHISNSHPLSLTSDQY     AMNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIVADAGAFLRHAALQDIGKNIV     ANNAPVERIPORGAKACPERILLESSEN     ANNAPVERIPORGAKACPERILLESSEN     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAPVERIPORGAK     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR     ANNAP CHEMINAR		1	1		sequence		nucleotide insertion
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DLGPPIVGSLGPPDLITTIEGGGRSPRYALIVE   VGESWPQDQPWTKLMYKVVYTCLRALIVE   MARVGGASSLENTVDLHINNSHPLSLTSDQY     AVAIQDLVEGMEPOGPGES     AVAIQDLVEGMEPOGPGES     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIQDLVEGMEPOGPGES     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNY     AVAIAPVERIVADAGAFLRHAALQDIGKNE     AVAIAPVERIVADAGAFLRHAALQDIGKNE     AVAIAPVERIVADAGAFLRHAALQDIGKNE     AVAIAPVERIVADAGAFLRHAALQDIGKNE     AVAIAPVERIVADAGAFLRHAALQDIGKNE     AVAIAPVERIVADAGAFLRHAALQDIGKNE     AVAIAPVERIVADAGAFLRHAALAALAALAALAALAALAALAALAALAALAALAALAAL	1	ļ	1				TVWAVSEELLPNSGHGPDGEVPKDKEGGVF
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984   2334   A   8321   1   1243	ì	1	1	1		1	MARVGGASSLENIVDLHISNSHPLSLISDQI
TIREVYTERDKATERRIA VLPYELEFKEPLPE	Į.			1	1		KAYLQDLVEGMDFQGPGES
TIREVYTEIRDKATRRILAVLPYELIFKEPLPE	004	2224	<del>                _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _   _  </del>	8321	1	1243	ANMAPVEHVVADAGAFLRHAALQDIGKNIY
YVRLVTEFSKKTGDYPSLSATDIQVALTYQL   EARFVGVSHLKQEPQKVKVSSIQHPETTLHIS   GFILPYKPKPPOETEKGHSACEPENLEFSSFM   FWRNPLPNIDHELQELLIDREDVPSEEEEEE     NGFEDRKDDSDDDGGGWTFSNIKOJQQELE   QCDVPEDVRYGCLTTDFAMQNVLLQMGLHV   LAVNGMLIRRARSYLRGGFKTSDMSRV   KVLNPRGLRSVSLPTFKGGKYANPHLTEDQRF   PQLRLSQKARQKTNVPAPDYIAGVSPFVENDI   SSRSATLQVRDSTLTGAGRKYANPHLTEDQRF   PQLRLSQKARQKTNVPAPDYIAGVSPFVENDI   SSRSATLQVRDSTLTGAGRKYANPHLTEDQRF   PQLRLSQKARQKTNVPAPDYIAGVSPFVENDI   SSRSATLQVRDSTLTGAGRKYANPHLTEDQRF   PQLRLSQKARQKTNVPAPDYIAGVSPFVENDI   SSRSATLQVRDSTLTGAGRAFUNPASRKKFV   KKR   RNNNIRQFMKVCISQQARWITPVVPVLWET   EAGRSLELKSLRPAWATWGNPISTKINK     986   2336   A   8325   89   1172   KMNPTDIADTILDESIYSNVYLYL   FSYREPCTKE   GRKAFGELFLPPLYSLVVFGLLGNSVVVLVL   FKYRLRSMTDVYLLKLAISDLLFVFSLPFWG   YYAADQWYGGLGLCKMISWMYLVGFYSGIF   FVMLMSIDRYLAIVAVFSLRARTLTYGVITS   LATWSVAVFSLRGHTFYLTYGVITS   LATWSVAVFSLRGHTFYCKT   KYSLNSTTWKVLSSLENILGLVIPLGIMLFCY   SMIRTLOHCKNEKKNKAVAMMFAVVVLFLG   FWTPYNIVLFLETLYELEVLQDCTFREYLDVA   QATETLAPHCCNPHTYFFLGEKFRKYILQL   FKTCRGLFVLCQYCGLLQIYSADTPSSSYTQS   TMDHDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDHDAL   TMDHDAL   TMDHDHDAL	0521	1		TIREVVTEIRDKATRRRLAVLPYELRFKEPLPE			
EALFVGVSHLKQEPQKVKVSSIQHFETLHIS	i						VVRI VTEFSKKTGDYPSLSATDIOVLALTYQL
GFILPYKPKPPQETEKGHSAGEPENLEFSSFM   FWRNPLPNIDHELQELLIDGEDYPSEEEEEE   NGFEDRKDDSDDDGGWTPSNIKQIQGELE   QCDVPEDVPVQCLTIDFSNIKQIQQELE   QCDVPEDVPVQCLTIDFSNIKQIQQELE   QCDVPEDVPVQCLTIDFSNIKQIQQELE   QCDVPEDVPVQCLTIDFSNIKQIQQELE   QCDVPEDVPVQCLTIDFSNIKQIQQELE   QCDVPEDVPVQCLTIDFSNIKQIQQELE   QCDVPEDVPVQCLTIDFSNIKQILHMEFSNIP   KVLNPRGLRYSLPTFKGGKYAINPHLTEDQRF   PQLRLSQKARQKINVFAPDYLAGYSPVENDI   SSRSATLQVFDSTLGAGRRILNPNASRKKFV   KKR   RXNNIRQFIMKVCISQQARWLTPVVPVLWET   EAGRSLELKSLRPAWATWGNPISTKINK   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR   KKR		1	1	1		1	EAREVGUSHI KOFPOKUKUSSSIOHPETPLHIS
FWRNPLPNIDHELQELLIDRGEDVPSEEEEEEE   NGFEDRKIDSDIDGIGGGWTFSNIKQIQQELE   QCDVPEDVRVGCLTTDFAMQNVLLQMGLHV   LAVNGMLIREARSYIL RCIGYTTSDMSRV     FCSHCOKKILKKVSVTVSDDGTLHMHFSRNP     KVLNPRGLRYSLFTFKGGKYAINPHATEDQRF     PQLRLSQKAQKINVPAPPYIAGVSPFVENDI     SSRSATLQVRDSTLGAGRRRLNPNASKKEV     KKR     RRNNIRQFIMKVCISGQARWLTPVVPLWET     EAGRSLELKSIRPAWATWGMPISTKINK     KKR     RRNNIRQFIMKVCISGQARWLTPVVPVLWET     EAGRSLELKSIRPAWATWGMPISTKINK     KMNPTDIADTTLDESIVSNYYLYESPEPCTKE     GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL     FKYKRIRSMIDVYLLNAISDLLFVFSLPPWG     YYAADQWVFGLGLCKMISWMYLVGFYSGIF     FVMLMSIDRYALAVIAVSIRARITLTYGVITS     LATWSVAYFASLFGFLFSTCYTERMITYCKT     KYSLNSTTWKVLSSLEDINIGLUPIPLGIMLFCY     SMIRTL OHCKNEKKNKAVKMIFAVVVLFLG     FWTPYNIVLELTLIVELELQCTFERYLJOL     FKTCRGLFVLCQVGGLQINYSADITPSSYTQS     TOTAL     FKTCRGLFVLCQVGGLQINYSADITPSSYTQS     TOTAL     FKTCRGLFVLCQVGGLQINYSADITPSSYTQS     GSYDGVIKEVNVSPCTOPQCQLSKGQSYSN     VTFTSNIGSKSSKAVHGILMGVPVPFPPEPG     GCKSGINCPIGQKATYSYLKPVSKYPSIK     LVVEWQLQDDKNQSLFCWEIPVQIVSHL     VAEWQLPSATLCYFCRCKIGLGAALFPRSAR     ALAASALPAQGSRWPVLSSPGLPAAFSFPAC     PQRSYSTEREKPQQHQKTKMIVLGFSNPTNWV     RTRIKAFLIWAYFDKEFSITEFSGAAQAFAH     VSKLLSGCKEDLEELLVAKEVLHALKEKVTS     LPDNHKNALAANIDEIVFTSTIGDISTYDEKG     RKFVNILMGFWYLTSANIPSETLRGASVFQVK     GRYSTIEREFSQAAQAFAH     VSKLLSGCKEDLEELLVAKEVLHALKEKVTS     LPDNHKNALAANIDEIVFTSTIGDISTYDEKG     RKFVNILMGFWYLTSANIPSETLRGASVFQVK     GRYSTIEREFSQAAQAFAH     VSKLLSGCKEDLEELLVAKEVLHALKEKVTS     LPDNHKNALAANIDEIVFTSTIGDISTYDEKG     RKFVNILMGFWYLTSANIPSETLRGASVFQVK     GRYSTIEREFSQAAQAFAH     VSKLLSGCKEDLLEELVAKEVLHALKEKVTS     LPDNHKNALAANIDEIVFTSTIGDISTYDEKG     RKFVNILMGFWYLTSANIPSETLRGASVFQVK     GRYSTEREFSQAQAFAH     VSKLLSGCKEDLEELVAKEVLHALKEKVTS     LPDNHKNALAANIDEIVFTSTIGDISTYDEKG     RKFVNILMGFWYLTSANIPSETLRGASVFQVK     GRYSTEREFSQAQAFAH     VSKLLSGCKEDLEELVAKEVLHALKEKVTS     LPDNHKNALAANIDEIVFTSTIGDISTYDEKG     GRYSTEREFSQAQAFAH     VSKLLSGCKEDPLOTT     GRYSTEREFSQAAGAFAH     VSKLLSGCKEDPLOTT     GRYSTEREFSQAAGAFAH     VSKLLSGCKEDPLOTT	1		1	}	1		CELL DANDADOLLER CHEV CREVILLE ELSERM
NGFEDREDDEGGGWITENIKQIQQELE	İ	1	1				OLUTE I VLVLI OLI I INDICEDINGGEGEGEGE
QCDVPEDVRVGCLTTDFAMQNVLLQMGLHV	1		1		ľ	1	+ WKNYLYNIUMELQELLIUKGED Y FSEEEEEEE
LAVNIGMLIREARSYILRCHGCFKTTSDMSRV   FCSHCGKNKLKKVSVDDOTLIHMHSRNP   KVLNPRGLRYSLPTPKGGKYAINHHSRNP   KVLNPRGLRYSLPTPKGGKYAINHHSRNP   KVLNPRGLRYSLPTPKGGKYAINHHSRNP   KVLNPRGLRYSLPTPKGGKYAINHHSRNP   KVLNPRGLRYSLPTPKGGKYAINHHSRKKPV   KKR   RRNNIRQFIMKVCISGQARWLTPVVFVLWET   EAGRSLELKSLRAWATWGNPISTKINK   KKR   RRNNIRQFIMKVCISGQARWLTPVVFVLWET   EAGRSLELKSLRAWATWGNPISTKINK   KMPTDIADTTLDESIYSNYYLYESPKPCTKE   GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL   FKYKRLRSMITDVYLLINLAISDLLFYSLPPWG   YYAADQWYFGLGLCKMISWMYLVGFYSGIF   FVMLMSIDRYLAIVHAVFSLRARTLTYGVTIS   LATWSVAVFASLPGFLSTYFRRNHTYCKT   KYSLNSTTWKVLSSLEINILGLVPLGIMLFCY   SMIIRTLQHCKNEKKNRAVKMPAVVVLFLG   FVTPYNIVLELETLVELEVLQDCTFERYLDQA   IQATETLAFVHCCLNPITYFICGERRKYTLQQ   FKTCRGLFVLQQYCGLQLIVSADIPSSSYTQS   TMDHDLHDAL   FKTCRGLFVLQQYCGLQLIVSADIPSSSYTQS   TMDHDLHDAL   FKTCRGLFVLQQYCGLQLIVSADIPSSSYTQS   TMDHDLHDAL   FKTCRGLFVLQQYCGLQLIVSADIPSSSYTQS   TMDHDLHDAL   FKTCRGLFVLQQYCGLQLIVSADIPSSSYTQS   TMDHDLHDAL   FKTCRGLFVLQQYCGLQLIVSADIPSSSYTQS   GSVDGVIKEVNVSPCPTQPQQLSKGQSYSVN   VTFTSNIQSKSSKAVHGLIMGVVPVPPPPPPP   GCKSGINCPIQKDKTYSYLNKLPVKSEYPSIK   LVVEWQLQDDKNQSLFCWEPPQIVSHL   LVVEWQLQDDKNQSLFCWEPPQIVSHL   LVTEWQLQDDKNQSLFCWEPPQIVSHL   LVTEWQLQDDKNQSLFCWEPPQIVSHL   LVTEWQLQDDKNQSLFCWEPPQIVSHL   VSEVLSGKFLEVPQQHQKTKMIVLGFSNPINWV   RTRIKAFLUMAYFDKEFSITEFSGAKQAFAN   VSKLLSGCKFPLLEELVAKEVLHALKEKVTS   LPDNHKNALAANDEIVFTSTGDISIYYDEKG   RKFVNILMCFWVLTASNFEILRGSSVFQVK   LGNQNVETKQLLSASYFQREFTQGVKPDWT   LAREHSKLLE   LPDNHKNALAANDEIVFTSTGDISIYYDEKG   RKFVNILMCFWVLTASNFEILRGSSVFQVK   LGNQNVETKQLLSASYFQREFTQGVKPDWT   LAREHSKLLE   LPDNHKNALAANDEIVFTSTGDISIYYDEKG   RKFVNILMCFWVLTASNFEILRGSSVFQVK   LGNQNVETKQLLSASYFQREFTQGVKPDWT   LAREHSKLLE   LPDNHKNALAANDEIVFTSTGDISIYYDEKG   RKFVNILMCFWVLTASNFEILRGSSVFQVK   LGNQNVETKQLLSASYFQREFTGGVKPDWT   LAREHSKLLE   LPDNHKNALAANDEIVFTSTGDISIYYDEKG   RKFVNILMCFWVLTASNFEILRGSSVFQVK   LGNQNVETKQLLSASYFQREFTGGVAFTD   LPTTLRFPMLSIGGREFSCTGAHTDIMDDW   LDCAFTCGVHCHGQGKYPCLQVFNLSHFG   GKALLFFYFFKCHQDRNDL   LDCAFTCGVHCHGQGKYPCLQVFNLSHFG   GKALLFFYFFKCHQDRNDL   LDCAFTCG	]		1	]		1	NGFEDRKDDSDDDGGGWITPSNIKQIQQELE
FCSHGGNKTLKKVSVTVSDGTLHMHFSRNP   KVLNPRGLRYSLPTPKGGKYANPHLTEDQRF   PQLRLSQKARQKTNVFAPDYLGVSPFVENDI   SSRSATLQVRDSTLGAGRRUNPNASRKKFV   KKR   RRNNIRQFIMKVCISGQARWLTPVVPVLWET   EAGRSLELKSLRPAWATWGNPISTKINK   KKR   RRNNIRQFIMKVCISGQARWLTPVVPVLWET   EAGRSLELKSLRPAWATWGNPISTKINK   KMNPTDIADTTLDESIYSNYVLYESPKPCTKE   GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL   FKYKRLRSMTDVYLLNLAISDLLFVPSLPFWG   YYAADQWVFGLGLCKMISWMYLVGFYSGIF   FYMLMSIDRYLALVHAVFSLRARITLTGVITS   LATWSVAVFASLPGFLFSTCYTERNHTYCKT   KYSLNSTTWKVLSSLEINILGLVIPLGIMLFCV   SMIRRTLQHCKNEKKNKAVKMIFAVVVLFLG   FWTPYNIVLFLETLVELEVLQDCTFERYLLDY   QATETLAFVHCCIDCTFERYLLDY   QATETLAFVHCCIDCTFERYLLDY   GCKSGINCPIOKDKTYSVINKLPVKSEYPSIK   LVVEWQLODDKNOSLCWEDPVQIVSHL   LVVEWQLODDKNOSLCWEDPVQIVSHL   LVVEWQLODDKNOSLCWEDPVQIVSH   LVVEWQLODDKNOSLCWEDPVQIVSH   VSKLLSQCKFDLLGLGAALFPRSAR   ALASALPAGGSRWPVLSSFGLFAATSFPAC   PQRSYSTEEKPQQHQKTKMVLGFSNPINWV   RTRIKAFLIWAFTPGISTSTGDISTYYDEKG   RRFVNILMCFWYLTSANIPSETLRGASVFQVK   LGNQNVETKQLLGAALFPRSAR   ALASALPAGGSRWPVLSSFGLFAATSFPAC   PQRSYSTEEKPQQHQKTKMVLGFSNPINWV   RTRIKAFLIWAFTPGISTSTYDEKG   RRFVNILMCFWYLTSANIPSETLRGASVFQVK   LGNQNVETKQLLSASYFQREFTQGVKPDWT   LAREHSKLLE   RSSHPMS   SAFFLRPQOHDSGEREPFSQTPGLMQPFSIPVQ   TILQGSRRRQGRTAFPASGKKRETDYSDGDPL   DVHKRLPSSTGDRAVMLGFSMMGFSVLMF   FLLGTTILKFPMLSIQRESTCTAHTDIMDDW   LDCAFTCGVHCHQGGKYCQLOVFNLSIFIG		i	1				QCDVPEDVRVGCLTTDFAMQNVLLQMGLHV
FCSHGGNKTLKKVSVTVSDGTLHMHFSRNP   KVLNPRGLRYSLPTPKGGKYANPHLTEDQRF   PQLRLSQKARQKTNVFAPDYLGVSPFVENDI   SSRSATLQVRDSTLGAGRRUNPNASRKKFV   KKR   RRNNIRQFIMKVCISGQARWLTPVVPVLWET   EAGRSLELKSLRPAWATWGNPISTKINK   KKR   RRNNIRQFIMKVCISGQARWLTPVVPVLWET   EAGRSLELKSLRPAWATWGNPISTKINK   KMNPTDIADTTLDESIYSNYVLYESPKPCTKE   GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL   FKYKRLRSMTDVYLLNLAISDLLFVPSLPFWG   YYAADQWVFGLGLCKMISWMYLVGFYSGIF   FYMLMSIDRYLALVHAVFSLRARITLTGVITS   LATWSVAVFASLPGFLFSTCYTERNHTYCKT   KYSLNSTTWKVLSSLEINILGLVIPLGIMLFCV   SMIRRTLQHCKNEKKNKAVKMIFAVVVLFLG   FWTPYNIVLFLETLVELEVLQDCTFERYLLDY   QATETLAFVHCCIDCTFERYLLDY   QATETLAFVHCCIDCTFERYLLDY   GCKSGINCPIOKDKTYSVINKLPVKSEYPSIK   LVVEWQLODDKNOSLCWEDPVQIVSHL   LVVEWQLODDKNOSLCWEDPVQIVSHL   LVVEWQLODDKNOSLCWEDPVQIVSH   LVVEWQLODDKNOSLCWEDPVQIVSH   VSKLLSQCKFDLLGLGAALFPRSAR   ALASALPAGGSRWPVLSSFGLFAATSFPAC   PQRSYSTEEKPQQHQKTKMVLGFSNPINWV   RTRIKAFLIWAFTPGISTSTGDISTYYDEKG   RRFVNILMCFWYLTSANIPSETLRGASVFQVK   LGNQNVETKQLLGAALFPRSAR   ALASALPAGGSRWPVLSSFGLFAATSFPAC   PQRSYSTEEKPQQHQKTKMVLGFSNPINWV   RTRIKAFLIWAFTPGISTSTYDEKG   RRFVNILMCFWYLTSANIPSETLRGASVFQVK   LGNQNVETKQLLSASYFQREFTQGVKPDWT   LAREHSKLLE   RSSHPMS   SAFFLRPQOHDSGEREPFSQTPGLMQPFSIPVQ   TILQGSRRRQGRTAFPASGKKRETDYSDGDPL   DVHKRLPSSTGDRAVMLGFSMMGFSVLMF   FLLGTTILKFPMLSIQRESTCTAHTDIMDDW   LDCAFTCGVHCHQGGKYCQLOVFNLSIFIG	1	ŀ		1			LAVNGMLIREARSYILRCHGCFKTTSDMSRV
KVLNPRGLRYSLPTRKGGKYAINPHLITEDQRF   POLRLSQKARQKINVAPDYJAGSYSFVENDI)   SSRSATLQVRDSTLGAGRRRLNPNASRKKFV   KKR   SRNIRQFIMKVCISGQARWLTPVVPVLWET   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPAWATWGPISTKINK   EAGRSLEILKSLRPHYLOLGINSVVVLVL   FKYRKIRSSMTDVYLLINGSULFVPSEIPFWG	İ					1	FCSHCGNKTLKKVSVTVSDDGTLHMHFSRNP
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SSRSATLQVRDSTLGAGRRRINPNASRKKFV KKR	}				ł	i	POLDI SOKAROKTNYFAPDYIAGYSPFVENDI
985   2335   A   8322   352   529   RRNNIRQFIMKVCISGQARWLTPVVPVLWET EAGRSLELKSLRPAWATWGNPISTKINK     986   2336   A   8325   89   1172   KMNPTDIADITILDESIYSNYTYLYSEISPECTKE GIKAFGELELPLYSLVFVFGLLGNSVVVLVL     FKYKRLRSMTDVYLLNLAISDLLFVFSLPFWG YYAADQWVFGLELCKMISWMYLVGFYSGIF FVMLMSIDRYLAIVHAVFSLRARTLTYGVITS     LATWSVAVFASLPGFLFSTCYTERNHTYCKT     KYSLNSTTWKVLSSLEINILGLUPLGIMLFCY SMIIRTLQHCKNEKKNKAVKMIFAVVVLFLG FWTPYNIVLFLETLVELEVLQDCTFERYLDYA     QATETLAFVHCCLNPIYFFLGEKFRKYTLQL FKTCRGLFVLCQYCGLLQIYSADIPSSSYTQS TMDHDLHDAL     987   2337   A   8326   3   470   SLSAMRFLAATFLLLALSTAAQAEPVQFKDC GSVDGVIKEVNVSPCPTQPCQLSKGQSYSVN     VIFTSNIQSKSSKAVVHGILMGVPVPFPPPPD GCKSGINCPIQKKTYSYLNKLPVKSEYPSIK LVVEWQLQDDKNQSLFCWEPVQIVSHL     VIKMALAARLPGFLHSRSLPGAVELRPA     VAEVELSQCKFDLEELVAKEVLHALKEKVTS     PORSYSTEEKPQQHQKTKMIVLGFSNPINWV     RTRIKAFLIWAYFDKEFSITEFSEGAKQAFAH     VSKLLSQCKFDLEELVAKEVLHALKEKVTS     LPDNHKNALAANDEIVFTSTGDISIYYDEKG     RKFVNILMCFWYLTSANIPSETLRGASVFQVK     LGNQNVETKQLLSASYEQVK     LGNQNVETKQLLSASYEQVK     SGFHQLLIQNIFCVYHTRLKTSQGLCLLSL     KSLHPMS     990   2340   A   8361   210   1115   ASFPLRPQGHDSGEREPFSQTPGLMQPFSIPVQ     UTLQGSRRRQGTAFPASGKRETDYSDGDPL     DVHKRIPSTGERAVAMLGFAMMGFSVLMF     FLLGTTILKPFMLSIQREESTCTAIHTDIMDDW     LDCAFTCGVHCHGQGKYPCLQVFVMLSHEG     OKALLHYYBELSAVONPKCFYTPKCHQDRNDL	ì	1			i		CODE ATT OVED STI CAGRERI NENASRKKEV
985   2335   A   8322   352   529   RRNNIROFIMKVCISGQARWLTPVVPVLWET	[	1		]			
2336   A   8325   89   1172	[						KKK
SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN   SAGRIELEKSLRPAWAL WOMPISIAINAN	985	2335	A	8322	352	529	RRNNIRQFIMKVCISGQARWLIPVVPVLWEI
See	'03		'	ļ			EAGRSLELKSLRPAWATWGNPISTKINK
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FKYKRLRSMTDVYLLNLAISDLLFVFSLFWG YYAADQWVFGLGLCKMISWMYLVGFYSGIF FVMLMSIDRYLAIVHAVFSLRARTLTYGVITS LATWSVAVFASLPGLFSTCYTFERNHTYCKIT KYSLNSTTWKVLSSLEINILGLVIPLGIMLFCY SMIRTLQHCKNEKKNKAVKMIFAVVVLFLG FWTPYNIVLFLETLVELEVLQDCTFERYLDYA IQATETLAFVHCCLNPIJFFLGEKFRKYILQL FKTCRGLFVLCQYCGLLQIYSADTPSSSYTQS TMDHDLHDAL  987 2337 A 8326 3 470 SLSAMRFLAATFILLALSTAAQAEPVQFKDC GSVDGYMKEVNVSPCPTQPCQLSKGQSYSVN VTFTSNIQSKSSKAVHGILMGVPVPFPPEPD GCKSGINCPIQKDKTYSYLNLPVKSFYPSIK LVVEWQLQDKNQSLFCWEIPVQIVSHL VVEWQLQDKNQSLFCWEIPVQIVSHL VVEWQLQDKNQSLFCWEIPVQIVSHL VVEWQLQDKNQSLFCWEIPVQIVSHL VVEWQLQDKNQSLFCWEIPVQIVSHL VVEWQLQDKNQSLFCWEIPVQIVSHL VREYLPSATLCYFCRCRLGLGAALFPRSAR ALASALPAQGSRWPVLSSPGLPAAFASFPAC PQRSYSTEEKPQQHQKTKMIVLGFSNPNWV RTRIKAFLIWAYFDKEFSITEFSEGAKQAFAH VSKLLSQCKFDLLEELVAKEVLHALKEKVTS LPDNHKNALAANDEIVFTSTGDISIYYDEKG RKFVNILMCFWYLTSANIPSETLRGASVFQVK LGNQNVETKQLLSASYEFQREFTQGVKPDWT LARIEHSKLLE  989 2339 A 8349 67 185 MSGFHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS GFHQLLIQNLFCVYHTRLKTSQGLCLLSL KSLHPMS GSFHQLLIQNLFCVYHTRLKTSQGLCLLSL SLHPMS TILGSRRRQGRTAFPASGKKRETDYSDGDPL DVHKRLPSSTGEDRAVMLGFAMMGFSVLMF FLLGTTILKPFMLSIQREESTCTAIHTDIMDDW LDCAFTCGVHCHQGKYPCLQVFVNLSHPG OKALLHTYNEEAVOINPKCFYTPKCHQDRNDL	900	2330	Α	0323	"		GIKAFGELFLPPLYSLVFVFGLLGNSVVVLVL
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=A spartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine V=Valine, W=Tryptophan,
			1	amino acid	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
		1	]	residue of	sequence	/=possible nucleotide deletion, \=possible
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PCT/US01/03800 WO 01/57188

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
1	uence	١	09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
seq-	delice	ļ	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
uence			1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
(	1			residue of	sequence	Y=Tyrosine, X=Unknown,sup codor,
<b>,</b>		1		peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-Americ Acid F=Glutamic Acid.
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	location	corresponding	I=Isoleucine, K=Lysine, L=Laucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
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nence			914	amino acid	of peptide	T=Threonine V=Valine, W=Tryptophan,
1		1	\	residue of	sequence	V=Typesine X=Unknown, *=Stop codon,
		l	1	peptide	Joque	/=possible nucleotide deletion, \=possible
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1						DOEL GKI SI DKVFRERESLNASIVDAINQAAL
1		İ			1	CVCIPCI RVFIKDIHVPPRVKESMUMUVEAL
		1				DDVD ATVI FSEGTRESAINVALGKKVAVILA
		- 1		ì		EARK AROINOA AGEASAVLAKAKAKAKAEAIK
1		1		ì	1	I A A A L TOHNGDAA A SLTVAEQY V SAFSKLA
1						POSNTILL PSNPGDVTSMVAOAMGVYGALL
1			Ì	(		KAPVPGTPDSLSSGSSRDVQGTDASLDEELD
			1			VKMS
			- 10431	134	941	NIDENI LESEMMDPCSVGVOLRTTNECHKTY
1002	2352	A	8421	154	7	VTD UTGEKTI OELSSNDMLLLOLRIGM ILS
				l l		ADUTICEHHVKIYIDRFEDLOKSCCDPFNIHKN
1.		1	-			AKKNI HVIDI DDATFL SAKEGRUL VPU WAL
· .		1		1		PRCTOINGSVDVDTEDROKRKPESDGK1AK
1		1		}		AT BSI OFTNPGROTEFAPETGKREKKKLIKN
		1		- 1		ATACSDROVIPAKSKVYDSOGLLIFSGMDLC
1	}					DCLDEDCLGCFYACPACGSTKCGAECRCDR
					i	WI VEOTETEGGETIHNKHAG
i			8427	3	1416	TEWGLSGSCPGCSPLEPGSRGRGAAAWRILL
1				1 4		10.00 mm n
1003	2353	A	0427	-	14.0	CRRLPEPSPFLTQPNLAQSQPPAPVPVTDPSV MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEI

				B 11:4-1	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
IO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in		corresponding	I=Isoleucine K=I.vsine L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uenœ	l	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
ence		(	914	ng to first		T=Threonine V=Valine, W=Tryptophan,
		1	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	}		}	residue of	sequence	/=possible nucleotide deletion, \=possible
	ĺ	ſ	1	peptide	}	nucleotide insertion
	Ì	ì		sequence		SLDTENIDEILNNADVALVNFYADWCRFSQM
	1	<del>                                     </del>			}	SLDIENIDEILINADVALVII TAB WEIG GAL
	l	1		(	l	LHPIFEEASDVIKEEFPNENQVVFARVDCDQH
	ì	1		l .		SDIAQRYRISKYPTLKLFRNGMMMKREYRGQ
	ł		ì	ļ		RSVKALADYIRQQKSDPIQEIRDLAEITTLDRS
		1	1	Į.		KRNIIGYFEQKDSDNYRVFERVANILHDDCAF
	1	}				LSAFGDVSKPERYSGDNIIYKPPGHSAPDMVY
	1	1				LGAMTNFDVTYNWIQDKCVPLVREITFENGE
	l .	1	1		}	DI TEECI PEI II FHMKEDTESLEIFONEVARQU
		]	1	1		ISEK GTINEL HADCDKFRHPLLHIQKTPADCP
	į			1	}	I VIAIDSERHMYVEGDEKDVLIPGKLKUFVFUL
		1	1	1		HSGKLHREFHHGPDPTDTAPGEQAQDVASSP
	}	1		1	i	PESSFQKLAPSEYRYTLLRDRDEL
	1			1		GLSRKLRAGFLPGFCRVSPCGSWVVETLVKM
1004	2354.	A	8432	910	387	ACAAARSPADQDRFICIYPAYLNNKKTIAEGR
			)			RIPISKAVENPTATEIQDVCSAVGLNVFLEKN
	ı		i i			RIPISKAVENPI ATEIQUI COAVOLITITE COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENTRA COENT
		1	ì			KMYSREWNRDVQYRGRVRVQLKQEDGSLC
	J	ļ		}		LVQFPSRKSVMLYAAEMIPKLKTRTQKTGGA
	1	ì		1	ļ	DOSLOGEGSKKGKGKKKK
1000	0256	A	8453	90	530	QSHETKMQSGTHWRVLGLCLLSVGVWGQD
1005	2355	^	0433	1 30		GNEEMGGITQTPYKVSISGTTVILTCPQYPGSE
	Į.		ì		1	II WOHNDKNIGGDEDDKNIGSDEDHLSLKEF
	1	1	(	1		SELEOSGYYVCYPRGSKPEDANFYLYLKARG
		1	!			NPGLONRYHRLFREDHSKGHSQ
					307	AVORIRHEMNIFRLTGDLSHLAAIVILLLKIW
1006	2356	Α	8458	3	307	KTRSCAGISGKSOLLFALVFTTRYLDLFTSF1S
	1					LYNTSMKVWYAIHRNVFHLQCTGLWTLNLC
	i			ì		OI CIEN
	}					GAGAGGDWAAMDKLKKVLSGQDTEDRSGL
1007	2357	A	8459	43	553	SEVVEASSLSWSTRIKGFIACFAIGILCSLLGT
•		1				VLLWVPRKGLHLFAVFYTFGNIASIGSTIFLM
	- {		İ			GPVKQLKRMFEPTRLIATIMVLLCFALTLCSA
		ļ			į	FWWHNKGLALIFCILQSLALTWYSLSFIPFAR
	1	- 1	1		}	FWWHNKGLALIFCILQSLALI WISDSIN COL
	ľ	- [	(	ì		DAVKKCFAVCLA
1008	2358	A	8462	487	150	AQDIRSVHSLGQKSTFVKHFRTLSHLHGLPDP
1000	2556	1 11	0.00		j	PPHWPPQERSPPSHPCMPSHRPQIPQLSNSGPS
	- 1	1	-	- [		DPRWGCVGPSMPTSTCLPGAVEASTTKASLP
	l	-		1		KCPVDSSLPTPEACFL
			0465	134	954	ETDVKTSI FI I RTOLEPTGTVGNTIMTSQPVP
1009	2359	Α	8465	134	75.	NETTIVI PSNVINFSOAEKPEPINQGQDSLAAL
		1	1			I HAFIKVIGTIOILCGMMVLSLGIILASASFSPI
		1	i			FTOVTSTLLNSAYPFIGPFFFIISGSLSIA1EKKI
	ł	- 1		}		TKLLVHSSLVGSILSALSALVGFIILSVKQATL
Ì		- )	}	}		NPASLQCELDKNNIPTRSYVSYFYHDSLYTTI
1	l	- 1	1		į.	CYTAKASLAGTLSLMLICTLLEFCLAVLTAVI
		- 1	}	1		RWKQAYSDFPGSVLFLPHSYIGNSGMSSKMT
1	ļ		}			KWKQA 13DFFG3 VLFLFFI3 I GH3GHIGHGI
1						HDCGYEELLTS
1010	2360	A	8468	2	473	KYRYRPYPVMRKICQVGPAGLAFILNISPVA
1010	2300	^	5100	1		HRVALCHLAGCQEQAAWYHTLQILFFLVSA
1	1			ì		FFSCPVPEKYFPGSCDIVGHGHQIFHAFLSICT
	ŀ	Ì	1			LSQLEAILLDYQGRQEIFLQRHGPLSVHMAC
1		1		-		SEFFI AACSAATAALLRHKVKARLIKKUS
L					409	TELSOLEKAHPPADMGRRKSKRKPPPKKKM
1011	2361	Α	8478	5	409	GTI FTOFTCPFCNHEKSCDVKMDRARNIGV
1				1		SCTVCLEEFQTPITCILGNLGFFQRVGRGLES
}				1		PCSSGPLCALVQGQSRPEEQVPPSDFCGVRR
1						PLOSOPECAL VQQQAG ELQ TITOL CO TIE
1			-			RAGFQCQ
1010	2362	A	8481	2810	1652	RTSTQKWQSVFNDSQEHLERFYCNPENDRM
	1 2302	10	1 0701		1	RMKYGGQEFWADLNAMNVYETTEFDQLRR
1012		1		1	1	LSTPPSSNVNSIYHTVWKFFCRDHFGWREYP

	CEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID NO: of	hod	ID NO:	beginning	nucleotide	D-Acceptic Acid F=Glutamic Acid
O: of ucl-	peptide	nou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
otide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
d-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
ence	daice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
.1100				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
			-	peptide		-possible nucleotide deletion, \-possible
	1	ļ		sequence		nucleotide insertion SVIRLIEEANSRGLKEVRFMMWNNHYILHNS
						FFRREIKRRPLFRSCFILLPYLQTLGGVPTQAP
			l	1	Į.	PPLEATSSSQIICPDGVTSANFYPETWVYMHP
	Ì	1		1		SQDFIQVPVSAEDKSYRIIYNLFHKTVPEFKYI
		1		Į.		ILQILRVQNQFLWEKYKRKKEYMNRKMFGR
	1					DRIINERHLFHGTSQDVVDGICKHNFDPRVCC
		İ	1			KHATMFGQGSYFAKKASYSHNFSKKSSKGV
			1		1	HFMFLAKVLTGRYTMGSHGMRRPPPVNPGS
			İ			VTSDLYDSCVDNFFEPQIFVIFNDDQSYPYFV
			-			OVEEVENTVSI
	1	<u> </u>			517	IENCRTRLRQAWHEVCGNKMAAPIPQGFSCI
013	2363	A	8488	2	317	SPET GWWFROPVLVTOSAAIVPVRTKKRFTF
		Į.			ì	PLYOPK FK TEK EFMOHARKAGLVIPPEKSUK
		-	1		ł	IHLACTAGIFDAYVPPEGDARISSLSKEGLIER
						TERMKKTMASQVSIRRIKDYDANFKIKDFPE
		1	\	l		KAKDIFIEGSPLY
		+	8501	363	17	VIRTGYVYICIIYAOLMYTYYIRTAYVYICIL
014	2364	Α	8301	303	1	A OT MYTYVI YTHSLCIHMYSIRTAY VYICII)
	1				AOIMYTYVFYTHRLCIHMYSIRTDYVYICILY	
					AQLMYTYVFYTHSYMSDE	
215	02/5	A	8504	3	2190	NSSEHFSQAPQRLSFYSWYGSARLFRFRVPP
015	2365	Α.	8304			AVLLRWLLQVSRESGAACTDAEITVHFRSGA
						PPVINPLGTSFPDDTAVQPSFQVGVPLSTTPR
		)	ļ	1		NASVNVSHPAPGDWFVAAHLPPSSQKIELKO
		1		1		LAPTCAYVFQPELLVTRVVEISIMEPDVPLPC
			ļ	1	1	TLLSHPSYLKVFVPDYTRELLLELRDCVSNG
			1		[	LGCPVRLTVGPVTLPSNFQKVLTCTGAPWPG RLLLPSPPWDRWLQVTAESLVGPLGTVAFS
		1	i			VAALTACRPRSVTIQPLLQSSQNQSFNASSG
						LSPSPDHQDLGRSGRVDRSPFCLTNYPVTRE
		İ		Ì	)	MDVVSVHFQPLDRVSVRVCSDTPSVMRLRI
		ĺ	1	[	1	NTGMDSGGSLTISLRANKTEMRNETVVVAC
		1	\			NAASPFLGFNTSLNCTTAFFQGYPLSLSAWS
		1	1	1		PANI HPYPETDNWYLSLOLMCPENAEDCEC
				İ		AVVHVETTLYLVPCLNDCGPYGQCLLLKKF
	1	Į				VI VASCSCK AGWRGWSCIDNSIAQI VAQQ
		-	1	1	l l	AATI II TI SNI MFLAPIAVSVRRFFLVEASV
	- 1	1	t	i i	[	AVTMFFSTFYHACDOPGEAVLCILSYDILQ
		1	1			CDFLGSGAAIWVTILCMARLKTVLKYVLFL
				}		GTT VIAMSLOLDRRGMWNMLGPCLFAFVI
	1			1		A SMW A VRCGHRROCYPTSWORWAFYLLP
	}	1		1	1	VSMASVGIAIYTSMMTSDNYYYTHSIWHIL
		1				AGSAALLLPPPDQPAEPWACSQKFPCHYQI
	1	1	1		1	KNOREELYAVT
1016	2266	$-\frac{1}{A}$	8511	1	453	KWYPSGPVRIPGRFYYKLPAGHRRCRMAPA
1016	2366	^	3311	1 -		KGGEKKKGRSAINEVVTREYTINIHKRIHGV
	-		İ		1	FKKRAPRALKEIRKFAMKEMGTPDVRIDTR
			- 1		1	NKAVWAKGIRNVPYRIRVRLSRKRNEDEDS
	1		- [			NKLYTLVTYVPVTTFKNLQTVNVDEN
1015	22/2	$ +$ $\overline{A}$	8513	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSD
1017	2367	I A	1 6515	1 .		LSAKWADNFMAEGCGGSKEHSFQHPFLQA
		1				GMFLGEFSCLAAFYLLRCRAAGQSDSSVDF
	ì			1	}	OPENPLL FLPPALCDMTGTSLMYVALNMIS
		ĺ				SSEOMLEGAVITETGLESVAFLGRELVLSQV
		1		1		GILATIAGLVVVGLADLLSKHDSQHKLSEV
		1				GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPI
			J			AVGTEGLFGFVILSLLLVPMYYIPAGSFSGN
,	- 1	- 1		1	1	RGTLEDALDAFCQVGQQPLIAVALLGNISSI
		Į.	I	1	}	FFNFAGISVTKELSATTRMVLDSLRTVVIWA

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence	}	ł	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1		1	amino acid residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1		sequence	/-possible nucleotide deletion, \-possible
		ł		peptide sequence		nucleotide insertion
		<u> </u>	<del> </del>	Sequence	<del> </del>	SLALGWEAFHALQILGFLILLIGTALYNGLHR
						PLLGRLSRGRPLAEESEQERLLGGTRTPINDA
		1	)	]		1 s
1010	22.00	A	8518	324	694	SPFWTEKRRMEKPLFPLVPLHWFGFGYTALV
1018	2368	^	6516	324	05.	VSGGIVGYVKTGSVPSLAAGLLFGSLAGLGA
						YOLYODPRNVWGFLAATSVTFVGVMGMRS
		j	1	1		YYYGKFMPVGLIAGASLLMAAKVGVRMLM
		Ì		ļ		TSD
1019	2369	A	8526	2	1787	VSAAAVNMEPPDAPAQARGAPRLLLLAVLL
1019	2309	^	0520	1 -		AAHPDAQAEVRLSVPPLVEVMRGKSVILDCT
		1	ı		1	PTGTHDHYMLEWFLTDRSGARPRLASAEMQ
		1	i		Ì	GSELQVTMHDTRGRSPPYQLDSQGRLVLAEA
			1			QVGDERDYVCVVRAGAAGTAEAAARLNVF
		Í		1		AKPEATEVSPNKGTLSVMEDSAQEIATSNSRN
	1		1			GNPAPKITWYRNGQRLEVPVEMNPEGYMTS
			1			RTVREASGLLSLTSTLYLRLRKDDRDASFHC
	1	1	ļ	1		AAHYSLPEGRHGRLDSPTFHLTLHYPTEHVQ
l		ì	1	ĺ		FWVGSPSTPAGWVREGDTVQLLCRGDGSPSP
		1				EYTLFRLQDEQEEVLNVNLEGNLTLEGVTRG
		1		1	1	QSGTYGCRVEDYDAADDVQLSKTLELRVAY
			1	1		LDPLELSEGKVLSLPLNSRAVVNCSVHGLPTP
1	1			1		ALRWTKDSTPLGDGPMLSLSSITFDSNGTYVC
ļ		j	İ			EASLPTVPVLSRTQNFTLLVQGSPELKTAEIEP
j		}				KADGSWREGDEVTLICSARGHPDPKLSWSQL
Ì				1		GGSPAEPIPGRQGWVSSSLTLKVTSALSRDGI
	1	1	1		Ì	SCEASNPHGNKRHVFHFGTVSPQTSQAGVAV
ł	1	1	Ì			MAVAVSVGLLLLVVAVFYCVRRKGGPCCRQ
}						RREKGAP PRVRLLRPSRSRSCRGLLSTRAPGPSPFRSLHS
1020	2370	Α	8530	2	1200	SPLLPHAMKSPFYRCQNTTSVEKGNSAVMGG
				]	j	VLFSTGLLGNLLALGLLARSGLGWCSRRPLR
i	1	1	1			PLPSVFYMLVCGLTVTDLLGKCLLSPVVLAA
		1	1			YAQNRSLRVLAPALDNSLCQAFAFFMSFFGL
		1	1	}		SSTLQLLAMALECWLSLGHPFFYRRHITLRLG
		1				ALVAPVVSAFSLAFCALPFMGFGKFVQYCPG
						TWCFIQMVHEEGSLSVLGYSVLYSSLMALLV
1		- {	1			LATVLCNLGAMRNLYAMHRRLQRHPRSCTR
1	}	1			1	DCAEPRADGREASPQPLEELDHLLLLALMTV
		1				LFTMCSLPVIYRAYYGAFKDVKEKNRTSEEA
<u> </u>		1		ļ	1	EDLRALRFLSVISIVDPWIFIIFRSPVFRIFFHKI
1		-				FIRPLRYRSRCSNSTNMESSL
			- 0505	<del></del>	237	RRGEIDMATEGDVELELETETSGPERPPEKPR
1021	2371	A	8536	1	237	KHDSGAADLERVTDYAEEKEIQSSNLETAMS
	1	- [			1	VIGDRRSREQKAKQER
<u></u>			<del></del>	<del>                                     </del>	541	RKERRRRRRRMEAVVFVFSLLDCCALIFLSV
1022	2372	A	8537	94	541	YFIITLSDLECDYINARSCCSKLNKWVIPELIG
		1				HTIVTVLLLMSLHWFIFLLNLPVATWNIYRYI
1	1	- 1	1			MVPSGNMGVFDPTEIHNRGQLKSHMKEAMI
						KLGFHLLCFFMYLYSMILALIND
			-	<del> </del>	431	RMMKCPQALLAIFWLLLSWVSSEDKVVQSPL
1023	2373	A	8540	26	431	SLVVHEGDTVTLNCSYEVTNFRSLLWYKQEK
1				1		KAPTFLFMLTSSGIEKKSGRLSSILDKKELSSIL
				1	1	NITATQTGDSAIYLCAVEAQCSLVTCSLYSNS
1		1	-	1		TAEALQL
	1_				J	GVRLRYSPIAVVMVGEAGRDLRRRRAVAVT
1024	2374	A	8544	1731	743	AEKMAVLAPLIALVYSVPRLSRWLAQPYYLL
						SALLSAAFLLVRKLPPLCHGLPTQREDGNPCD
		1	1	1	1	SALLSAAPLL V KALFFLUNGLF I QALDONI CD
	- 1	İ				TOWNEY FOR A STATE OF A STATE OF THE OWNER WNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OW
						FDWREVEILMFLSAIVMMKNRRSITVEQHIGN IFMFSKVANTILFFRLDIRMGLLYITLCIVFLM

	000 ·	174-2	0.79	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	SEQ ID NO:	beginning	nucleotide	De Aspartic Acid E-Glutamic Acid,
NO: of	NO: of	noa	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			) 314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
			]	peptide	Joquenee	/=possible nucleotide deletion, \=possible
		1	1			nucleotide insertion
			<u> </u>	sequence	<u> </u>	TCKPPLYMGPEYIKYFNDKTIDEELERDKRVT
		1	1	1		WIVEFFANWSNDCQSFAPIYADLSLKYNCTG
	}		}	]		LNFGKVDVGRYTDVSTRYKVSTSPLTKQLPT
			ļ	ì	1	LILFQGGKEAMRRPQIDKKGRAVSWTFSEEN
	1	1				VIREFNLNELYQRAKKLSKAGDNIPEEQPVAS
	1	1	j	}		TPTTVSDGENKKDK
		[ _	<b></b>			TVSFHKTMASLKCSTVVCVICLEKPKYRCPA
1025	2375	Α	8546	2194	1707	CRVPYCSVVCFRKHKEQCNPETRPVEKKIRS
		Į		1	Ì	ALPTKTVKPVENKDDDDSIADFLNSDEEEDR
	1	1		İ	1	VSLQNLKNLGESATLRSLLLNPHLRQLMVNL
	1	}	1	1	ł	DQGEDKAKLMRAYMQEPLFVEFADCCLGIV
	ł		ì	İ	1	
		1				EPSQNEES THE CHILD THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN
1026	2376	A	8547	1078	594	VGMELPAVNLKVILLGHWLLTTWGCIVFSGS
1020	20,70	1			1	YAWANFTILALGVWAVAQRDSIDAISMFLGG
	}	1	ŀ			LLATIFLDIVHISIFYPRVSLTDTGRFGVGMAIL
		Į	1	1	İ	SLLLKPLSCCFVYHMYRERGGELLVHTGFLG
		Į.	1			SSQDRSAYQTIDSAEAPADPFAVPEGRSQDAR
			1		1	GY CONTROL OF A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGING WITH A LONGI
1027	2377	A	8557	1	340	DFLGPASPQEEGGSESSTMTELETAMGMIIDV
1027	2377	1,,	000			FSRYSGSEGSTQTLTKGELKVLMEKELPGFLQ
	1		1	į.	Ì	SGKDKDAVDKLLKDLDANGDAQVDFSEFIVF
		1	1			VAAITSACHKYFEKAGLK
1028	2378	A	8569	20	963	KMAATLGPLGSWQQWRRCLSARDGSRRLLL
1028	23/8	^	0505			LLLLGSGQGPQQVGAGQTFEYLKREHSLSKP
ł .						YQGEAPRPCFLRDWELQVHFKIHGQGKKNL
	1		1	j		HGDGLAIWYTKDRMQPGPVFGNMDKFVGLG
	1	1	1		ļ	VFVDTYPNEEKQQERVFPYISAMVNNGSLSY
1	1	Ì	ł		1	DHERDGRPTELGGCTAIVRNLHYDTFLVIRY
		1	į			VKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
			1			YYFGTSSITGDLSDNHDVISLKLFELTVERTPE
					ļ	EEKLHRDVFLPSVDNMKLPEMTAPLPPLSGL
ì						ALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK
İ		-	<u> </u>	1		RFY
			8572	<del> </del>	578	AAAASHRSRARSRPRRVSSGPAPRRAQSSAG
1029	2379	Α	8372	1.	1 3.0	PVASGLDSAPLCTMARALCRLPRRGLWLLLA
	l		1			HHI FMTTACOEANYGALLRELCLTQFQVDM
1			ł	1	(	EAVGETLWCDWGRTIRSYRELADCTWHMAE
			1	-		KLGCFWPNAEVDRFFLAVHGRYFRSCPISGR
]						AVRDPPGSILYPFIVVPITVTLLVTALVVWQS
1		1	i	1	1	KRTEGIV
			10001	1252	372	DSSTVKGGSESRHLCLIPDLKGKARTREASSG
1030	2380	A.	8574	1352	3/2	SPICGRRISLCISAKSSWTYRSGRLSWQSIKG
				1	1	THITTOALROPLHRAPLLPGOLCWSPRPLEK
						NIK AMGRPI LIPILLLLOPPAFLOPGGSTGSGP
}				1		SYLYGVTQPKHLSASMGGSVEIPFSFYYPWEL
1	1	1		1	Ĭ	AIVPNVRISWRRGHFHGQSFYSTRPPSIHKDY
				1		VNRLFLNWTEGQESGFLRISNLRKEDQSVYF
1			Ì	1		CRVELDTRRSGRQQLQSIKGTKLTITQAVTTT
						CKYELDI KKOUKŲŲLŲSIKUI KLIII ŲK TITI
			Ì			TTWRPSSTTTLAGLRVTESKGHSESWHLSLDT
			1	1		AIRVALAVAVLKTVILGLLCLLLLWWRRRKG
	}				1	SRAPSSDF
1031	2381	- A	8580	905	340	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQL
1031	4381	^	5560			AFDDFQESCAMMWQKYAGSRRSMPLGARIL
	]	1			1	FHGVFYAGGFAIVYYLIOKFHSRALYYKLAV
	ļ					FOLOSHPEAOEALGPPLNIHYLKLIDRENFVDI
	1	1				VDAKLKIPVSGSKSEGLLYVHSSRGGPFQRW
						HLDEVFLELKDGOOIPVFKLSGENGDEVKKE
		<del></del> _	0502	2550	961	RRRPRLLPGAEPCEPRVGPRRADMGCSAKAR
1032	2382	A	8393	2558	1 301	WAAGALGVAGLLCAVLGAVMIVMVPSLIKQ
1032	2382	A	8593	2558	961	RRRPRLLPGAEPCEPRVGPRRADMGCSAKAR WAAGALGVAGLLCAVLGAVMIVMVPSLIKQ

SEQ ID No. of nowl- peptide colored peptide uence where the period peptide colored peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide peptide pep			,		D4:-4-4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
in melectide could sequence   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister   Sister		SEQ ID	Met	SEQ	Predicted		De A spartic Acid. E=Glutamic Acid.
10.000   10.000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.0000   10.000		l .	hod	1		***	F=Phenylalanine, G=Glycine, H=Histidine,
Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   Course   C	nucl-	peptide					I-Icolaucine K=I vsine I =I cucine.
### Bid in the author of peptide residue of peptide of peptide of peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Peptide sequence   Pept	cotide	seq-	1			corresponding	14-14 othionine N=A coargaine P=Proline
914   ng to first   samino acid residue of peptide   sequence   sequence   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   victorial   v	seq-	uence					M=Methodine, N=Asparagne, 1 110mms,
amino acid   residue of peptide   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence	,	ļ	[	914			T. T V-Velice W-Triptophen
Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible   Popsible		ŀ	ł	l			I=Inreonine, v=vaine, w=Itypiophan,
		ĺ	1			sequence	Y=1yrosine, X=Unknown,stop codon,
QVLKNYRIPESILSFNMWKEPIPFYLSYYFYER   WMPSELLGGER/DWERGPYYVJKSFRNNT   WMPSELLGGER/DWERGPYYVJKSFRNNT   WMPSELLGGER/DWERGPYYVJKSFRNSN   WMPSELLGGER/DWERGPYYVJKSFRNSN   WMPSELLGGER/DWERGPYNTYLGFTGVQNI   SRIHLUGKWGLSKVDFWHSDQCMMINGTS   GQMWPFMFPSESELFYSPACRESKKLMYKE   GSVFEGIPTYRFVAPKTLFANGSIYPPNEGFC   CLESGIQNYSTCRYSAPLFLSHPHFLNADPVL   AEAVTGLIPRNQEAHSLEIDHFVTOIPMNCSS   KLQLSLMKSVAGGGTOKLEPVLYPLLWFA   ESGAMEGETLJHTFYTQLVLMFKVMHYAQVY   LLALGCVLLLVPVIQURSQEKCYLFWSSKK   GSKDKEAIQAYSESLMTSAPKGSVLQEAKL   WMSCALGOVALFFYDTOIPMNCSS   GSKDKEAIQAYSESLMTSAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL   WMSCALGOVALSTAPKGSVLQEAKL	1	1	Į		peptide	}	/=possible nucleotide deterior, /-possible
VMMPSEILKGEKPQVPRERGPYYYREFRHINGT	(	1	1	[	sequence		nucleotide insertion
TENNNDTYSELEYRTTG-GPGKSHIGSESDYV   MPNILUGAAVMENREMTIKLIMTLAFTITL   GERAFMINTVGEIMWGYKDPLVNLINKYPT   GMPPFKDYRGITAELINNDSDGLTGTGTGVQN   SRIHI-VDKWIGLSKVDF WHSDQCMMINGTS   GQMWPFMPFESELEYSPPACAGEN, MAYKE   SQVFEGIPTYREVAPKTLFANGSIYPPNEGFCP   CLESGION-VSTCERS-SAPLFI SHPH-NADPVL   AEA-VTGLHPNOEAHSI-ELDHEVTGIPMNCS-V   KLQISLYMKSVAGGGTKKEREVLYPLLWFA   ESGAMEGETI HTTYTQL VILMPKVMHYAQVV   SALGISLYMKSVAGGGTKKEREVLYPLLWFA   ESGAMEGETI HTTYTQL VILMPKVMHYAQVV   SALGISLYMKSVAGGGTKKEREVLYPLLWFA   ESGAMEGETI HTTYTQL VILMPKVMHYAQVV   SALGISLYMKSVAGGGTKKEREVLYPLLKYQ   FALLIC VILL VPI/CQURSQEKCYLYPLSSKK   GKDKEAIQAYSESLMTSAPKGSVLQEAKL   VITSCHIPFAGGGVKAFSSLMTSAPKGSVLQEAKL   VITSCHIPFAGGGVKAFSSLMTSAPKGSVLQEAKL   VITSCHIPFAGGGVKAFSGKOKLC-VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VITSCHIPFAGGGVKAFSGKOKLL   VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VNMGDRISMVQDPGSQAPTSWISSGCVFQTI   VNMGDRISMVQDGSQAPTSWISSGCVFQTI   VNMGDRISMVQDGSQAPTSWISSGCVFQTI   VNMGDRISMVQDGSQAPTSWISSGCVFQTI   VNMGDRISMVQDGSQAPTSWISSGCVFQTI   VNMGDRISMVQDGSQAPTSWISSGCVFQTI   VNMGDRISMVQDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			+				QVLKNVRIDPSSLSFNMWKEIPIPFYLSVYFFD
MPNILVLGAAVMMENKEMTLKLIMTLAFTI-   GERAFMINTVOELMWGYKDPLVNLINKYFP     GMFPKUNFGLFAELINNSDGLFTOFTGVOW)     SRIHLI-VOKWIGLSKVFWHSDOCHMINGTS     GOMMPFFMIPESSLEFYSPEACRSMKLMYKE     SGVFEGIPTYREVAPTLEANGSIPPHEGFCP     CLESGIONYSTCRSAPLILSHPHILNAPVI-   ABAYTGLHPMQEAHSLFLDIHPVI-PDEMPKS-   KLQLSI-MKSVAGIGGTGKIEPVI-PLIMPS-   KLQLSI-MKSVAGIGGTGKIEPVI-PLIMPS-   KLQLSI-MKSVAGIGGTGKIEPVI-PLIMPS-   ESGAMEGETLIHTYTQL-VLMPK-METY-AQYV     LLALGOVILLI-VVI-QUIRSQBK-VLT-WSSSIK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     GSKDKEAIQAYSSLMTSAFKGSVI-QEAK     FALLSLU-SSSLWSLSLCPEITOA     VTISCIUPFAGE     PMMGTIGGKYCMDPAVIAGVI-SKRS-PGOKIT     VTISCIUPFAGE     CONTROL	1		ļ	}	,		VMNPSEILKGEKPQVRERGPYVYREFRHKSNI
GERAFMINTYGEIMWGYKDPLYNLINKYPF   GMPPPKDKPGLAELNINSDGGITTOFTGYON    SRIHLVDKWNGLSKVDFWHSDQCMMINGT    GQMWPPFMPESELSENSYBEACHSKMKMYKE    GCRIGNYSTGESELFYSPEACRSKKLMYKE    SCYPEGIPTYREVAPKTLFANGSIVPPNEGFCP    CLESGIQNYSTGESAPLFLSHPHANDPVL     AEAVTGLHPNGEAHSLELDHIPVTGIPMNCS    KLOLSLYMKSVAGGGTOKERPVLPLUWFA    ESGAMEGETLHITPYTGLVJMPKWHHYAQVI    LALGCYLLL VPWIQGIRGNECKVLFWSSKK    GSKDKEALQAYSESLMTSAPKGSVLQEAKL    GSKDKEALQAYSESLMTSAPKGSVLQEAKL    GSKDKEALQAYSESLMTSAPKGSVLQEAKL    CONTROL     AHLPDTLLPPHSPTVTPKSFGCKAFSRS    FCLLSLVSSSLSSLSLCPTIQA    VTTSCHPFAFGLGVRASELAEIDMPYLLKYQ    PMMQTIGGK YCMDPAVLAGVLSKKSPGDKIL    VNMGDRISHWVQDPGSQAPTSWBSEQVPQTI    VNMGDRISHWVQDPGSQAPTSWBSEQVPQTI    VNMGDRISHWVQDPGSQAPTSWBSEQVPQTI    EVITTITELQREPTVTPDQVLARAKYLKRHG    FASAGGAGTYFCSUGGKKKALIVG    HOWERSTANDARD     AMASTLEYSPSLRRLVGPAAGFSRAARADL    HVKKNOVGKVGDQLLAIKGGGKKKALIVG    HCMPGPRMTPRFDSNNVVLEDMGNPVGTN    KTPIPTSLRKREGEYSKVLALAONPVPVT    KTPIPTSLRKREGEYSKVLALAONPVPVT    KTPIPTSLRKREGEYSKVLALAONPVPVT    TQYLQPRSPEECKMFACAKLACTPSLRAGSR    VAYRPISASVLSRPEASRTGEGSTVPNGAQNTV    VAGSGAGGTYFGOSLIGVARNFSLKQQLFSV    ALGEFALSEAMGLCLMVFALIFINGGAATVG    VAGSGAGGTYFOSLIGVARNFSLKQQLFSV    ALGEFALSEAMGLCLMVFALIFINGGSPITDT    CQGLI GDOWLLAALGSLTTCPKLLVRVVYGR    QSFKNYAGENFOWPFONOPOSPITION     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRANDARD     GRA			1			1	TFNNNDTVSFLEYRTFQFQPSKSHGSESDYIV
GMPPENDKPGLFAELNNSDSGLFTGFTGVQNI   SRIHLVDKWIGLSKVDFWHSDQCNMINGTS   SRIHLVDKWIGLSKVDFWHSDQCNMINGTS   SRIHLVDKWIGLSKVDFWHSDQCNMINGTS   GQMWPPEMTPESSLEFYSPEACRSMKLMYKE   SGYEGIPTYREVAPKTLFANGSIVPPNEGGCP   CLESIGIONVSTCRFSAPLFLSIPHPLANDPVL   AEA/TGLHPNOEANISLEDIDIPYTGIPMNCSV   KLQLSLYMKSVAGIGGTGEPVVLPLLWPA   ESGAMEGETLHTYTQLVLMPAMDPVL   AEA/TGLHPNOEANISLEDIDIPYTGIPMNCSV   KLQLSLYMKSVAGIGGTGEPVVLPLLWPA   ESGAMEGETLHTYTQLVLMPAWIMTAQVY   LLALGCVLLLVPVICQIESQEKCYLFWSSSKK   GSKDKRSAQAYTSSIMTSARKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GSKDKRSAQAYTSSIMTSAPKGSVAQEAKL   GRAVPRSQDLSCOPCROVLARAKYLKRHG   F			1	1			MPNILVLGAAVMMENKPMTLKLIMTLAFTIL
SRIHLVDKWNGLSKVDFWHSDQCNMINGTS GQMPPEMPTESSLEFYSERSMKLMYKE SGYEGIPTYRFVAPKTLFANGSIYPPNEGFCP CLESGIONVSTCEPSAPLELSHPHTLNADPVL AEAVTGLHPNQEAHSLFLDIHPVTGPHNCSV KLQLSLYMKSVAGIGQTGKIPVVLPLLWFA ESGAMEGETLHITFYTQLVLMPKVMHYAQYV LLALGCVLLLVPVICQIRSQEKCYLFWSSSKK GSKDKEAQAVSSISINTSAPROSVLQBAKL  1033 2383 A 8595 595 767 AHLPDTLLLPFHSPTVPTPRSFQCSQKACFSRS FCLLSLVSSSLVSLSLCPPTQA  1034 2384 A 8597 640 164 VTTSCUIPFAFGLGVKASERLAEIDMPYTLLKYQ PMMQTIGGKYCMPDAVIAGVLSKKSFGDKIL VNMGDRTSMVQDFGSQAFTSWISESQVFQTT EVLTTHITELGRFFTWTPDYLRGQLGVYSL GAGYVRSSQDLSCDFCNDVLARAKYLKRHG F  1035 2385 A 8603 936 204 AMASTLEYSFSPLRRLVGPAAGFSRAARADL SWDPMAFFTGLWGPFTWTPDYLRGQLGVYSL GAGYVRSSQDLSCDFCNDVLARAKYLKRHG F  1036 2386 A 8606 1 562 PTRAHSFDLCCSPFCRRLIGREGGEPTSPV TOYLOPRSFEECKMFACAKLACTPSLIRAGSR VAYRPISASVLSKPEASRIGEGTVYNGAQNG VAGSGAGIGTVGSLIGVAMPLIKAGSR VAYRPISASVLSKPEASRIGEGTVYNGAQNG VAGSGAGIGTVGSLIGVAMPLIKAGSR VAYRPISASVLSRPEASRIGEGSTVYNGAQNG VAGSGAGIGTVGSLIGVAMPLIKAGSR VAYRPISASVLSRPEASRIGEGSTVYNGAQNG VAGSGAGIGTVGSLIGVAMPLIKAGSR VAYRPISASVLSRPEASRIGEGSTVYNGAQNG VAGSGAGIGTVFGSLIGVAMPLIKAGSR VAYRPISASVLSRPEASRIGEGSTVYNGAQNG VAGSGAGIGTVFGSLIGVAMPLIKAGSR VAYRPISASVLSRPEASRIGEGTVFTDT GMVAHINNSELKAKGVGCHDNAQNIFGNSF EELRAACLRKGELFEDLEPSSIGFKDLG GFSKNYQNISWGRRKDINNPLFINDGISPTDI CQGLIGDCVLLAAIGSLTTCFRLLTRYVRGG GSYKKNYAGIFFGGWANGVVVDDL PTKNDKLVFVHSTERSFWSALLEKAYAKLS GSYERALSGGSTMEGLEDTIGAVQSFQUQPF PONLLRLIKKAVERSSLMGCSEVTSDSLES MTDKMLVKGHFGWAYSVTGLQDVHNSKMSAGG RNFGTFWTNPGKLSTPGDPFEDDAGON VCCTLVALMQKNWRHARQQGAQLQTIGFV LYAYRKEFQNIQDVHLKKEFFTKYQDHGFSEL FTNSRVSQLRIPPGFWIIFSFFPHRDADFL LRVFTEKHESSWELLDENYAGQQQQQLQTIGFV LYAYRKEFGNIQDVHLKKEFFTKYQDHGFSEL FTNSRVSQLRIPPGFWIIFSFFPHRDADFL LRVFTEKHESSWELLDENYAGQCQGLKXSED DDDQDFFLIRKIVAGGEGGIVTSFEDPHDDGDDAGON VCCTCLVALMQKNWRHARQQGAQLQTIGFV LYAYRKEFGNIQDVHLKKEFFTKYQDHGFSEL FTNSRVSQLRIPPGFWIIFSFFPHRDADFL LRVFTEKHESSWELLDENYAGCQCGLKYSED DDDQDFFLIRKIVAGGEGGIVTSFTEDPHDDGDDAGON VCCTCLVALMQKNWRHARQQGAQLQTIGFV LYAYRKEFGRINGFFECDDAGDHSGT LRVFTEKHESSWELLDENYAGCQCGLGKYSED DDDDGFFISSFCCLLKTMFTFTLIMDDWFTCDCDDHSGT LNSTEMBLIUFERGERGCLG	Į	İ					GERAFMNRTVGEIMWGYKDPLVNLINKYFP
GOMMPPPMIPESSLEFYSEACRSMKLMYKE   SGYEGIPTYRVAPKTLFANGSYPPNEGFCP   CLESGION/STCRFS&PLFLSIPHPLNADPYL   AEA/TGLHPNOEAHSIELDIPHPYTGIPMNCSV   KLQLSLYMKSVAGIGOTGKIEPVVLPLWPA   ESGAMEGETLHIFTYTQLYMPAWCHTAQYV   LLALGCVLLIVPVICQIRSQEKCYLFWSSSKK   GSKDKSAIQAYSESIMTSAPKGSVLQEAK!   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CON		1	1	1	1		GMFPFKDKFGLFAELNNSDSGLFTGFTGVQNI
GOMMPPPMIPESSLEFYSEACRSMKLMYKE   SGYEGIPTYRVAPKTLFANGSYPPNEGFCP   CLESGION/STCRFS&PLFLSIPHPLNADPYL   AEA/TGLHPNOEAHSIELDIPHPYTGIPMNCSV   KLQLSLYMKSVAGIGOTGKIEPVVLPLWPA   ESGAMEGETLHIFTYTQLYMPAWCHTAQYV   LLALGCVLLIVPVICQIRSQEKCYLFWSSSKK   GSKDKSAIQAYSESIMTSAPKGSVLQEAK!   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CONTROL   CON	l	1					SRIHLVDKWNGLSKVDFWHSDQCNMINGTS
SGYEGIPTYRPVAPKTLFANGSIYPPNEGGP	l .						GOMWPPFMTPESSLEFYSPEACRSMKLMYKE
CLESGIQNYSTCRTSAPLELSHPHENADPVL     ARANTGLHPNQEAHSI-EJDHPVTGIPMNCSV     KLQLSLYMKSVAGIGOTGKIEPVVLPLLWFA     ESGAMEGETLHTFYTQLWKPVMHVAQYV     LLALGCVLLVPVICQIRSQEKCYLFWSSKK     GSKDKEAJQAYSESLMTSAPKGSVLQEAKL     1033   2383   A   8595   595   767     AHLPDTLLEPHSFTVTFKSFQCSQKACFSRS     FCLLSLVSSSLVSLSLCPPLTQA     A   8597   640   164   VITSCIIPFAFGGVASETLAEIDMFYLLKYQ     PMMQTIGGKYCMDPAVIAGVLSKSFGDKIL     VMGDRTSMVQDPGSQAFTSWISESQVPQTT     EVLTTRITELQRRPFTWTPDQYLRGGLCAYSG     GAGYVRSSQDLSCDFCNDVLARAKYLKRIG     FVANTSKIPFAFTLVGPAAGFSRAARDL     SWDPMAFFTGLWGPFTCVSRVLSHHCFSTTG     SLSAJQKMTRVRVVDNSALGNSPYHRAPRCI     HVYKKNGVGVCDQLLAIKGGKKKALIVG     HCMFGPRNTTRFDSNNVVLEDINGRYGTRI     KTPITSLKREGEYSKVLAIAQNFV     TRAHSPDLCSSFCRRLLGREAGEPTSV     TQYLOPRSPECKMFACIACTPSLIRAGSR     VAYRISASVLSRPASRTGEGSTVPNGAQNG     VSQLJQREFGTSAISRDDTAAKTGAGAATVG     VAGSGAGIGTVFGSLIGYARNFSLKQQLFSY     ALIGHALSKAGVGQHDMAQNFGNQSF     GYFKLSSEASLDGSGEDEPRGSCAEPIFTDT     GMVAHINISRIKAKGVGQHDMAQNFGNQSF     GYFKLSGGSTMEGLEDFTGGVAQSFQLQRP     PQNLLRLRRAVERSSLMGCSEVTSSELES     MTDKMLVVFWSTERSSETSWSALLEKAYAKLS     GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP     PQNLLRLRRAVERSSLMGCSEVTSSELES     MTDKMLVRCHASYSVDFLNNFTLEICNL     PTRNBKLVFVHSTERSSETSWSALLEKAYAKLS     GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP     PQNLLRLRRAVERSSLMGCSEVTSSELES     MTDKMLVRGHASYSVTLQDVHYRGKMETLI     RVRNPWGREWNGAWSDSAREWEVASDIQ     MQLIHKTEGGFFWSYOPILNNFTLEICNL     TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC     RNHPGTF WYNPOFKISLEPTKYQDHGFSE     FTNSREVSQLRLPPGEVIIIPSTFEPHRDADFL     LRVTTERHSESWELDENNYAGQLGEKVSED     DMDQDFLHLPHTWRGKEIGYPELQRLINR     MAIKFKSFKTKGFGLDACRGMINDKDOG     KIGLLEFKILWKLIKKWLKKMINKDNGCHANN     KIGLLEFKILWKLIKKWLKMINKDNGCHANN     MAIKFKSFKTKGFGLDACRGMINDKDOG     KIGLLEFKILWKLIKKWLIKKMINKDNGCHANN     DNDILIDFSFISCFLRLKINKKKINKMINGLOCHANN     DNDILIDFSFISCFLRLKINKKINKMINGVLVARYA     DNDILIDFSFISCFLRLKINKKINKMINGVLVARYA     DNDILIDFSFISCFLRLKINKINKENGVLVARYA     DNDILIDFSFISCFLRLKINTETHT IMDFKNT	1	l	}				SGVFEGIPTYRFVAPKTLFANGSIYPPNEGFCP
AEA/TGLIPMOGARIST.FUDIPMYTGIPMNCSY   KLQLSLYMKSVAGIGGTOKIEPVVLPLLWFA   ESGAMEGETLHTEYTQLVLMFKVMTAQTY   LLALGCVLLLVPMCQUISQEKCYLFWSSSKK   ESCAMEGETLHTEYTQLVLMFKVMTAQTY   LLALGCVLLLVPMCQUISQEKCYLFWSSSKK   GSKOKEALQAYSESLMTSAPKGSVLQEAKL   GSKOKEALQAYSESLMTSAPKGSVLQEAKL   AHLPDTLLLPPHSPTVPTFKSFQCSKACFSRS   FCLLISLVSSSLVSILSLCPLTQA   TCLLISLVSSSLVSILSLCPLTQA   TCLLISLVSSSLVSILSLCPLTQA   TCLLISLVSSSLVSILSLCPLTQA   TCLLISLVSSSLVSILSLCPLTQA   TCLLISLVSSSLVSILSLCPLTQA   TCLLISLVSSSLVSILSLCPLTQA   TCLLISLVSSSLVSILSLCPLTQA   TCLLISLVSSLVSILSLCPLTQA   TCLLISLVSSLVSILSLCPLTQA   TCLLISLVSSLVSILSLCPLTQA   TCLLISLVSTSPPLTRALGCRAFT WTLKTYPTTLGARPTT WTPOQYLRGGLCAYSG   GAGYVRSSQDLSCDFCNDVLARAKYLKRHO   F	1				1	1	CLESGIONVSTCRFSAPLFLSHPHFLNADPVL
KLQLSLYMKSVAGIGGTGKIEPVVLPLLWFA			ł	ŀ			AFAVTGI HPNOEAHSLFLDIHPVTGIPMNCSV
ESGAMEGETLHTFYTQLVLMWMHYAQYU   LALGCVLLLYPVICQIRSQEKCYLFWSSSKK     GSKDKEAIQAYSESLMTSARKOSVLQEAKL     1033   2383   A   8595   595   767   AHLPDTLLLPHSFTYFRSFQCSQKACFSRS     FOLLSLVSSSLVSLSLCPPLTQA     1034   2384   A   8597   640   164   VITSCIIFFAFGLGVRASERI AEIDMPYLLKYQ     PMMQTIGQKYCMDPAVIAGVLSRKSPGDKIL     VNMGDRTSMYQDFGSQAPTSWISSGVVFQTI     EVLTTRITLQRIFFTYDQVLRGGLCAYSG     GAGYVRSSQDLSCDFCNDVLARAKYLKRHG     F		ì	Į.	j	1		KLOLSLYMKSVAGIGOTGKIEPVVLPLLWFA
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TQYLQPRSPEECKMFACAKLACTPSLIRAGSR VAYRPISASVLSRPEASRTGEGSTVFNGAQNG VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY AILGFALSEAMGLFCLMVAFLILFAM  SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDIINNPLFINDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGYYELQRLINR MAKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1						KTPIPTSLRKREGEYSKVLAIAQINFV
TOYLOPRSPELKMFACALACTISLIKAGISK VAYRPISASVLSRPEASRTGEGSTVFNGAQNG VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY AILGFALSEAMGLFCLMVAFLILFAM SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLKKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLNR MAKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1036	2386	TA	8606	1	562	PTRAHSFDLCCSPCRRRLLGREEAGEEPTSPV
VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY AILGFALSEAMGLFCLMVAFLILFAM  SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDIINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCFKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDIJIDFDSFISCFLRLKTMFTFFLTIMDPKNT	1 1050	2000					TOYLOPRSPEECKMFACAKLACIPSLIKAGSK
VAGSGAGIGTYFGSLIIGYARNPSLKQQLFSY AILGFALSEAMGLFCLMVAFLILFAM  1037 2387 A 8615 2 2364 SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDIINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFFGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSQQTLPPGEFUIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGI LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1	1		ļ			VAYRPISASVLSRPEASRTGEGSTVFNGAQNG
AILGFALSEAMGLFCLMVAFLILFAM  SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDIINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRIGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1		-	1	1	1	VSQLIQREFQTSAISRDIDTAAKFIGAGAATYG
1037 2387 A 8615 2 2364 SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHIDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDIINPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKLLKWKLKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	ŀ	l l	1	1			VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY
GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGPSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKIL WKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDI.IIDFDSFISCFLRLKTMFTFFLTMDPKNT				1		1	AILGFALSEAMGLFCLMVAFLILFAM
GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGPSEI FTNSREVSSQLRLPPGEYJIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKIL WKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDI.IIDFDSFISCFLRLKTMFTFFLTMDPKNT	1027	7297	ΙΔ-	8615	2	2364	SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT
EELRAACLRKGELFEDPLFFAEPSSLGFKDLG PNSKNVQNISWQRPKDIINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDILIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1037	2367	^	0015	_		GMVAHTNNSRLKAKGVGOHDNAQNFGNQSF
PNSKNVQNISWQRPKDIINPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTIFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1		1			1	EELRAACLRKGELFEDPLFPAEPSSLGFKDLG
CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT			1		1		PNSKNVONISWORPKDIINNPLFIMDGISPTDI
QSFKKNYAGIFHFQIWQFGQWVNVVVDDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT			i			1	COGILGDCWLLAAIGSLTTCPKLLYRVVPRG
PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDIJIIDFDSFISCFLRLKTMFTFFLTMDPKNT			i				OSEKKNYAGIFHFOIWQFGQWVNVVVDDRL
GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGPSEI FTNSREVSSQLRLPPGEYIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT			J		1	1	PTKNDKLVFVHSTERSEFWSALLEKAYAKLS
PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	i						GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP
MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT				1	1		PONLLRLLRKAVERSSLMGCSIEVTSDSELES
RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT				1	1		MTDKMI.VRGHAYSVTGLODVHYRGKMETLI
MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1		1		-	1	RVRNPWGRIEWNGAWSDSAREWEEVASDIO
TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1			j			MOLI HKTEDGEFWMSYODFLNNFTLLEICNL
RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGPSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1	!			1		TROTI SGDYKSYWHTTFYEGSWRTGSSAGGC
VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	-	Ì				1	PNILIPGTEWTNPOFKISI PEGDDPEDDAEGNV
LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1					ļ	VVCTCI VAI MOKNWRHAROOGAOLOTIGEV
FTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT			1				A ACTOR APPROPRIATE REPLEASED A ACTOR APPROPRIATE REPLEASED A ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR ACTOR APPROPRIATE REPLEASED AND ACTOR APPROPRIATE REPLEASED AND ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR ACTOR AC
LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLJIDFDSFISCFLRLKTMFTFFLTMDPKNT			-				ETICPEVSOI DI PROEVIIIPETEEPHEDADEI
DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLJIDFDSFISCFLRLKTMFTFFLTMDPKNT	1	į	1				LINGUE ASSOCIATE DEAVISATION UNDER AGED
MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT		<b>†</b>	-				LKALIEVUSES A ETDEAMI VEGT GER ASED
KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT			ł			1	DWDOOLTHELY CECL DACEON LEDONEDAY
LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT	1	:	l		i		MAIKEKSEK I KUFULDAUKUMINLMUADUSU
DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT						1	KLGLLEFKILWKKLKKWMDIFKEUDQDHSGI
DDDLIIDFDSFISCFLRLK IMF I FFL I MDPKN I GHICLSLEQVLGEGWEGICRIAPACPSTPPPPS			Ì				LNSYEMRLVIERAGIKLNNK VMQ VL VAK I A
GHICLSLEQVLGEGWEGICKIAPACPSTPPPPS	1						DDDLIIDFDSFISCFLKLK1MF1FFL1MDFKN1
	-	i	1				GHICLSLEQVLGEGWEGICKLAPACPSTPPPPS

SEQ ID NO: of	SEQ ID	Met	I CEO I			
			SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	p=pncnylalatific, U=Otycine, II Tibudano,
eotide	seq-	{	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
- 1		ì	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			, , ,	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ĺ				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ŀ		]	1		Sequence	/=possible nucleotide deletion, \=possible
		1		peptide	ļ	nucleotide insertion
				sequence		SDVPGPASCPRLFPPWDLLPVSTVAADDHVGI
					1	1
		Į.		<b>\</b>		EAL
1020	2388	A	8621	3	1494	RSRMARAPLGVLLLLGLLGRGVGKNEELRLY
1038	2300	^	8021	"	1 *	HHLFNNYDPGSRPVREPEDTVTISLKVTLTNL
		i .	1		1	ISLNEKEETLTTSVWIGIDWQDYRLNYSKDDF
			1		1	GGIETLRVPSELVWLPEIVLENNIDGQFGVAY
1	ļ		1		1	DANVLVYEGGSVTWLPPAIYRSVCAVEVTYF
	ł	1	1	1	į	DANVLY IEGGSVI WELLALIKSVEAVEVILL
h	1	1	1		i	PFDWQNCSLIFRSQTYNAEEVEFTFAVDNDG
	l	1	1	ì	-	KTINKIDIDTEAYTENGEWAIDFCPGVIRRHH
	1	1	1	l	-	GGATDGPGETDVIYSLIIRRKPLFYVINIIVPCV
	ļ				1	LISGLVLLAYFLPAQAGGQKCTVSINVLLAQT
		1	1	1	1	VFLFLIAQKIPETSLSVPLLGRFLIFVMVVATLI
;	ł	1	ļ	Ì	1	VMNCVIVLNVSQRTPTTHAMSPRLRHVLLEL
	1	1	1	i		LPRLLGSPPPPEAPRAASPPRRASSVGLLLRAE
	ĺ	í	ſ	1		ELILKKPRSELVFEGQRHRQGTWTAAFCQSL
	1		1	1		ELILKKPRSELYFEUQKIRQUI WIAAI CQSE
·	1	1	1	1	1	GAAAPEVRCCVDAVNFVAESTRDQEATGEE
l	1		1	1		VSDWVRMGNALDNICFWAALVLFSVGSSLIF
l		i	l l			LGAYFNRVPDLPYAPCIQP
1039	2389	A	8636	i	900	PGRERPGGGGARRRPQHLPALLPSERPDCATL
1039	2309	^	0030	1.	1	OAMENELPVPHTSSSACATSSTSGASSSSGCN
	1	ł	1			NSSSGGSGRPTGPQISVYSGIPDRQTVQVIQQ
		1		i		ALHRQPSTAAQYLQQMYAAQQQHLMLQTA
Į.				ļ		ALQQHLSSAQLQSLAAVQQASLVSNRQGST
		1	1	1		SGSNVSAQAPAQSSSINLAASPAAAQLLNRA
	j		1	Į	i	SGSNVSAQAPAQSSSINLAASI AAAQEENTO
	1			ĺ		QSVNSAAASGIAQQAVLLGNTSSPALTASQA
l			1			QMYLRAQMLIFTPTATVATVQPELGTGSPAR
ļ	)	ļ	1	1	ł	PPTPAQVQNLTLRTQQTPAAAASGPTPTQPVL
			1			PSLALKPTPGGSQPLPTPA
<u> </u>	-		8645	98	1388	ASQLAFGGKLTSTPSRDFQGCGRGAVTCCSF
1040	2390	A	8043	70	1300	HEHRHQSGRCLSTGMAPNLKGRPRKKKPCPQ
	1		1		J	RRDSFSGVKDSNNNSDGKAVAKVKCEARSA
}		(	1			LTKPKNNHNCKKVSNEEKPKVAIGEECRADE
	1		1			QAFLVALYKYMKERKTPIERIPYLGFKQINLW
1			l.	}		TMFQAAQKLGGYETITARRQWKHIYDELGG
1	1	1				IMPUAAUKLUUTETTIAKKU WATIITDEEU
1	1		1	1	1	NPGSTSAATCTRRHYERLILPYERFIKGEEDKP
ſ	1		1			LPPIKPRKQENSSQENENKTKVSGTKRIKHEIP
1	1	1	}		1	KSKKEKENAPKPQDAAEVSSEQEKEQETLISQ
1	1	1	1			KSIPEPLPAADMKKKIEGYQEFSAKPLASRVD
	1					PEKDNETDOGSNSEKVAEEAGEKGPTPPLPSA
1	1	ì				PLAPEKDSALVPGASKQPLTSPSALVDSKQES
1	1	1				KLCCFTESPESEPQEASFPRLPHHTGHRWQTR
	1	1				MRRRMTNCPPWQITLPTAP
1	1		L			LLQEMCTKTIPVLWGCFLLWNLYVSSSQTIYP
1041	2391	A	8646	113	1492	LUCEMCIVILA FACRICA CO CO CO CO CO CO CO CO CO CO CO CO CO
1				1		GIKARITQRALDYGVQAGMKMIEQMLKEKK
						LPDLSGSESLEFLKVDYVNYNFSNIKISAFSFP
		1		1		NTSLAFVPGVGIKALTNHGTANISTDWGFESP
					Į	LFVLYNSFAEPMEKPILKNLNEMLCPIIASEVK
		1		1		ALNANLSTLEVLTKIDNYTLLDYSLISSPEITE
		i		1		NYLDLNLKGVFYPLENLTDPPFSPVPFVLPER
	1	1		1		SNSMLYIGIAEYFFKSASFAHFTAGVFNVTLS
				1	j	DUDING HOUSE TELESCOPERATE TO ALL ALLES
1	1	1		1		TEEISNHFVQNSQGLGNVLSRIAEIYILSQPFM
						VRIMATEPPIINLQPGNFTLDIPASIMMLTQPK
	1			1		NSTVETIVSMDFVASTSVGLVILGQRLVCSLS
		1		1		LNRFRLALPESNRSNIEVLRFENILSSILHFGVL
	1			1		PLANAKLQQGFPLPNPHKFLFVNSDIEVLEGF
	1	1				LLISTDLKYETSSKQQPSFHVWEGLNLISRQW
1		}		1		
	1	1				RGKSAP
	1	1	,			
1042	2392	A	8672	538	170	ARRIARTRESKAAVSQDNVPALQPGKKKKLR LGGKKKKFKFFRLPKEFKKQLMYSPSNFKKM

						- Contains
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	l=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			amino acid residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ			Sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
		<u> </u>		sequence		TSLAGNTVQCLNKLKYVIYSAQYPAYGNITT
		1	İ	Į.		LOMITSTDHVLEODFWICFTFYSVKERQI
	0202		8688	359	17	GLKTRAPATPTFOREVLGPAKQDMQRRCPRI
1043	2393	Α	0000	339	1 1	GLMTSLLKPIKRRWRDYKRWKSGGFTGESC
		į	ł			HHADTLGDRGGLQGDHSELLQWQKRILRTE
				ļ		GEPSPKYISKNIFPICSYITGFL
1044	2394	A	8718	292	1490	GTVKTSVATPITAGHSCSSGGVLQVKSPATQS
1044	2394	^	0710	->-		GFKFTSKMEDFNMESDSFEDFWKGEDLSNYS
		1		\		YSSTLPPFLLDAAPCEPESLEINKYFVVIIYAL
					Ī	VFLLSLLGNSLVMLVILYSRVGRSVTDVYLL
		}		1		NLALADLLFALTLPIWAASKVNGWIFGTFLC
	1	}		\		KVVSLLKEVNFYSGILLLACISVDRYLAIVHA
		i i		ĺ		TRTLTQKRYLVKFICLSIWGLSLLLALPVLLFR
	}	1		1		RTVYSSNVSPACYEDMGNNTANWRMLLRIL
		1			1	PQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQK HRAMRVIFAVVLIFLLCWLPYNLVLLADTLM
j		1	1	1		RTQVIQETCERRNHIDRALDATEILGILHSCLN
		}	1			PLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDS
ļ		1				RPSFVGSSSGHTSTTL
				<del> </del>	3184	FRANLAITVANRRGAQGGKMHTCCPPVTLEQ
1045	2395	Α	8724	254	3104	DLHRKMHSWMLQTLAFAVTSLVLSCAETIDY
		1	Ì	1	1	YGEICDNACPCEEKDGILTVSCENRGIISLSEIS
ł	1	1				PPRFPIYHLLLSGNLLNRLYPNEFVNYTGASIL
ļ	1	1			İ	HLGSNVIQDIETGAFHGLRGLRRLHLNNNKL
						FLURDDTFLGLENLEYLOVDYNYISVIEPNAF
ł	ì	Ì		ľ	1	GKLHLLOVLILNDNLLSSLPNNLFRFVPLTHL
		1				DLRGNRLKLLPYVGLLOHMDKVVELQLEEN
	i	1	ļ		}	PWNCSCELISLKDWLDSISYSALVGDVVCETP
Ì		ł	1		Ì	FRIHGRDLDEVSKQELCPRRLISDYEMRPQTP
		1				LSTTGYLHTTPASVNSVATSSSAVYKPPLKPP
1	1	ĺ				KGTRQPNKPRVRPTSRQPSKDLGYSNYGPSIA
			•			VOTKSPVPLECPTACSCNLQISDLGLNVNCQE
						RKIESIAELQPKPYNPKKMYLTENYIAVVRRT
}			1	-		DLLEATGLDLLHLGNNRISMIQDRAFGDLTN
ì		-				LRRLYLNGNRIERLSPELFYGLQSLQYLFLQY
	ì			1		NLIREIQSGTFDPVPNLQLLFLNNNLLQAMPS
1		1				GVFSGLTLLRLNLRSNHFTSLPVSGVLDQLKS
		-		ļ		LIQIDLHDNPWDCTCDIVGMKLWVEQLKVG
				1	i	VLVDEVICKAPKKFAETDMRSIKSELLCPDYS
1	1	1				DVVVSTPTPSSIQVPARTSAVTPAVRLNSTGA
				}		PASLGAGGGASSVPLSVLILSLLLVFIMSVFVA
			1			AGLFVLVMKRRKKNQSDHTSTNNSDVSSFN
		ļ				MQYSVYGGGGGTGGHPHAHVHHRGPALPK
	1		j	1		VKTPAGHVYEYIPHPLGHMCKNPIYRSREGN
1	1	1				SVEDYKDLHELKVTYSSNHHLQQQQQPPPPP
		1				QQPQQQPPPQLQLQPGEERRESHHLRSPAYS
1				1		VSTIEPREDILLSPVQDADRFYRGILEPDKHCST
	1		{	1		TPAGNSLPEYPKFPCSPAAYTFSPNYDLRRPH QYLHPGAGDSRLREPVLYSPPSAVFVEPNRNE
1						YLELKAKLNVEPDYLEVLEKQTTFSQF
						SPSAAGGLAWVSLALGSGSRGRDHSGSGVGT
1046	2396	A	8736	28	452	SPSAAGGLAWVSLALGSGSRORDHSGSGVGT AMAGALVRKAADYVRSKDFRDYLMSTHFW
		j		}		AMAUALVKKAADI VKONDENDI LIMSI NI W
						GPVANWGLPIAAINDMKKSPEIISGRMTFALC
		-	1	1		CYSLTFMRFAYKVQPRNWLLFACHATNEVA
		1	1	1		QLIQGGRLIKHEMTKTASA
		1				The same of the control of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the
1047	2397	A	8741	673	924	ALPGTPOOTVTLNTDGKVKSFTSPHSNPNLPP
1047	2397	A	8741	673	924	ALPGTPQQTVTLNTDGKVKSFTSPHSNPNLPP AKFFTSLQSLNWSSHLPPSPATESVGKRGNAK
1047	2397	A	8741	673	924	ALPGTPOOTVTLNTDGKVKSFTSPHSNPNLPP

			aro.	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning		F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	<b>\</b>	in	nucleotide	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location		M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence	1		914	ng to first	acid residue	Q=Glutamine, K=Arginile, S=Serile,
uciico		ļ	ļ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	ì	}	peptide	•	/-possible nucleotide deletion, \-possible
ł		1	1	sequence		nucleotide insertion
			<b></b>	Sequence	<del> </del>	VAVPNGQPPSAARYMPREVPPRFRCQQDHK
			ł			VLLKRGQPPPPSCMLLGGGAGPPPCTAPGAN
1	1	1	ì	]		PNNAQVTGALLQSESGTAPDSTLGGAAASNY
i	1		1			ANSTWGSGASSNNGTSPNPIHIWDKVIVDGS
<b>\</b>			1			ANSI WUSUASSINIUI SETTI III W DICTI DOS
1	1	ì				DMEEWPCIASKDTESSSENTTDNNSASNPGSE
1					•	KSTLPGSTTSNKGKGSQCQSASSGNECNLGV
ĺ		1	1			WKSDPKAKSVQSSNSTTENNNGLGNWRNVS
1	1					GQDRIGPGSGFSNFNPNSNPSAWPALVQEGTS
1	1	1		Ĭ		RKGALETDNSNSSAQVSTVGQTSREQQSKME
1	1	{				NAGVNFVVSGREQAQIHNTDGPKNGNTNSL
Í		1	1		1	NLSSPNPMENKGMPFGMGLGNTSRSTDAPSQ
Į.		1	1			STGDRKTGSVGSWGAARGPSGTDTVSGQSNS
		1		1		GNNGNNGKEREDSWKGASVQKSTGSKNDS
	1	1	1	1	1	WDNNNRSTGGSWNFGPQDSNDNKWGEGNK
1		1		1		MTSGVSQGEWKQPTGSDELKIGEWSGPNQPN
1		1	1	1	1	WISOASAGE MYCALOSDETVIO TO SOLICO CO
1	ļ	1	1			SSTGAWDNQKGHPLLENQGNAQAPCWGRSS
1	1					SSTGSEVEGOSTGSNHKAGSSDSHNSGRRSY
i	1	1	1		ł	RPTHPDCQAVLQTLLSRTDLDPRVLSNTGWG
	1	1				QTQIKQDTVWDIEEVPRPEGKSDKGTEGWES
i i	1	1	ļ	1		AATQTKNSGGWGDAPSQSNQMKSGWGELS
	1	1	j			ASTEWKDPKNTGGWNDYKNNNSSNWGGGR
1		1				PDEKTPSSWNENPSKDQGWGGGRQPNQGWS
1	1		1			SGKNGWGEEVDQTKNSNWESSASKPVSGWG
1		1	l l			EGGQNEIGTWGNGGNASLASKGGWEDCKRS.
l			1			PAWNETGRQPNSWNKQHQQQQPPQQPPPPQ
i	ı		1			PEASGSWGGPPPPPPGNVRPSNSSWSSGPQPA
1	Ì	1				TPKDEEPSGWEEPSPQSISRKMDIDDGTSAWG
	ļ		1			TPKDEEPSGWEEPSPQSISACAADDEDAH PTP
1	1	İ	ŀ			DPNSYNYKNVNLWDKNSQGGPAPREPNLPTP
	}	}	ļ	1		MTSKSASDSKSMQDGWGESDGPVTGARHPS
ĺ		-	1			WEEEEDGGVWNTTGSQGSASSHNSASWGQG
1	1			ł		GKKQMKCSLKGGNNDSWMNPLAKQFSNMG
1			1			LLSQTEDNPSSKMDLSVGSLSDKKFDVDKRA
		1	1	}	ľ	MNLGDFNDIMRKDRSGFRPPNSKDMGTTDS
1	1	- 1	1	}		GPYFEKGGSHGLFGNSTAQSRGLHTPVQPLN
1		ļ	· I	1		SSPSLRAQVPPQFISPQVSASMLKQFPNSGLSP
1			1	1		GLFNVGPQLSPQQIAMLSQLPQIPQFQLACQL
1					1	LLQQQQQQLLQNQRKISQAVRQQQEQQLA
	1			1	I	RMVSALQQQQQQQQRQPGMKHSPSHPVGPK
		-	1	1	1	PHLDNMVPNALNVGLPDLQTKGPIPGYGSGF
1			1			SSGGMDYGMVGGKEAGTESRFKQWTSMME
				1	1	SSGGMD YOM VOOR EAG LESKING WISHINE
		ĺ		}	1	GLPSVATQEANMHKNGAIVAPGKTRGGSPY
ł	- (	1	[		1	NQFDIIPGDTLGGHTGPAGDSWLPAKSPPTNK
		1				IGSKSSNASWPPEPQPGVPWKGIQNIDPESDP
	1	-		1	1	VVTPGSVLGGTATSPIVDTDHQLLRDNTTGS
Ĭ					1	NSSLNTSLPSPGAWPYSASDNSFTNVHSTSAK
1	1					FPDYKSTWSPDPIGHNPTHLSNKMWKNHISS
1						RNTTPLPRPPPGLTNPKPSSPWSSTAPRSVRG
						WGTQDSRLASASTWSDGGSVRPSYWLVLHN
			j	J		LTPQIDGSTLRTICMQHGPLLTFHLNLTQGTA
1	1	1		1		LIPQIDGSTERTICINQUOTEETFICHETQGTA
			i			LIRYSTKQEAAKAQTALHMCVLGNTTILAEF
1		1	1	-		ATDDEVSRFLAQAQPPTPAATPSAPAAGWQS
			j	- 1		LETGQNQSDPVGPALNLFGGSTGLGQWSSSA
		1				GGSSGADLAGASLWGPPNYSSSLWGVPTVED
-				ĺ	1	PHRMGSPAPLLPGDLLGGGSDSI
				<del></del>	1207	VPWKRQDEQLSLQVETLYLDSPAVIHLLSPTF
1049	2399	A	8748	200	1387	LPPSSLPPFLQIVDSSSSACTLDSFFPFLAPWDS
	[	i		1		PODCGFKDHOPLTLQALTVELARWTLMLLLS
1	1	1	İ	1		PQDCGFKDMQFLTQALT VELARW TEMEDES
		-				TAMYGAHAPLLALCHVDGRVPFRPSSAVLLT
1	1	1	-	1	1	ELTKLLLCAFSLLVGWQAWPQGPPPWRQAA
	.			l		PFALSALLYGANNNLVIYLQRYMDPSTYQVL
		- 1	1	1	1	

			000	The disease	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
{		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ				peptide	354.2	/=possible nucleotide deletion, \=possible
1	1	1		sequence		nucleotide insertion
	<del> </del>	<del>                                     </del>	+	Sequence		SNLKIGSTAVLYCLCLRHRLSVRQGLALLLL
				· ·		MAAGACYAAGGLQVPGNTLPSPPPAAAASP
	1	Į.				MPLHITPLGLLLLILYCLISGLSSVYTELLMKR
						QRLPLALQNLFLYTFGVLLNLGLHAGGGSGP
						GLLEGFSGWAALVVLSQALNGLLMSAVMKH
1	1	1				GSSITRLFVVSCSLVVNAVLSAVLLRLQLTAA
		1				FFLATLLIGLAMRLYYGSR
1050	2400	A	8758	3	1660	WVSSMGFEELLEQVGGFGPFQLRNVALLALP
1030	2400	1 **	0.50			RVLLPLHFLLPIFLAAVPAHRCALPGAPANFS
1						HQDVWLEAHLPREPDGTLSSCLRFAYPQALP
}	1			1		NTTLGEERQSRGELEDEPATVPCSQGWEYDH
	Ì					SEFSSTIATESQWDLVCEQKGLNRAASTFFFA
}	1	1			}	GVLVGAVAFGYLSDRFGRRRLLLVAYVSTLV
	1			1 .		LGLASAASVSYVMFAITRTLTGSALAGFTIIV
		1	ŀ			MPLELEWLDVEHRTVAGVLSSTFWTGGVML
		1		t		LALVGYLIRDWRWLLLAVTLPCAPGILSLWW
	I			1		VPESARWLLTQGHVKEAHRYLLHCARLNGR
						PVCEDSFSQEAVSKVAAGERVVRRPSYLDLF RTPRLRHISLCCVVVWFGVNFSYYGLSLDVS
		[				GLGLNVYQTQLLFGAVELPSKLLVYLSVRYA
1			2	1	1	GRRLTQAGTLLGTALAFGTRLLVSSDMKSWS
į.				1		TVLAVMGKAFSEAAFTTAYLFTSELYPTVLR
		1		}	1	QTGMGLTALVGRLGGSLAPLAALLDGVWLS
ĺ			1		İ	LPKLTYGGIALLAAGTALLLPETRQAQLPETI
		1		1		QDVERKSAPTSLQEEEMPMKQVQN
	1	<del>                                     </del>	0750	515	1625	EIRTPVAVSSAPSGDSEGDEEETTQDEVSSHTS
1051	2401	A	8759	313	1023	EEDGGVVKVEKELENTEQPVGGNEVVEHEV
		1		1		TGNLNSDPLLELCQCPLCQLDCGSREQLIAHV
1	1	1				YOHTAAVVSAKSYMCPVCGRALSSPGSLGR
		-				HLLIHSEDORSNCAVCGARFTSHATFNSEKLP
1				1		EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYP
						AGILLVCNNCAAYRKLLEAQTPSVRKWALRR
						QNEPLEVRLQRLERERTAKKSRRDNETPEERE
1	1					VRRMRDREAKRLQRMQETDEQRARRLQRDR
}				1		EAMRLKRANETPEKRQARLIREREAKRLKRR
				İ		LEKMDMMLRAQFGQDPSAMAALAAEMNFF
		1				QLPVSGVELDSQLLGKMAFEQNSSSLH
1052	2402	A	8763	1106	70	RHGHGGRDRRGGGRVARPGGLGRYPGRGAA
						ASLVFVPTRRRSGPSGTASVAAMAYHSGYGA
						HGSKHRARAAPDPPPLFDDTSGGYSSQPGGY PATGADVAFSVNHLLGDPMANVAMAYGSSI
						ASHGKDMVHKELHRFVSVSKLKYFFAVDTA
1	1	1				YVAKKLGLLVFPYTHQNWEVQYSRDAPLPP
						RQDLNAPDLYIPTMAFITYVLLAGMALGIQK
		1		1		RFSPEVLGLCASTALVWVVMEVLALLLGLYL
	ļ	1				ATVRSDLSTFHLLAYSGYKYVGMILSVLTGL
1						LFGSDGYYVALAWTSSALMYFIVRSLRTAAL
		1		i	1	GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY
]		1	ł			WLTFHLVR
	100	<del> </del>	07/0	2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVF
1053	2403	A	8768	1 4	/12	YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW
1						PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE
			1			VLMDCAHLVKANSIQGCKMNNVNVVYTPW
						SNLKKTADMDVGOIGFHROKDVKIVTVEKK
			1			VNEILNRLEKTKVERFPDLAAEKECRDREER
						NEKKAQIQEMKKREKEEMKKKREMDELRSY
			1			SSLMKVENMSSNODGNDSDEFM
1054	2404	$\frac{1}{A}$	8769	344	527	REATTLACRNSCWVFSRCSLGACKPTVCSMP
1034	2404	^	3707	1		SLSRQGSQTLCLRLAEYCMESVDSQRLLLS
				<del></del>		

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutarnine, R=Arginine, S=Serine,
uence			914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
i	<u> </u>	1		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			}	residue of	sequence	/=possible nucleotide deletion, \=possible
			1	peptide		nucleotide insertion
		<u> </u>	<u> </u>	sequence	1104	QQESPAAGAARMNCKEGTDSSCGCRGNDEK
1055	2405	A	8770	430	1104	KMLKCVVVGDGAVGKTCLLMSYANDAFPEE
				1		VUPTVFDHYAVTVTVGGKOHLLGLYDTAGQ
	1	ļ		i		EDYNOLRPLSYPNTDVFLICFSVVNPASYHNV
		1	l l	ł		OFEWVPELKDCMPHVPYVLIGTQIDLRDDPK
ì		}	j	Į	}	TI ARLI YMKEKPLTYEHGVKLAKAIGAQCYL
		1				ECSALTQKGLKAVFDEAILTIFHPKKKKKRCS
				ļ	,	EGHSCCSII
	2106	<del> </del>	8773	261	332	NPRIOLSGNSCCAGSCRVWLSEQ
1056	2406	A	8778	3	477	PAGIRHEOARGADRMGKCRGLRTARKLRSH
1057	2407	Α	0//0	1	1	RRDOKWHDKOYKKAHLGTALKANPFGGAS
		1				HAKGIVLEKVGVEAKOPNSAIRKCVRVQLIK
1						NGKKITAFVPNDGCLNFIEENDEVLVAGFGR
			ļ	1		KGHAVGDIPGVRFKVVKVANVSLLALYKGK
l						KERPRS
1058	2408	A	8808	171	881	PGLSQEPSGSMETVVIVAIGVLATIFLASFAAL
1038	2400	1				VLVCRQRYCRPRDLLQRYDSKPIVDLIGAME
ł						TOSEPSELELDDVVITNPHIEAILENEDWIEDA
}		1	1		ĺ	SGLMSHCIAILKICHTLTEKLVAMTMGSGAK MKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
1				ļ	1	DPKLLDARTTALLLSVSHLVLVTRNACHLTG
		1	-		l .	GLDWIDQSLSAAEEHLEVLREAALASEPDKG
				]		LPGPEGFLQEQSAI
		l			100	MRLQGAIFVLLPHLGPILVWLFTRDHMSGWC
1059	2409	Α	8809	246	757	EGPRMLSWCPFYKVLLLVQTAIYSVVGYASY
Ì		-			i	LVWKDLGGGLGWPLALPLGLYAVQLTISWT
1	1	1				VI VI FETVHNPGLALLHLLLLYGLVVSTALI
		1	1	J		WHPINKLAALLLLPYLAWLTVTSALTYHLWR
1	ļ		1			DSLCPVHQPQPTEKSD
1000	2410	A	8810	304	381	PKLSVYPLOSHHCLSEPFOSLVCCLA
1060	2410	$\frac{\Lambda}{\Lambda}$	8820	1673	848	SCKTENLLEMWWFQQGLSFLPSALVIWTSAA
1061	2411	1	0020	19,75		FIFSYITAVTLHHIDPALPYISDTGTVAPEKCLF
1			1		1	GAMLNIAAVLCIATIYVRYKQVHALSPEENVI
						IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA
		Ì				HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH
		1				GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS
{		1	-	1		GNFGTDLEQKLHWNPEDKGYVLHMITTAAE
		l l				WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL
						TLYDTAPCPINNERTRLLSRDI GGAPPASVPARESPVSGAQGSSRTRGHKRAA
1062	2412	A	8824	1	763	GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA
	Ì	- 1		1		YSLAPATPEVKVACSEDVDLPCTAPWDPQVP
	1	1	1			YTVSWVKLLEGGEERMETPQEDHLRGQHYH
Ì				1	1	QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR
				İ		CTLQDPDGQRNLSGKVILRVTGCPAQRKEET
		1	1	1		FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI
1						FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT
						ELV
			- 6006	147	627	CETSTSSAGHAPCRHAAOGPPAEPTGLRLCSE
1063	2413	A	8826	147	027	HORI HAWPPGPRRPSLWPPKNGKWHSGKRT
		İ				AGGRPORRPSRROSORPSAWSGSPRMHSPGQ
	Ì			1		KCSLMCPHRSODSLSTAIFQRSPGANTGRALH
Į.		1	1			CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL
					1	
				}	1	TR
1051			0025	2087	1869	I KOTI KSOMTOEASDEAEDMKEAMNRMIDE
1064	2414	A	8835	2982	1869	LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKOVSELSOLYKEAOAELEDYRKRKSLEDV
1064	2414	A	8835	2982	1869	LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKQVSELSQLYKEAQAELEDYRKRKSLEDV TAFYTHKAEHEKLMQLTNVSRAKAEDALSE
1064	2414	A	8835	2982	1869	LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKOVSELSOLYKEAOAELEDYRKRKSLEDV

PCT/US01/03800

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
nence			, , ,	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	!	1	l	peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion VAKLEKQLLEEKAAMTDAMVPRSSYEKLQS
			1	}		SLESEVSVLASKLKESVKEKEKVHSEVVQIRS
				<b>\</b>	1	FVSOVKREKENIOTLLKSKEQEVNELLQKFQ
						OAOEELAEMKRYSESSSKLEEDKDKKINEMS
				}	}	KEVTKIKEALNSLSOLSYSTSSSKRQSQQLEA
	ĺ .	1				LOOOVKOLONOLAECKKOHQEVISVYRMHL
			-			LYAVQGQMDEDVQKVLKQILTMCKNQSQK
						K PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROP
1065	2415	A	8841	3	663	AAATAASLSPRGCRLRTPSSDVGPSRAPPPSA
1005		-		}		APLPTGRAQMSPSGRLCLLTIVGLILPTRGQTL KDTTSSSSADATIMDIQVPTRAPDAVYTELQP
•		}	1		}	TSPTPTWPADETPQPQTQTQQLEGTDGPLVT
				1	]	DPFTHKSTKAAHPTDDTTTLSERPSPSTDVQT
		1	1			DPOTLKPSGFHEDDPFFYDEHTLRKRGLLVA
						AVI.FITGIIILTSGKCRQLSRLCRNHCR
1066	2416	A	8853	3806	2204	FVGEOEGGCEAGAGRGAOTYPGEAGERWFG
1066	2410	^	0000	5555		RRRRGRVVSRKKMSLKSERRGIHVDQSDLL
		1	1	İ		CKKGCGYYGNPAWQGFCSKCWREEYHKAR
				1		QKQIQEDWELAERLQREEEEAFASSQSSQGA QSLTFSKFEEKKTNEKTRKVTTVKKFFSASSR
i		٠.				VGSKKEIQEAKAPSPSINRQTSIETDRVSKEFIE
	}	j		1	1	FLKTFHKTGQEIYKQTKLFLEGMHYKRDLSIE
				-		FOSECAODFYHNVAERMOTRGKVPPERVEKI
'			İ			MDOJEKYIMTRLYKYVFCPETTDDEKKDLAI
				1	1	QKRIRALRWVTPQMLCVPVNEDIPEVSDMVV
		1	1	1		KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI
				1		KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE
j	1	1	İ			KLDAQSLNLSQEDFDRYMSGQTSPRKQEAES
}	1			ł	1	WSPDACLGVKQMYKNLDLLSQLNERQERIM
	1					NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI
}		ļ	}	]		KPPNOPLAAIDSENVENDKLPPPLQPQVYAG
1067	2417	A	8855	1372	1513	SNMREVGCGWLVPVIPAFWEAEVGGSLEARS
1007	2417	1	***			LRQAWATKQDPISKKK
1068	2418	A	8856	1530	1583	PCRPGMECNSMISVHCNL
1069	2419	A	8857	1530	1583	PCRPGMECNSMISVHCNL PYPQGGYPQGPYPQEGYPQGPYPQGGYPQGP
1070	2420	A	8866	293	1675	YPQSPFPPNPYGQPQVFPGQDPDSPQHGNYQ
						EEGPPSYYDNQDFPATNWDDKSIRQAFIRKVF
}		}		1		LVLTLOLSVTLSTVSVFTFVAEVKGFVRENV
1						WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL
		1	- 1			VALSVLTASLSYMVGMIASFYNTEAVIMAVG
	1	-	ļ		j	TTTAVCETVVIFSMOTRYDFTSCMGVLLVSM
1	1	1	ļ	1		VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA
1		ļ		1		VDTQLLLGNKQLSLSPEEYVFAALNLYTDIIN
1	1	1		(	1	FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY
		- 1		1		TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC
				1		HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSC
1		ļ	}	ļ		EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS
(	-		1			GDMRSGGLIPVLSPE
			9068	2	358	ARGNTLYHLPRLCRKLNLRWFSASTLYDVQF
1071	2421	A	8868	1 4	330	DDKMGSNTFFKRNDCRYVMISCKADMAYDN
	}		1			VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII
						LNGEKLKVFPVRSGT*QGCSVWP
1		-	8870	33	658	MESVLSKYEDQITIFTDYLEEYPDTDELVWIL
1072	2422	1 A				
1072	2422	A	0070		İ	GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI
1072	2422		0070			GKQHLLKTEKSKLLSDISAKLWFTYKKAFSFT GGTGPSSDAGWGCMLRCGQMMLAQALICRF LGRDWSWEKQKEQPKEYQRILQCFLDRKDC

	oro m	Mat	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=A spartic Acid E=Glutamic Acid,
NO: of	NO: of	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	)	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
scq-	uence	}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	}	1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ì	Ì	1	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	peptide	sequence	/=possible nucleotide deletion, \=possible
			ļ			nucleotide insertion
				sequence	<b></b>	CYSIHQMAQMGVGEGKSIGEWVLGPNTVAQ
		1		į.		GV*KNLA/LFDEW\NSLGLVYVSM\DNPSGSIA
		1				RFPKKLCRVLPL\SADTAGLTGP
	Ì	l	1			DFSV*GDVDIEVTCPICLQLLTEPLSLNCGLRL
1073	2423	Α	8879	146	412	*QVCITA*IKESVIISGG*SSSPVCHTTFQPANL
	l l		1		1	RTSRYLPT*SIKSLGPDEPQEG
						HLQGRSIRTLQLTGENEKNCEVSERIRRSGPW
1074	2424	A	8884	67	435	KEISFGDYICHTFQGDCWADRSPLHEAAAHG
			1	}		RLLALKTLIAQGVNVNLWTL/DRVSSLHEACL
		1				RELACK I CLAUDY WAY OF PROGENT CONTROL OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGENT OF THE PROGE
	1					*GPVACAKPYWKMVPRHGGTVTGPPLLMV
1075	2425	A	8896	1294	248	RSGDRNGLTHQLGGLSQGSRNQSYRSRSRSR
1075	2.120	1				SRERPSAPRGIPFASASSSVYYGSYSRPYGSDK
		1				PWPSLLDKEREESLRQKRLSERERIGELGAPE
	1		į.			VWGLSPKNPEPDSDEHTPVEDEEPKKSTTSAS
			ļ			TSEEEKKKKSSRSKERSKKRRKKKSSKRKHK
			1		1	KYSEDSDSDSDSETDSSDEDNKRRAKKAKKK
		1	1		]	EKKKHRSKKYKKKRSKKSRKESSDSSSKES
			- {	1	{	QEEFLENPWKDRTKAEEPSDLIGPEAPKTLTS
	İ	-	1			QDDKPLNYGHALLPGEGAAMAEYVKAGKRI
	İ	j	1			PRRGEIGLTR*RNCHHLNAQVM**VVSRHRR
	1					MEAVRTAKREPESTVLMRREPLHPFNPRRET
	- [		1			KERE
1076	2426	A	8899	146	789	GRSTEAEKEPAFDERTGKGRRLPRAGEFHG*E
1076	2420	n	0000	1		*APGPGPRSFQVSRKMPEEIPPGARKHPFSGKS
[	- [				1	FYLDLPAGKNLQFLTGAIQQLGGVIEGFLSKE
<b>\</b>	1	}	İ			VSYIVSSRREVKAESSGKSHRGCPSPSPSEVR
	}	ļ	1			VETSAMVDPKGSHPRPSRKPVDSVPLSRGKE
i			-			LLQKAIRNQK**CTVQQLSHCRLY\GEKTTAK
		- [	1			RSOREHVOOOSQEHGKWPDLKGPR
	- 105		8901	352	3	AKIGAYKYIOELWRKKQSDVMHFLLRVRCW
1077	2427	Α	8901	1 332	-	QYPALHRAGTEWQLSALHRAPRSTQPDKAC
	1		ì	i		RLGYKAKOGYIIYRICVRRGGWKCPVPKAVT
	1		1	1		\YGKPVHHGVN*LKFAQSLQSVAEEQ
			8905	536	781	ACPAENREVPEMAAGQAPHAGPGAGPGQPA
1078	2428	A	6903	1 330	, 0.	PALPFAATPGSRGQALCRGGRRRQHLHGPLH
1	- 1			ļ		RP*OAAPALHAGCOLAPHPPT
			0012	121	376	NI.IWKLCYTERRLVILDNYDLASE/YEANKYI
1079	2429	Α	8912	121	1 370	CNRIIQFKPGQDKYFTLGLPTGSTPL*CYPKLI
			ı			EVNKNGHLSFKYVKTFSMDEY
				101	1788	SSESPSDPGRMAMTWIVFSLWPLTVFMGHIG
1080	2430	A	8920	381	1700	GHSLESCEPITLRMCODLPYNTTFMPNLLNHY
1				1	1	DOQTAALAMEPFHPMVNLDCSRDFRPFLCAL
i	İ		i			YAPICMEYGRVTLPCRRLCQRAYSECSKLME
1				}	1	MFGVPWPEDMECSRFPDCDEPYPRLVDLNLA
1	- {	Ì	1			GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY
		1	i	1		SFLHVRDCSPPCPNMYFRREELSFARYFIGLIS
	}	}	1	Į	1	IICLSATLFTFVTFLIDVTRFRYPERPIKCYAV
		1		1	1	WHMMVSLIFF\GFLLEDRVACNA\SIPAQYKA
1	ļ	-	1			STVTQGSHNKACTMLFMILYFFTMAGSVWW
		i		1	1	VILTITWFLAAVPKWGSEAIEKKALLFHASA
1		}	}	J		VILITI WILLANDIVIECDNIECUCEUCI VD
1	1	1		1		WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD
1						VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR
1	}	- [	1	1	1	VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL
	-	1		1	1	VVIGCYFYEQAYRGIWETTWIQERC
1081	2431	A	8922	56	420	EERTKMSTGPDVKATVGDISSDGNLNVAQEE
1081	2431	^	0,22	1 3		CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG
1		J	1			TLANFVF\CSVRHGLALILQLCNFSIYTQQMN
	- 1	-				LSIAIPAMVNNTAPPSOPNASTERPST
		1	1	1		THE STREET AND THE STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STR
1082	2432	A	8923	355	1079	PFGTPSSTMAVVKNKCLMKGGKKGVKKKVV

					The second and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	İ	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	Ì	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence	ì		914	ng to first	acid residue	Q=Glutamine, K=Arginine, 5-Settile,
	1		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	Į		1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1	peptide		/=possible nucleotide deletion, \=possible
	ł		1	sequence	(	nucleotide insertion
			<del>                                      </del>			GPFSKKDQYDVKAPAMFNIRNTGK/TLVART
	}	1	1	1		QGTQIASDGLKGLLFEVSLADLQNDEVAFRK
ì	1	Į.	1	ļ		FKLITEDVODKNCLTNFYGMDLTCDKICSMV
ļ	1	(	İ			EKWSTMIEAHVDVKTTDGYFFHLFCVGFTKK
}	1	1	1			HNNQILKTSYA*HQQS/RQIQKKMMEIMT*EV
l	1			i		OTNDLKEVVNKLIPDNIGKDTEKV/CPIYPLH
}	1	1	1	1	ļ	DVFIRKVKMLENPGFER\MELRGGGSSS
			1			LTWPQPHIPSCPAMSEETLQSKLAAAKKKLP
1083	2433	Α	8948	28	385	WGAVQGSRAMSDLLLLLDLTLLLLLMLLGF
	1	1	-	ì	1	AGYSGQLAGVAVSAGSPPIRYKFHVEPYGET
ļ	ł	1	1	Į	Ì	AGYSGQLAGVAVSAGSFFFKTRTHVEFTGET
1	1	,				GWLLT/ESCSISPKLCSIAVH*DNPAWF
1084	2434	A	8950	156	318	HYTPINTDTIENSENNKCW*GY*E\VGLIHHW
1004	2454	1	0,77	1	9	WGGKRVQPFWKRVWQKRTLNLRV
1006	2435	+ <u>A</u>	8956	16	413	HMGQLGYFIQCWWECKRLISF\WKTI*QSPAK
1085	2433	^	6930	10		*TIVTSVDTAIPIS/GI/YPKRMSSKCHQETCAR
1		1	l	\		MEILAPFTATIKGKOLTCPLVEERIDY\MWYS
	1	i i				HKYYIKVKRNL*VTITH\TWVNLNILMFEIILW
1			Į			VSHKYY
			1-00-60	060	1026	H*KILQVGRAQRAHXSRL*SQLLRRLRHESHL
1086	2436	A	8962	868	1026	NPGARGCSEARLHRCTPAWTT
	1				1220	LHVKHLGHFQLVFSEVICHCILMPVS*ELQRL
1087	2437	Α	8985	58	330	*ERSVCAFHVCIQTYVCLQVYACMCVYYICM
	1	1	1		1	FVYSVYGCGLCTCVCMDVYICVCVQEFL
1	ĺ		[			N*KWILHVNVRIQSIFF/IKRNQK/INSHELKLD
1088	2438	A	8989	394	404	KKFLDMMSNA*STKKHDKLD/LIKFKT/LCSA
		1			1	KKFLDMMSNA*SIKKHDALD/LIAFAT/DCSA
1	1		ı	}		KYTVKRIKIHPTDLEKMLRNHLSDKD*YS/GV
1			1	ļ.	)	YKDLSKLNRRKTE/S*/VKKWVKDLSRYFIKE
İ	1	İ	{	1	_	VISMENKHKKIFSTS
1089	2439	A	8991	60	329	MALTPESPSSFPGLAATGSSVPEPPGGPNATL
1007	12437	1				NSSWDSPTEPSSLEDLEATGTIGTLLSDMGVV
	]			1		GVEDNAYTLEVNSRYMRAVGIM*IHL
1090	2440	A	8996	2	351	SNITITLT*MKKYDNTFCW*GCGQIG/T/LIYC
1090	2440	1.7	0,,,,	-		WQESKFIQAFWSKIQQYLA*ISIHILFDPAFLFL
	-	ĺ	-			GGYPGGTQSVFLTGVLVSSVFYNMKMLHTR
	1		Í			LLIAALFIIVOYWKQSKDHYI
	<del> </del>		8997	97	456	YPLPVCSYLSGPRGEHWNSLGGKSSCPLPLPT
1091	2441	A	8997	31	130	LVSSRFKISKVIVVGDLSVGKTCLINR*GGAG
1	1	1	1			AELGRVGPSLARWAGSRSQHLVPSQ\VCKDS
ı			1		İ	FDKNYKAPIGADFEMERFEVLGIPF
				+	811	SSFIKRHILIFEDDWHQTTCCHHPHHP\F*RCQ
1092	2442	Α	8999	548	011	FHIFYVSVQNSISPSLSVSSSHPDRPDHEVHQH
	1					RAAHHHQHGQGPLGHGLVARVG
1		-				ALLGLQQPAQSLILSRSSVMGVRGLQGFVGS
1093	2443	A	9002	3	2745	ALLULQU'AQSLILSASS VING VACCOTTAND
1	1					TCPHICTVVNFKELAEHHRSKYPGCTPTTVVD
	1					AMCCLRYWYTPESWICGGQWREYFSALRDF
-				1		VKTFTAAGIKLIFFFDGMVEQDKRDEWVKRR
			1		1	LKNNREISRIFHYIKSHKEQPGRNMFFIPSGLA
			1			VFTRFALKTLGQETLCSLQEADYEVASYGLQ
1						HNCLGILGEDTDYLIYDTCPYFSISELCLESLD
						TVMLCREKLCESLGLCVADLPLLACLLGNDII
					ĺ	PEGMFESFRYKCLSSYTSVKENFDKKGNIILA
1		1			1	VSDHISKVLYLYOGEKKLEEILPL/VTKQSSFL
		1		1	1	*RNGIISFTRT/INLHGFSKNPKV**LWTNK*YP
		İ		1		- MOUSI INTIMIDITOR BILLIAN
						PVOTPNPGKKFPCVOMLNPGKKFPCVQALNP
						RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP GEKFPCIHI/PEPROEVPTCSDPEPRQEVPTCTG
						RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP GEKFPCIHI/PEPRQEVPTCSDPEPRQEVPTCTG PESRREVPMCSDPEPROEVPMCTGPEPRQEVP
						RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP GEKFPCIHI/PEPRQEVPTCSDPEPRQEVPTCTG PESRREVPMCSDPEPROEVPMCTGPEPRQEVP
						RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP GEKFPCIHI/PEPRQEVPTCSDPEPRQEVPTCTG PESRREVPMCSDPEPRQEVPMCTGPEPRQEVP MCTGPEAROEVPMCTDSEPROEVPMCTDSEP
						RVQTPNPGKKFPCVQMLNPGKKFPCVQALNP GEKFPCIHI/PEPRQEVPTCSDPEPRQEVPTCTG PESRREVPMCSDPEPROEVPMCTGPEPRQEVP

SEQ ID   NO. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   N
nucle- oside seq- uence    Deptide oside seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq- uence   Seq
1094   2444   A   9021   97   834   185   1094   185   1095   2445   A   9022   1   537   2447   A   9032   716   357   2447   A   9032   716   357   2447   A   9032   716   357   2447   A   9032   716   357   2447   A   9032   716   357   2447   A   9032   716   357   2448   A   9038   230   652   449   A   9043   185   372   1100   2450   A   9045   763   584   RISCHERS INCHERS INCHERS INCHERS INCHERS INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS IN INCHERS I
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1096   2446   A   9022   1   537   LV.NSYEDFVPFEGARTLEPLAUSEDELS   LEARNESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD   VL. NSKENESSELS STREETINSOSD
1096
residue of   peptide   sequence   y=Tyrosine, X=Unknown, **Stop codon,   y=possible   nucleotide deletion,   y=possible   nucleotide deletion,   y=possible   nucleotide   nucleotide   nucleotide   peptide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucleotide   nucl
Peptide
PICTOPISKQEDSMCTHAEINQKLPVATDFE   LEALMCTNPEIKQEDPTHAEINQKLPVATDFE   LEALMCTNPEIKQEDPTHAEINQKLPVATDFE   LEALMCTNPEIKQEDPTHAEINQKPTYCPKQQVTM   DTELKVARTHHVQAESYLVYNIMSSGEIEK   NTLEDELDQALPSQAFIYRPIRQRVYSLLE   CQDVTSTCLAVKEWFVYPONPLRHPDLVR   QMTIPGGTPSLKILWINQEPEIQVREIDTLL   CFNLSSSREELQAVESFPQALCCLLIYLFVQ   DTICLEDLHAFIAQALCLQGKSTSQLVNLQ   DYINPRAVQLOSLLVRGITTU.VINSACOF   WKTSDFMPWNVPIGKLFHQVXLOSEKGY   WKTSDFMPWNVPIGKLFHQVXLOSEKGY   VEVL/CRTK*ISAHQPQPEGSRALQGLHEGE   HWPSPLGLTPRREVGKTGLQLPQDGLWY   VEVL/CRTK*ISAHQPQPEGSRALQGLHEGE   THMPSPLGLTPRREVGKTGLQLPQDGLW   WKTSDFMPWNVPIDGKLFHQVXLOSEKGY   VEVL/CRTK*ISAHQPQPEGSRASKGATAFTQLPADDL   VEVL/TSSPLGLYSRHMKVAFGRTSSGKSS   NAML WDKVLPSGIGHTNCFLSVEGTDGD   YVLMTEGSDEKKSVKTVNDK*AFGRTSSGKSS   NAML WDKVLPSGIGHTNCFLSVEGTDGD   YVLMTEGSDEKKSVKTVNDK*AFGRTSSGKSS   NAML WDKVLPSGIGHTNCFLSVEGTDGD   YVLMTEGSDEKKSVKTVNDK*AFGRTSSGKSS   NAML WDKVLPSGIGHTNCFLSVEGTDGD   YVLMTEGSDEKKSVKTVNDK*AFGRTSSGKSS   NAML WDKVLPSGIGHTNCFLSVEGTDGD   YVLMTEGSDEKKSVKTVNDG*ALHAHMKDA   AGCLVRVFWPKAKCALLRDDLVLVQFG*CVTTELDSWIDKFCTKSSTREITNSGSDT   YVLNTSXVEDSVFVPFGGAGRATPFALRFLAAC   LLHRARRSSALCPRPRSWGVSGGGAGA   PTSSSCCLSAASHLSIGSSPNMAGARRIRR   LAKEKIEGCHICTSVTTGEPQVFLGKDKAFT   DYVPDIDSQCQCITYICCERSLIFGCCFGVNA*   FAYGQTGAGKTYTMGTGFD   TSSSCCLSAASHLSIGSSPNMAGARRIRR   LAKEKIEGCHICTSVTTGEPQVFLGKUKGAKAFT   TSSSCCLSAASHLSTGNAMSSACLSTRIPTNSCSDT   TSSSCCLSAASHLSTGNAMSSACLSTRIPTNSCSDT   TSSSCCLSAASHLSTGNAMSSACLSTRIPTNSCSDT   TSSSCCLSAASHLSTGNAMSSACLSTRIPTNSC   LAHCNFRHAGFPPLSCLSLFNRWEYRRPA   GKFLVFVPLGFCQC*ODIDLLTSRSACLLPKCWDYRRPAASIIFQTTFFINSK   LAHCNFRHAGFPPLSCLSLFNRWEYRRPA   GKFLVFVPLGFCQC*ODIDLLTSRSACLLPKCWDYRRPAASIIFQTTFFINSK   LAHCNFRHAGFPPLSCLSLFNRWEYRRPA   GKFLVFVPLGFCQC*ODIDLLTSRSACLLPKCWDYRRPAASIIFQTTFFINSK   TSSWGYGERWINGGGFCGGACRESTICHCWFEK   HSJWK/TV*QFLKRI,YLHLPHNNSWIAFLGIS   KKIKTCPONSCTSMLINHAKKYLAFLCIK   TNFSQQFYHLWVPSHIFWQTTCGRLPHKT   G*AALDHLKVFDRIPLPYDKKKQMAYSAT   VYRRPPPRASALGHTMACNTOWKYDMK   TMGEKRKYYYQKICYQKK   HITCHTPLSCLSCTSMANCLCPLVFTPLS   LTFEMESLPVARQECSGTISAHNCLCPLVFTPLS   LTFEMESLPVARQE
LEALMCTNPERKQEDPTNVQPEVKQQVTM     DTELK VARTHHVQAESYL.VYNIMSSGEEK     NTLEDELDQALPSQAFIYRPIRQRVYSLLLE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLLE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLLE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLLE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLLE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLLE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLLE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLLE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLIVE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLIVE     CDTLATESSEE     CQDVTSTCLAVKEWFVYYRPIRQRVYSLLIVE     DTLCLEDLAHAIQALCQGKSTSQLVNLQ     DTLCLEDLAHAIQALCQGKSTSQLVNLQ     DYNTPRAVQLQSLLIVEQGLHEGE     HHWPSPLGLTPRREVGKTGLQLPDQLHY     WKTSDFWWNYPGGSLFRLWPSCCCRVIVGA     HHWPSPLGLTPRREVGKTGLQLPDQLHY     AREACRAKTDFPGRFFLWPSCCCRVIVGA     THMAEPYSPLKHFVLAKKAITAHPQLLE     TEGSHFVAATVKPLAKKAITAHPQLLE     TEGSHFVAATVKPLAKKAITAHPQLLE     TEGSHFVAATVKQLAHALHMOKD     AGCUVRVFWPKAKCALLRDDLVMCPGV     VMTEGSBEKKSVKTVQLAHALHMOKD     AGCUVRVFWPKAKCALLRDDLVMCPGV     THMAEPYSPLKHFVLAKKAITAHPQLLE     THMAEPYSPLKHFVLAKKAITAHPQLLE     THMAEPYSPLKHFVLAKKAITPQLLE     THMAEPYSPLKHFVLAKKAITPQLLE     THMAEPYSPLKHFVLAKKAITPQLLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLKHFVLAKKAITPQLE     THMEESLEVANGEGOETALIC     THMAEPYSPLKHFVLAKKAITPQLE     THMAEPYSPLLIFT     THMEESLEVANGEGOETALIC     THMAEPYSPLLIFT     THMEESLEVANGEGOETALIC     THMAEPYSPLLIFT     THMEESLEVANGEGOETALIC     THMAEPYSPLLIFT     THMEEPYSPLLIFT     THMAEPYSPLLIFT     THMAEPYSPLLI
DTELLKVARTHHVQAESYLVYMINSGEEICE     NTL DELL DQAL PSQASTYRPIRQR VYSILLE     CQDVTSTCL AVKEWFVYPGNPLRHPDLVR     QMTIPGGTTPSLKILWI.NQEPBIQVRRLDTILL     CPNLSSRRELQAVESPPQALCCLIYLFVQ     DTILCLEDLHAFIAQALCLQCKSTSQLVNLQ     DYNPRAVQLGSLLVAGYLQSEKGY     VEVL/CRTK*1SAHQIPQPEGSRLQGLHEGGE     WKTSDFMPWNVFDGKLFHOKYLQSEKGY     VEVL/CRTK*1SAHQIPQPEGSRLQGLHEGGE     WKTSDFMPWNVFDGKLFHOKYLQSEKGY     VEVL/CRTK*1SAHQIPQPEGSRLQGLHEGGE     WKTSDFMPWNVFDGKLFHOKYLQSEKGY     VEVL/CRTK*1SAHQIPQPEGSRLQGLHEGGE     WKTSDFMPWNVFDGKLFHOKYLQSEKGY     VEVL/CRTK*1SAHQIPQPEGSRLQGLHEGGE     WKTSDFMPWNFDGKLFHOKYLQSEKGY     VEVL/CRTK*1SAHQIPQPEGSRLQGLHEGGE     WKTSDFMPWNFDGKLFHOKYLQSEKGY     VEVL/CRTK*1SAHQIPQPEGSRLQGLHEGGE     WKTSDFMPWNFDGKLFHOKYLQSEKGY     WKTSDFMPWNFDGKLFHOKYLQSEKGY     WKTSDFMPWNFDGKLFHOKYLQSEKGY     WKTSDFMPWNFDGKLFHOKYLQSEKGY     WKTSDFMPWNFDGKLFHOKYLQSEKGY     WKTSDFMPWNFDGKLFHOKYLQSEKGY     THAMPONF SERVEL     WKTSDFMPWNFDGKLFHOKYLQSEKGY     WKTSDFMPWNFLKKKLAGYSGKTLFALT     LAKEKLEGCHICTSVTPGEPQVFLGKDKAFJ     DYVPDIDSQQEQTYQCEBLIEGCFGYNAF     AYQCTJGAGKTYTMGTGFD     FFFFNFCKSFKVPKPGCKEESTGTLFKNTL     LAKEKLEGCHICTSVTPGEPQVFLGKDKAFJ     DYVPDIDSQQEQTYQCEBLIEGCFGYNAF     AYQCTJGAGKTYTMGTGFD     FFFNFCKSFKVPKPGCKEESTGTLFKNTL     LAKEKLEGCHICTSVTPGEPQVFLGKDKAFJ     DYVPDIDSQQEQTYQCEBLIEGCFGYNAF     AYQCTJGAGKTYTMGTGFD     FFFNFCKSFKVPKPGCKEESTGTLFKNTL     LAKEKLEGCHICTSVTPGEPQVFLGKDKAFJ     GQHSTTPSLKKKLAGYSGMCL     SQULRRL     GQHSTTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     LACKPRINGTGFFRAMGFP     GKFLVTLVETGFQCGFDGLTLFKNTL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     GQHSTPSLKKKLAGYSGMCL     SQULRRL     SQUL
NTLEDELDQALPSQAFTYRPRGRYYSLLLE
CQDVTSTCLAVKEWFVYPGPLRHPDLVR
OMTIPGGTPSLKIL.WLNQEPEIQVRR.LDT/LCPUL.SSRSELQ.ADSSPEQAL.CC.LIYLFVQ
CFNLSSSRELQAVESPFQALCCLLYLFVQ   DTLCLEDLHAFIAQALCQKSTSQLVNLQ    DYNPRAVQLGSLVRQLUTILVLVNSACGF    WKTSDPMPWNVFDGKLFH(KYLQSKEQLVHEGE    WKTSDPMPWNVFDGKLFH(KYLQSKEQL)   VEVL/CRIK*ISAHQPQFEGSRLQGLHEGE    HHWPSPLGLTPRREVGKTGLQLPQDGLWV    VEVL/CRIK*ISAHQPQFEGSRLQGLHEGE    HHWPSPLGLTPRREVGKTGLQLPQDGLWV    VEVL/CRIK*ISAHQPQFEGSRLQGLHEGE    HHWPSPLGLTPRREVGKTGLQLPQDGLWV    VEVL/CRIK*ISAHQPQFEGSRLQGLHEGE    HHWPSPLGLTPRREVGKTGLQLPQDGLWV    KDKLSUGEVLSRRHWVAFFGRTSSGKSS    NAMLWDKVLPSGIGHITNCFLSVEGTDGDB    YLMTEGSDEKKSVKTVNQLAHALHMDKD    AGCLVRVFWPKAKCALLRDDLVLVDCPG    VITELDSWIDKFCTKSSTREITNSGSDT    VLNNSVEDFVPFEGAGRTLPFALRACALLAGDLVLVDCPG    VITELDSWIDKFCTKSSTREITNSGSDT    VLNNSVEDFVPFPEGAGRTLPFALRACALLAGDLVLVDCPG    VITELDSWIDKFCTKSSTREITNSGSDT    VLNNSVEDFVPFPEGAGRTLPFALRACALLAGEKKEGCHICTSVTPGEPQVFLGKDKAF    DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNA*   FAYGQNGAGKTYTMGTGGP    FFFFTV*CKSPKVPKPGCKEESTGTLFKNTLI    GQHSETPSLKKKLAGYSGMCL*SQVLRRL    EDCLSPGGNCRES*CPYTPAWITERDPV    1097
DILCLEDLHAFIAQALCLOGKSTSQLVNSACOP
DYNPRAVOLGSILLVRGLTTLVLVNSAGGP
1094   2444   A   9021   97   834   AREACRAKTDEPGREERIUPSCCCRVIVGA
1094   2444   A   9021   97   834   AREACRAKTDEPGREERIUPSCCCRVIVGA
VEVL/CRTK*ISAHQIPQFGSRLQGLHEGEC   HHWPSPLGLTPREVGKTGLQLPQDGLWV
HHWPSPLGLTPRREVGKTGLQLPQDGLWV   AREACRAKTDFPGRRFRLWPSCCCRVIVGA
1094
T*HMAEPVSPLKHFVLAKKAITAIFDQLLE   TEGSHFVEATYKNPELDRIATEDDL VEMOX   KDKLSIIGEVLSRRHMK VAFFGRTSSGKSS   NAML WDK VLPSGIGHITNCFLS VEGTDGDB   YLMTEGSDEKKSVKTVNQLAHALHMDKD   AGCLVRVYWPKAKCALLRDDLVLVDGPGT   VTTELDSWIDKFCTKSSTREITNSGSDT   LVLNSRVEDFVPPEGAGRTLPFALAPLAAC   LLHRRARRSSALCPRPRSWGVSGGEGAGA   P*ITSSSCCL.SAA/SHLSIQSPNMAGARRIRI   LAKEKLEGCHCTSVTPGEHQTVFLOKDKAF   DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTIGAGKTYTMGTGPD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGGTELFSVARYCGSGTISAHCKSSACLIEKTMTIGSD   YVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGGTELFTSKKKKLAGYSGMCL*SQVLRRL   EDCLSPGGGNCRES*SGCYTTAMTERDVILKEL   EDCLSPGGGNCRES*SGCYTTAMTERDVILKEL   YVFDIDSQGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSQGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSQGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGNCRES*SGCYTTAMTERDVILGERGT   YVFDIDSGGGNCRES*SGCYTTA
TEGSHEVEATYKNPELDRIATEDDLVEMQC   KDKLSIIGEVLSRRHMKVAFFGRTSSGKSSN   NAMLWDKVLPSGIGHTINCFLSVEGTDGDB   YLMTEGSDEKKSVKTVNQLAHALHMDKDD   AGCLVRVFWPKAKCALLRDDLVLVDGPG   YTTELDSWIDKFCTKSSTREITNSGSDT   VLNSRVEDFVPPEGAGRILPFALRPLAAC   LLHRRARRSSALCRPRSWGVSGGEGAGA   P*ITSSCCLSAA/SHLSIQSPNMAGARRIR   LAKEKIEGCHICTSVTPGEPQYFLGKDKAF   DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNA: FAYGQTTGAGKTYTMGTGFD   FFFFNVCKSPKVPKPGCKEESTGTLFKNTL   GQHSETTSLKKKLAGYSGMCL*SQVLRRL   EDCLSPFGGNCES*SCPYTPAWITERDPV   ARSTGFWGEILWCGFLKRSLALSPRVKCSG   LAHCNFRHAGFPPJSCLSLPNSWEYRRPDV   GAFFLVFLYETGFQC/G*DGLDLLTSRSACI   LPKCWDYRREPAASIFQTTFFNSK   LPKCWDYRREPAASIFQTTFFNSK   TNPSQQPYLLWVPSHIFWQTTCGRLPHKTT   G*AALDHLKVFDRIPLYDKKKQMAVSAT   VVRPKP*RKFAYLGHWAQKVDWKYQAMT   TNGEKRKVYYQKLCYQKK   TNGGKRKVYYQKLCYQKK   TNSSQCPYHLWVPSHIFWQTTCGRLPHKTT   G*AALDHLKVFDRIPLYDKKKQMAVSAT   VVRPKP*RKFAYLGHWAQKVDWKYQAMT   TNGEKRKVYYQKLCYQKK   SLTSSWDYRRPPHPANFLYFK*RGF   LFLFKWSNGTSTSMLNAHHDQKWKKINI   RKIKTCPNSCTSMLNAHHDQKWKKINI   RKIKTCPNSCTSMLNAHHDQKWKKINI   SLTSSWDYRRPPPHPANFLYFK*RGF   LFLFKWSNGTLSSFLDFVNFQGFVFAFLLL   LFLFKWSNGTLSSFLDFVNFQGFVFAFLLL   LFLFKWSNGTLSSFLDFVNFQGFVFAFLLL   LFLFKWSNGTLSSFLDFVNFQGFVFAFLLL   LFLFKWSNGTLSSFLDFVNFQGFVFAFLLL   LFLFKWSNGTLSSFLDFVNFQGFVFAFLLL   LFLFKWSNGFLSSFLDFVNFQGFVFAFLLL   LFLFKWSNGFLSSFLDFVNFQGFVFAFLLL   LFLFKEMESLPVARVECSGTISAHCNLCLPG   DSPASAS*VAGITDMCRYTQLLFHAS   LFLFFKMESSHDTLLEREDVILKEL   DSPASAS*VAGITDMCRYTQLLFHAS   LFLFFKMESSHDTLLEREDVILKEL   DSPASAS*VAGITDMCRYTQLLFHAS   LFLFFKMESSHDTLLEREDVILKEL   DSPASAS*VAGITDMCRYTQLLFHAS   LFLFFKMESSHDTLLEREDVILKEL   DSPASAS*VAGITDMCRYTQLLFHAS   LFLFFKMESSCTISAHCNLCLFG   DSPASAS*VAGITDMCRYTQLLFHAS   LFLFFKMESSHDTLLEREDVILKEL   DSPASAS*VAGITDMCRYTQLLFHAS   LFLLFFEMESLPVARVECSGTISAHCNLCLFG   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPASAS*VAGITDMCRYTQLLFEDVILKEL   DSPA
NAML WDK VLPSGIGHITNCFLSVEGTDGDB   YLMTEGSDEKKSVKTVNQLAHALHMDKD    AGCLVRVFWPKAKCALLRDDLVLVDGPG7    VTTELDSWIDKFCTKSSTREITNSGSDT    1095
1095   2445   A   9022   1   537
AGCLVRVFWPKAKCALLRDDLVLVDGPGT
1095
1095
LLHRRARRSSALCPRPRSWGVSGGEGAGA
P*ITSSSCCLSAA/SHLSIQSPNMAGARRIRI
LAKEKIEGCHICTSVTPGEPQVFLGKDKAF    DYVFDIDSQQEQIYIQCEKLIEGCFEGYNA    FAYGQTIGAGKTYTMGTGFD    FFFFNTCKSPKVPKPGCKEESTGTLFKNTLI    GQHSETPSLKKKLAGYSGMCL*SQVLRRL    EDCLSPGGGNCRES*SCPYTPAWITERDPV    1097
DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNA' FAYQQTIGAGKTYTMGTGFD
1096
1096         2446         A         9029         1         285         FFFFN▼CKSPKVPKPGCKEESTGTLFKNTLI GQHSETPSLKKKLAGYSGMCL*SQVLRRL EDCLSPGGGNCRES*SCPYTPAWITERDPV           1097         2447         A         9032         716         357         ARSTGFWGEILWCGFLKRSLALSPRVKCSG LAHCNFRHAGFPPLSCLSLPNRWEYRRPPA GKFFLVFLVETGFQC/G*DGLDLTSRSACL LPKCWDYRREPAASIIFQTTFFINSK           1098         2448         A         9038         230         652         KVVVMSCEDINISGSFYRNKLKYLAFLCKR TNPSQGPYHLWVPSHIFWQTTCGRLPHKTR G*AALDHLKVFDRIPLPYDKKKQMAVSAT VVRPKP*RKFAYLGHWAQKVDWKYQAM TMGEKRKVYYQKICYQKK HSL/WK/TV*QGCGDIETLIHCW*E*K HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGIS RKIKTCPQNSCTSMLINAIHNDQKWKKINI RKIKTCPQNSCTSMLINAIHNDQKWKKINI RKIKTCPQNSCTSMLINAIHNDQKWKKINI RKIKTCPQNSCTSMLINAIHNDQKWKKINI RKIKTCPQNSCTSMLINAIHNDQKWKKINI RQSLALSPRLECSGTISAHCRLCPLVFTPLSG SLTSSWDYRRPPPHPANFLYFK*RRGF           1100         2450         A         9045         763         584         RQSLALSPRLECSGTISAHCRLCPLVFTPLSG SLTSSWDYRRPPPHPANFLYFK*RRGF           1101         2451         A         9050         275         2         LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLL FLL/FEMESLPVA/RVECSGTISAHCNLCPG DSPASAS*VAGITDMCRYTQLILFHAS           1102         2452         A         9053         449         1224         KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
1096
EDCLSPGGNCRES*SCPYTPAWITERDPV
1097
LAHCNFRHAGFPPLSCLSLPNRWEYRRPPA
GKFFLVFLVETGFQC/G*DGLDLLTSRSACL LPKCWDYRREPAASIIFQTTFFINSK
LPKCWDYRREPAASIIFQTTFFINSK
1098
TNPSQGPYHLWVPSHIFWQTTCGRLPHKTE
G*AALDHLKVFDRIPLPYDKKKQMAVSAT
VVRPKP*RKFAYLGHWAQKVDWKYQAMT   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVYYQKICYQKK   TMGEKRKVIYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQKK   TMGEKRKVYYQK   TMGEKRKVYYQKK   TMGEKRKVYYQK   TMGEKRKVYYQK   TMGEKRKVYYQK   TMGEKRKVYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYYQK   TMGEKRYY   TM
TMGEKRKVYYQKICYQKK
1099
HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGIS RKIKTCPQNSCTSMLINAIHNDQKWKKINI RQSLALSPRLECSGTISAHCRLCPLVFTPLSG SLTSSWDYRRPPPHPANFLYFK*RRGF LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLL FLL/FEMESLPVARVECSGTISAHCNLCLPG DSPASAS*VAGITDMCRYTQLILFHAS KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
RKIKTCPQNSCTSMLINAIHNDQKWKKINI  1100 2450 A 9045 763 584 RQSLALSPRLECSGTISAHCRLCPLVFTPLSG SLTSSWDYRRPPPHPANFLYFK*RRGF  1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPG DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
1100 2450 A 9045 763 584 RQSLALSPRLECSGTISAHCRLCPLVFTPLSG SLTSSWDYRRPPPHPANFLYFK*RRGF  1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPG DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
SLTSSWDYRRPPPHPANFLYFK*RRGF  1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPG DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
SLTSSWDYRRPPPHPANFLYFK*RRGF  1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPG DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
FLL/FEMESLPVA/RVECSGTISAHCNLCLPG DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
FLL/FEMESLPVA/RVECSGTISAHCNLCLPG DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKEL DEEDVLOECKAONRKLIEFLLKAECLEDLV
DEEDVLOECKAONRKLIEFLLKAECLEDLV
\[\n\*EEPPQDMDEKIRYKYPNISCELLTSDVSQ\]
NDRLGEDESLLMKLYSFLLNDSPLNPLLAS
TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKV
RNL*HST*NVMDISKYVNLHWGLNKSHSL
LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDV
SLV
CLINVDEOVVPEHI TI NVKKCSVSFWGI
1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVRRCSVSFWOLL WLYLQMYEIIKSPRFPIKMTDITKCW*GCM
AGMQVH/CW\WCVNVGKFWEMS*YYLLKI
ST/PYDPAIPLLGIYL*ETRVYIHPKTCMRMI

		1.	L 0.50	D -31 1	Dendistad	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	сопеspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		ŀ	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		]		peptide	Soquence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
	<del> </del>		<del> </del>	sequence		APFVLAVNC
1104	2454	A	9064	75	393	KWLFSSLNITGRGDIIGHLKWLDCR\NCSSFPI
1104	2434	1 "	700.	1 .5		KRNRQTHSTESNKLKAGHSFGYN*LIH*NS\V
ļ						KTDCGCGANSKGVVVVMKV\KTAQQKQTTS
						YMQIGTTKNSRAT
1105	2455	A	9065	366	778	DLLILRNLAFPELKRRNCISRFYLAYHLHKIYS
1105	2.55	'-				RSILLCNNCSGFYILSL*QYDVFFFNYFFFRDR
1		1				AWPCCPGWSAAWLTTVILAHYRRPGLERSCC
					ļ	LSLSSSWDHRRVPPCPANF*/YFSMGFTAFPRL
		Ì	1			VLNS*TQGI
1106	2456	A	9083	673	816	ESGSLIH*WWENKPAQPLWWEI*QHVQKLPT
		1				HFPCDPAIPLLGICPED
1107	2457	A	9086	580	18	KPSSGSFIRAIYIFLSTAHVPALFSVLVRTKLT*
		1	1			AFSQSSVLWAHKQQKTSLSLVIR/ERLQIKTA
	1	1				VRENFLPIRLAKILKLDNVKCWQG/SGSNMSL
1	l			İ		VHCWWEYNVIHIIWNSVTFPRKVEHVYITYA
Ì						PEISVR*IHGGLPTLVHQETHTSVFRGAPSVIP
	J					ETR\CRPTKESINKLLHIYTMEHYGDENK GGNDCSVTPTTEPGRKEIT*KRKF*EKTDRLP
1108	2458	Α	9093	540	1	GA/PPSRTPPTPYPCPHGDRLLPPSRPLPAGPA
	E'					SAFPPAERSRGHRRASL*RARWSAAVPRRSA
j		1	1		ļ	GSASEPVQSRWLRLPVGSDSPPAVPVRVCPAP
		1			1	DSRPAAPGSRLPDPGLDSPAPSRTPSSSVD*GG
						QRPPPPSGDSLSPPGCCRY
1100	2450	A	9099	1255	1425	HESYHVNPNLCNPVAPTSGAHSIG*KWPSWL
1109	2459	A	9099	1233	1425	GAVAHSCNPSTLVGRGGRITRGQELR
1110	2460	A	9103	242	70	EEOFFFFAVGMFP*VDFLAPASGELWDRLRLT
1110	2400	^	1,,,,			CSRPFTRHQSFGLAFLRVCSSLDSLDDSVVGP
1		-	1	1		SALLSSVL/NQGGRNVLEAREAAKHPTI*RQS
	1					LLRKQRNKRMAIP
1111	2461	A	9110	189	121	SFLSVRLECNGAIMAHCALPLPG
1112	2462	A	9113	100	910	RRRGGGSRPRRTPVPAPGPGPSFGMDVRFYP
						AAAGDPASLDFAQCLGYYGYSKFGNNNNYM
						NMAEANNAFFAASEQTFHTPSLGDEEFEIPPIT
				ļ		PPPESDPALGMPDVLLPFQALSDPLPSQGSEFT
1	1	ľ		İ		POFFPOSLDLPSITISRNLVEQDGVLHSSGLHM
		1	1			DQSHTQVSQYRQDPSLIMR\PSST*PDAARSG
	1		1			VMPPAQLTTINQSQLSAQLGLNLGGASMPHT SPSPPASKSATPSPSSSINEEDADEANRAIGEK
			1			RAAPDSGKKPKTPKK
	<u> </u>	1	1	2452	3051	FLRPSFALVPQAGVQWCALSWLQPPSPRFK*F
1113	2463	A	9120	3452	1005	SCLSLPSSWDYRHVPPRPANFFVLLVETGFLH
						VGQAGHEPLTSGDPPASASQSAGITGVSHQA
		Ì				WPSFFIFSRDTVLLCCSGWSRTSGLKQSACLS
	1					LLKCWDY
1111	10451	1,	0122	152	377	NQLPLQQWTFFIYETGFCSVAQAGVQCRDHS
1114	2464	A	9122	134	311	SLHP*PPG\SSDPPAPPS*VLGITGQRYHACLII
						YLYVQTVPQRV
1115	2455	1	9124	553	981	QRPLLRQQLGSWPTCRSLEGDLASPW**RLPG
1115	2465	Α	7124	333	701	SPRMRRSGT/ATLNLPLSPQGTVRTAVEFQVM
			1	1		TQTQSLSFLLGSSASLDCGFSMAPGLDLISVE
						WRLQHKGRGRGDLHLPDHHLSVPSSADHPA
						OOPSOFNGRNLYFLPLFR
1116	2466	A	9135	48	410	SASHEPAEHDGGADSLSASQPPRPAGRPAGA
1110	2400	10	1133	1 30 .	1	OHVHVPPWTDVLAGQDRRAPTAGDGAPWP
	r	ł		1		APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ
Į		1	1	1		70 00111101101101
						PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA
						PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA GAGGP*GSPAGRACGAAGCRPRPPRPAASSA *NSAGS*GLVEGT*PPGAGHGAPSPAVGARLS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  CPARTSVQGGTWTC*APAGRPAGLGGWEAE RESAPPSCSAGS*DAD*GAEPWGAGSRSWGS  KSGHWAKECLQPRIPPRPCPICVGPHWKSDCP TCPGAVPRAPGTLPQGSLTDSFPDLLSLVAED *CCLMASEASWTITELWVTLTVEGKSVP/CL NTEATHSTLPSFQGPVSLASITVVGIDGQASKP LKTPQLWCQLGQYSFMHYFLVIPTCPVPLLG* GILTKLSAFLTIPRLQPHLIAALSPSS
1118	2468	A	9154	471	2	AAGQVVVEVTSHLYLCITSDAAGLRLLPPAES ERGEGGHCPAEAPLPPRPQYCLAKHPLLRKLP EEKIKLDPYLTQHTKINSKQIKYLS/VRAKTTQ LVEGNIGVNLQNTELKQH*INGFLDTTPEAQE TKEKTNKLNFIKKVKRQLAEWEKIPQIA
1119	2469	A	9155	2	3187	ACPRLARRRRVVSLRRRRGWLRARWSRGQ NNMAARRITQETFDAVLQEKAKRYHMDASG EAVSETLQFKAQDLLRAVPRSRAEMYDDVHS DGRYSLSGSVAHSRDAGRESLRSDVFSGPSFR SSNPSISDDSYFRKECGRDLEFSHSNSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHPVSQ ESSWSQEYSFGPSAVLGDFGSSRLIEKECLEK ESRDYDVDHPGEADSV/LRGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGVGKLVTL RNVSTKKIPTVNRITPKTQGTNQIQKNTPSPD VTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRR KMSFDIIDKSDVFSRFGIEIIKWAGFHTIKDDIK FSQLFQTLFELETETCAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQEKIL*AVGLQ DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS SGCPLQVKKAEPEPMREEEKMIPPTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERTLLKEDPAYWFLSDENSLEYKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKKLLPWQRRGLLRAQG\LRG\ WKARRA\TTGTQTLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPQTSSPCPSADIDMKT METAEKLARFVAQVGPEIEQFSIENSTDNPDL WFLHDQNSSAFKFYRKVFELCPSICFTSSPH NLHTGGGDTTGSQESPVDLMEGEAEFEDEPP PREAELESPEVMPEEEDEDDEDGGEEAPAPG GAGKSEGSTPADGLPGEAAEDDLAGAPALSQ ASSGTCFPRKRISSKSLKVGMIPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV
1120	2470	A	9163 9166	272	523	PMSSLQGCFYTFKCIIFKGIFLLLISNLIAF**EK
1121	2471	A	7100	2/2		V/CSHITDSLKFIGKGWVGMVTHACNPGTLG G*GGWIA*VREFETSLGNM
1122	2472	C	9170	442	236	MNRRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRON*
1123	2473	A	9171	10	423	MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC LTWINALGKFFG

				T 19	Desdisted and	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D=Aspartic Acid, E=Glutarnic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ļ	in	nucleotide	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł		peptide	Sequence	/=possible nucleotide deletion, \=possible
		1	İ	sequence		nucleotide insertion
	0.454	<del>  </del>	9173	3	374	GPSPSLLVLLPOEPGGTGTPVRAGAGAGMWL
1124	2474	Α	91/3	3	} 3,4	WEDOGGLLGPFSFLMLMLLLETRNPVNACLL
		1	1	1	1	TGSLFVLLGVFSFEPVPSCRALQELKPRDRISA
		1		1		LAHRGGRHDPPENTLGAIR/OGS**WSNRR
	0.400	<del> </del>	9179	704	188	FSSSGLLFOCFOGIHVOKLTLOARPTLFSWWL
1125	2475	Α	91/9	704	100	CSKPPKETGELENAESGGDGGRRGGKQDNV
		į.	1			AWWRRM\OKG\DFPWDDEDFPQSGPFGGQA
1			i	1		LPMGFFYLYFRDPGREITWKHFVQYYLARGL
		1	1		}	VDRLEVVNKQSVRVIPAPGTSSEVRGEFKAE
Ì		1				YCRHKFISCKNVVFYFFQ
	2476	+	9183	153	233	MEYMAESTDRSPGHILCCECGVPISPN
1126	2476	A -	9185	1 1	321	LTGOLGSILLRVFSKSRAGLGARKLKAYRTM
1127	2477	Α	9185	1 1	321	EYMAESTDRSPGHILCCECGVPISPNPAQY\CV
		1	1			ACLRSSFHIYHCIPKLFIHPFSKTSSSAFITPSHY
						LITERSTIS
1100	2478	<del></del>	9186	183	847	VLKFLLLOTMDEOSOGMOGPPVPQFQPQKAL
1128	24/8	Α	9160	103	"	RPDMGVNTLANFRIEKKIGRGO\FSEVYRAAC
}				1	1	LALDGVPVALKKVOIFDLMDAKARADCIKEID
Ì		1	l			LI KOLNHPNVIKYYASFIEDNELNIVLELADA
		1	ļ	1		GDLSRMIKHEKKOKRLIPERTVWKYFVQLCS
1		Į.				ALEHMHSRRVMHRDIKPANVFITATGV VKLG
		ĺ				DLGLGRFFSSKTTAAHSLVGTPYYMSPERIHD
1	1	}	ì	1		NG
1129	2479	A	9190	1	370	GTSWKIPSAAVSESSPNGAAYASGLPCGVRG
1129	24/3	1	1,,,,	1		PPWAGLALLPSPTLMALLRRPTVSSDLDNIDT
		1	1		1	RATTIKIRVVATTTRARIEDMRHSATALTRPD
			Ì			ATTAQIPKLPVTTVCNRRANPGIPPSVL
1130	2480	A	9194	131	487	AYLKRLPVPESITGFARLTVSEWLRLLPFLGV
1130	2.00	1				LALLGYLAVRPFLPKKKQQKDSLINLKIQKEN
1	1	1	1	İ	1	PKVVNEINIEDLCLTKAAYCRCWRSKTFPAC
İ						DGSHNKHNELTGDNVGPLILKKKE
1131	2481	A	9201	184	605	KELVDEKSERGRAMDPVSQLASAGTFRVLKE
		1	1		}	PLAFLRALELLFAIFAFATCGGYSGGLRLSVD
1			1	ſ	1	CVNKTESNLSIDIAFAYPFRLHQVTFEG\PTCE
		Ì			1	GKERHKLALIGDSSSSAEFFGTVAGFAFLYSL
		1	-			AATGVYIFFQNKY
1132	2482	A	9206	1	852	GGGRAGAGSRDMGSTDSKLNFRKAVIQLTTK TQPVEATDDAFWDQFWADTATSVQDVFALV
1				1	1 .	PAAEIRAVREESPSNLATLCYKAVEKLVQGA
1	-				1	ESGCHSEKEKQIVLNCSRLLTRVLPYIFEDPD
1		ŀ	}	}		WRGFFWSTVPGAGRGGQGEEDDEHARPLAE
1		1		1		SLLLAIADLLFCPDFTVQSHRRSTVDSAEDVH
	1	}		1		SLEATABLEFCPDFT VQSHRRST VDSAEDVII SLDSCEYIWEAGVGFAHSPQPNYIHDMNRME
		1				LLKLLLTCFSEAMYLPPAPESWQH/RTHWFSS
		1		Į.		FVSSENRHALPLFTSLLNTVCAYDPVEYGIPY
1			1	1		
		1			<del></del>	NHLY GPRARVQGFSGADIVKFMALGSMYLVLTLIV
1133	2483	A	9208	1165	1463	AKVLRGAEPCCGPLKNRVLRPCPLP/VPLPPP
				1	1	HPQPSRGNPVGCLPTYKVVYKLLSWPLHSNS
			1	1		
					1.00	NVYFIV MAGAGPKRRALSAPVAEEKEEAREKIMAAK
1134	2484	A	9210	66	1586	RADGAAPAGEGEGVTLQGNITLLKGVAVIVV
		}				AIMGSGIFVTPTGVLKEAGSPGLALVVWAAC
			1		ĺ	AIMUSUIT VI FI GTTTEV COODVA VM DV
		1		1		GVFSIVGALCYAELGTTISKSGGDYAYMLDV
1		-				YGSLPAFLKLWIELLIIRPSSQYIVALVFATYL
	1	- 1	1	1	1	LKPLFPTCPVPEEAAKLVACLCVLLLTAVNC
1	- 1	í	1	1	[	THE TRANSPORT A SECURE OF A SECURITION ASSESSMENT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
				1		YSVKAATRVQDAFAAAKLLALALIILLGFVQI
						YSVKAATRVQDAFAAAKLLALIILLGFVQI GKGDVSNLDPNFSFEGTKLDVGNIVLALYSG LFAYGGWNYLNFVTEEMINPYRNLPLAIIISLP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ì	i	peptide		/=possible nucleotide deletion, \=possible
			]	sequence		nucleotide insertion
						IVTLVYVLTNLAYFTTLSTEQMLSSEAVAVDF
	ľ	į		{		GNYHLGVMSWIIPVFVGLSCFGSVNGSLFTSS
			1			RLFFVGSREGHLPSILSMIHPQLLTPVPSLVFT CVMTLFYAFSKDIFSVINFFSFFNWLCVALAII
		ļ	1			GMIWLRHRKPELERPIKVNLALPVFFILACLF
		İ		1		LIAVSFWKTTPWSVASDFTIILSGLPVYFFGV
			[	İ		WWKNKPKWAPPGHLSPRPSCVRSSCMVVPQ
		<u> </u>			<u> </u>	RDRLPPAYFCRPVVCVVTALDVG\SPESQEM
1135	2485	Α	9216	40	410	DLVAFEDVAVNFTQEEWSLLDPSQKNLYREV
		}		1		MOETLENLASIGEKWKDQNIEDQYKNPRNNL
	1		ł	1		RSLLGERVDENTEENHCGETSSQIPDDTLNK
	_				<u> </u>	RRRRSRYRRCSRFPRPGPLAVSMPHAFKPG
1136	2486	A	9223	3	983	DLVFAKMKGYPHWPARIDDIADGAVKPPPN
		1		1		KYPIFFFGTHETAFLGPKDLFPYDKCKDKYGK
		1	1			PNKRKGFNEGLWEIQNNPHASYSAPPPVSSSD
			1			SEAPEANPADGSDADEDDEG\RGVMAVTAVT
			1	1		ATAASDRMESDSDSDKSSDNSGLKRKTPALK
	-					MSVSKRARKASSDLDOASVSPSEEENSESSSE
						SEKTSDQDFTPEKKAAVRAPRRGPLGGRKKK
		]	1			APSASDSDSKADSDGAKPEPVAMARSASSSSS
			ŀ	\		SSSSDSDVSVKKPPRGRKPAEKPLPKPRGRK
•		1	ł			PKPERPPSSSSSD
	2487	$+_{A}$	9229	21	239	LFPRLECRDPVTVNCTLNLPGSKNAPTTASQV
1137	2487	Ι^	1227	7.		GSTWNYRGGLPHPTNFFVKTGFRCSQAGLKL
						RGSREPPAWA
1138	2488	A	9231	1664	2	TRSVGVNTCEVGVVTEPECLGPCEPGTSVNL
1130	2400	1	723.			EGIVWHETEEGVLVVNVTWRNKTYVGTLLD
				i		CTKHDWAPPRFCESPTSDLEMRGGRGRGKR
				· ·		ARSAAAAPGSEASFTESRGLQNKNRGGANG
	1		1			GRRGSLNASGRRTPPNCAAEDIKASPSSTNKR
		ł		Ì		KNKPPMELDLNSSSEDNKPGKRVRTNSRSTP
		ì				TTPQGKPETTFLDQGCSSPVLIDCPHPNCNKK
		1				YKHINGLRYHQAHAHLDPENKLEFEPDSEDK
1	1	1				ISDCEEGLSNVALECSEPSTSVSAYDQLKAPA
}	1	]	}	1		SPGAGNPPGTPKGKRELMSNGPGSIIGAKAGI
		İ				NSGKKKGLNNELNNLPVISNMTAALDSCSAA
						DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK
		1				ANNCKTDKN\PSKLKSARPIAPAPAPTPPQLIA IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPI
}	}	1		1		KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR
	1					KLKDKEGKETGSPKMDAKLGKLEDSKGASK
1				•		DLPGHFLKDHLNKNEGLANGLSESQESRMAS
						DEPOHERDHENINEGENINGESESQUINGES
1					1	IKAEADKVYTFTDNAPSPSIGS TRRGQPWRRRAAAAGILPGREAAACLPSC/A
1139	2489	A	9234	207	443	VTAAVSGLLVGYELGIISGALLQIKTLLALSC
1						A I WA A 20TF A DIE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE TOTTO TE T
						HEQEMGVSSLVIGALL MAQGNNYGQTSNGVADESPNMLVYRKV
1140	2490	A	9238	248	328	FVEAAVKMLGSLVLRRKALAPRLLLRLLRSP
1141	2491	A	9242	2	535	TLRGHGGASGRNVTTGSLGEPQWLRVATGG
1	1	ĺ				RPGTSPALFSGRGAATGGRQGGRFDTKCLAA
			Į.			ATWGRLPGPEETLPGQDSWNGVPSRAGLGM
	1			1		A I WORLPUTEE IL FUUDA MIU TI SKAULUM
		1	1			WPWAAALVVHCYSKSPSNKDAALLEAARA
						NMQEVSRNRCALLHSAAVQEYGYGN
1142	2492	A	9245	157	466	HLCFWFFVGLFLPEQQIMLFATLLRMAQGCL
				1		FALGNDFLNITTKAQA/TKEKLDKLDFIKIKTO
1			-			CTSMDAIEKTEPLTKWTKAFVSHVSYKRLLF
1		j				GICKEYSRQ
				1		
1143	2493	A	9247	264	115	GLPQQTSTIQPPGTPDGARDFTSTIQPPGAPDO ARDSTSIIRMGPEIPPP

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nucl-	peptide	1	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	1	USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ience			914	ng to first amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	}		peptide	sequence	/=possible nucleotide deletion, \=possible
	[	1	1	sequence	Ì	nucleotide insertion
	0404	ļ	9260	Sequence	401	KKVPGRLSEMSFSLNFTLPANTTSSPVT\DCG
1144	2494	A	9200	<b>'</b>	101	SLGLAAGIPLLVATALLVALLFTLIHRRRSSIE
		1	1	1	{	AMEESDRPCEISEIDDNPKISENPRRSPTHEKN
	1					TMGAQEAHIYVKTVAGSEEPVHDRYRPTIEM
	1			ļ		FRRR
1145	2495	A	9264	175	411	METIWIYQFRLIEIGDSTVGKSCLLHRFTQGR
1145	2493	1	1,20.	1		PGLRSPACDPTVGVDFFSRLLEIEPGKRIKLLL
	1		1			WDTAGQERFISIT
1146	2496	A	9277	592	814	MFTYLEGREGIKSQPKMEPHSVT\RLECSGMI
1140	2470	1	1			SAHCSLNLPGTSDSPASASR/VAGTTGMRHH
	į.	-				WLIFAFLVETGF
1147	2497	A	9279	1255	2	FRRGRRGEEEKEEEEEEGWVNGMENSHPI
	1			1		HHHHQQPPPQPGPSGERRNHHWRSYKLMIDI
						ALKKGHHKLYRYDGQHFSLAMSSNRPVEIV
				1	1	DPRVVGIWTKNKE\LELSVPKFKIDEFYVDQ\
	1		1		1	PPKQVTFAKLNDNIRENFLRDMCKKYGEVEI
		Ì	1			VEILYNPKTKKHLGIAKVVFATVRGAKDAVO HLHSTSVMGNIIHVELDTKGETRMRFYELLV
	1	1	ì			TGRYTPQTLPVGELDAVSPIVNETLQLSDALI
	1	1		1		RLKDGGLSAGCGSGSSSVTPNSGGTPFSQDT.
	1		1			YSSCRLDTPNSYG/QGTPLTPRLGTPFSQDSS
	1	1	1	}	1	SSRQPTPSYLFSQDPAVTFKARRHESKFTDA
	1				<u> </u>	NRRHEHHYVHNSPAVTAVAGATAAFRGSSD
	1				1	LPFGTVGGTGGSSGPPFKAQPQDSATFAHTPI
		1				PAOATPAPGFR
1110	1000	+A	9302	1026	6	IASIONADTMPGVGLLVSHFSTLVSRQRCPN
1148	2498	^	9302	1020		ADPONLTDVSIFLLLEVSGDPELQPVLAGLFL
						SMCLVT:VLGNLLIILAISPDSHLHTPMYFFFS?
	1	1	ł	ł	}	LSLPDV\GFTSTTVPK\MIVDI\QSRSRVISYAG
			-			CLTQKSLFAIFGGTEE\NMLLSVMAYDRFVA
	1	1		ļ		CHPLYHSAIMNPCFCAFLVLLSFFFLSLLDSQ
		)		j	}	HSWIVLQFTIIKNVEISNFVCDPSQLLKFACSI
	1		- 1			SIINSIFIYFHKDPERQLVLAGLFLSMCLVTVL
						GNLIIILDVSPDSHLPTPMYFFLSNLSLPDIGF
				1		STTVPKMIVDIQSHGRVIFYAGCLTQMSLFAI
	1					GGMEERHAPECDGL
1149	2499	A	9303	1	699	MASQEKDIFIGWGTIHLFRKPQRSFFGKLLRE
		-				FRLVAADRSMGRYMLFGVINLICTGFLLMW
	1					SSTNSIALT\SYTYLTIFDLFSLMTCLISYWVT
	]			1	1	RKPSPVYSFGFERLEVLAVFASTVLAQLGAL
			1	1	ĺ	ILKESAERFLEQPEIHTGRLLVGTFVALCFNL
			-			TMLSIRNKPFAYVSEAASTSWLQEHVADLSR
		1		1		SLCGIPGLSSIFLPRMNPFVLIDLAGAFALCIT
				<del> </del>	1 (02	YMLIEI DRSTSVTRAGVQWCSLGSLQPRTPGLLRSSC
1150	2500	A	9308	797	693	SLP
				1 205	406	VAIKELPVLWKWSKPTR\TAKEPPQTQQRAG
1151	2501	A	9309	205	400	SKTAAPPCQWSRMASEGPNIPCPGARHSDKC
	1					FLICTI
1122	1000		0214	913	504	KPSPLITPPAVVLPPSAVLNLVNTFSSFPQVEV
1152	2502	Α	9314	913	507	QGPLCGPRKGRLAVTIPFFGLS/LPKYMDHRF
	1			1		PPPHR\EIFFVFLAETGFHRASQAGPDLPTS/S/
				1		PPTSA/FPKCWEYRSEPQCLPGCLSFSGILLDL
						GTNVSLRAA
<u> </u>	2500		9315	392	1	HPHRPRPGFRSPARSSRPCPVLTSLLPPFPSPS
	2503	Α	9313	372	1,	PADDLVKAGRDRKDPQVR/ERRLRPNPGRLC
1153						
1153						GPR\PRPARARS/CHQPRLTRVCPRSPPPEARA
1153						GPR\PRPARARS/CHQPRLTRVCPRSPPPEARAPAPAAPARGRGAPKRNRPRTDTRAPRGSSAF

SEQ ID   SEQ ID   Not   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod   bod							11 11 11 11 11 11 11 11 11 11 11 11 11
Included	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Seq.   USSN   Goresponding   February   Goresponding   February   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding   Goresponding	1	h	hod		, -		D=Aspanic Acid, E=Glutamic Acid,
Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Sect	1						
1154	1	, -	1	4			1=150/eucine, N=Lysine, L=Leucine,
### ### ### ### ### ### ### ### ### ##	1 -	uence		1		1	M=Methornic, N-Asparagnic, 1-1 tonic,
residue of   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   popular   p	uence		1	914			
Peptide			ĺ				V=Transine Y=Linknown *=Ston codon
1154   2504   A   9321   331   433   MFC/QAQYGTRAPSQPRQHSASDPLITERIK PT	Ì					sequence	
1154   2504   A   9321   331   433							
PF		0504		0221		122	
1155	1154	2504	A	9321	331	433	1
1156   2506   A   9326   383   619   MISPSKTEGDPLPLPPEGGGGEVKGFGGGAVE	11.55	0606	<del> </del>	0224	190	275	
BAAQRHCRASVSLIRMRPFQGGSSRPARVPL   ROPDSPHLIREPPSPSP			<u> </u>		1		
1157   2507   A   9327   152   292   YERGRISQGGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGRAIGAGWQS   KEPL-WEGLQRSGSHPAGAQPGGAGAAMAQPRACSVTTIERRYSLKS   SESGLLVSCPDIGNLVVVFVSYFRGRRRRP!   KVAAVGGLLDLEGGEMI   KVAAVGGLLDLEGGEMI   KVAAVGGLLDLEGGEMI   KVAAVGGLLDLEGGEMI   KVAAVGGLABAGALPRAGILYPLAGIR WYGALDRWSGLSGHEJSHLALEISPR   KRYVRILLIGEGAEHVADPVSUTQNTVR   LMEAGLPOKQABRADELPRAGILYPLALDES   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGEGAEHVADPVSUSHTAMK   KRYVRILLIGISGVFLGGAGVYRGAVFTAMK   KRYVRILLIGISGVFLGGAEVYBGGVYRGAVFTAMK   KRYVRILLIGISGVFLGGAAVARIKVYLM   QTSRQRVVKRLRTSLFSSLGQEVAFSDKAGT   GELI   KRYVRILLIGISGVFLGAAVARIKVYLM   QTSRQRVVKRLRTSLFSSLGQEVAFSDKAGT   GELI   KRYVRILLIGISGVFLGAAVARIKVYLM   QTSRQRVVKRLRTSLFSSLGQEVAFSDKAGT   GELI   KRYVRILLIGISGVFLGAAVARIKVYLM   QTSRQRVVKRLRTSLFSSLGQEVAFSDKAGT   GELI   KRYVRILLIGISGVFLGAAVARIKVYLM   QTSRQRVVKRLRTSLFSSLGQEVAFSDKAGT   GELI   KRYVRILLIGISGVFLGAAVARIKVYLM   QTSRQRVVKRLRTSLFSSLGQEVAFSDKAGT   GELI   KRYVRILLIGISGVFLGAAVARIKVYLM   QTSRQRVVKRLRTSLFSSLGQEVAFSDKAGT   GELI   KRYVRILLIGISGVFLGAAVARIKVYLMICHTAM   CTSRQRVVKRLRTSLFSSLGQEVAFSDKAGT   GELI   KRYVRILLIGISGVFLGAAVARIKVYLMICHTAM   KRYVRILLIGISGVFLGAAVARIKVAGAAVAGASVAGAVARIPAGAAVAGASVAGAVARIPAGAAVAGASVAGAVARIPAGAAVAGASVAGAVARIPAGAAVAGASVAGAVARIPAGAAVAGASVAGAVARIPAGAAVAGASVAGAVARIPAGAAVAGASVAGAVAGASVAGASVAGASVAGASVAGASV	1156	2506	A	9320	363	019	FAAORHCRASVSILRMRRPGOGSSRPARVPL
1157   2507   A   9327   152   292   YERRGRSGGSHPAGAGPGGRAIGAGWGS   KEPLWEGLGRSGSIPLO   KEPLWEGLGRSGSIPLO   KEPLWEGLGRSGSIPLO   KEPLWEGLGRSGSIPLO   KEPLWEGLGRSGSIPLO   KEPLWEGLGRSGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPLO   KERNENGSIPL	1	1	1		· ·	1	
1158   2508	11.50	0507	<del>  </del>	0227	152	202	VERRORSOGGSHPAGAOPGGRAIGAGWOS
1158	1157	2507	A	9327	132	232	
LSKTFSVSSALAMLQERRCLYVVLTOSRCFL   VCMCFLTF[0.4]MVSGYLSSVTTIERRYSLKS   SEGILLVSCPDIGNLVVVFVSYFRGRRRPP   RVAAVGGLIDLEGGEM	1150	2509		0229	<del>-,</del>	430	
VCMCFLTFIQALMVSGYLSSVITTIERYSLKS	1138	2508	A	9328	1	1 430	LSKTESVSSALAMLOERRCLYVVLTDSRCFL
SESGLLVSCFDIGNLVVVVFVSYFRGRRRRP/   RVAAVGGLDLEGGEM    1169   2509   A	1			1	ļ		VCMCFLTFIOALMVSGYLSSVITTIERRYSLKS
RVAAVGGLDLEGGEM    RVAAVGGLDLEGGEM    RVAAVGGLDLEGGEM    LMEAGLPQKQAERADELFEAGLYVYKLDER     LMEAGLPQKQAERADELFEAGLYVYKLDER     LMEAGLPQKQAERADELFEAGLYVYKLDER     VLNALVYSVGLQWFKESDLSHLEILEISFE     VLNALVYSVGLQWFKESDLSHLEILEISFE     VLNALVYSVGLQWFKESDLSHLEILEISFE     VLNALVYSVGLQWFKESDLSHLEILEISFE     LA 9338   2			i	1			SESGLL VSCFDIGNL VVVVFVSYFRGRRRRP/
1159   2509   A   9334   108   383	}	}	ļ	1			
LMEAGLPQKQARADELFEAGLYIYYKLDER	1160	2500	<del>                                     </del>	0224	108	383	KGNOVNGNGNOLKRKHESMCPVSLTONTVR
1160   2510   A   9338   2   430	1139	2309	A	9334	108	303	LMEAGLPOKOAERADELFEAGLVIYVKLDER
1160		1	1	1			
	1160	2610	1	0239	-	430	
DITTOQELREEHKANVERVYHDVSQEATIEKI   RTKWIPLV/RWGDHAZGGYGKSYLPSGRSM   EAELPIMSQLTEIETCVEC	1100	2510	A	9336	-	450	
RTKWPLVRWGDHAEGPVGRSYLPSGRSM		1					DHTDOELREEIHKANVERVVHDVSQEATIEKI
EAELPIMSQLTEIETCVEC			]				RTKWIPLV/RWGDHA/EGPVGIKSYLPSGRSM
1161   2511   A   9341   1   390			1		İ		
AVG/CSPMSQVISMSAPFFLGKIIDAIYTNPTV	1161	2511	Α	9341	1	390	NSRVDDFVAPGLSEAGKLLGLEFPERQRLAA
OTSRQRVVKRLRTSLFSSILGQEVAFSDKAGT   GELT	1101	2311	Α.	7541	1.	1 0,0	AVG/CSPMSGVISMSAPFFLGKIIDAIYTNPTV
OTSRQRVVKRLRTSLFSSILGQEVAFSDKAGT   GELT	İ						DYSDNLTRLCLGLSGVFLCGAAANAIRVYLM
1162   2512   A   9343   84   837		1	1	1			
TLPPHYRYGMSPPGSVADKRKNPPWIRRRPV VVEPISDEDWYLFCGDTVEILEGKDAGKQGK VVQVIRQRNWVVVGGLNTHYRYIGKTMDYR GTMIPSEAPLLHRQVKLVDPMDRKPTEIEWR FTEAGERVRVSTRSGRIPKPEFPRADGIVPET WIDGPKDTSVEDALERTYVPCLKTLQEEVME AMGIKETR\NTRRSIGIEPGAEQLLPNFCPSLE G DSLALSPRLECSGAISAHCNLTPPGFTPFSCLS LPSSWAYRCASPHPDNFFVFLVESGFHHVGQ AGLKLLISSDPPTSAFPKCWDYRRD\SSAPAT FSSYQRNNPDLLNDTIMPNIK SSFPTCMRTVFHSNTSVSSLLHRRGHVTPQLTI HGGWRHHRDHTAIDEWDFNPSKFLIYTCLLL FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV VAGASVGAGWARNPRYRTEGEACVEFKA MLIAVGIHLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNILQFIFIALKLDRIHWPWLVVFVPLWILL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNILQFIFIALKLDRIHWPWLVVFVPLWILL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNILQFIFIALKLDRIHWPWLVVFVPLWHLD AIRRDF\CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGFEPTLHDCFPRP LGGDTLFHVEYTSVHGRERLSAKD PPILRWTPPSGKNFFFFFFESEFYSSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS							
TLPPHYRYGMSPPGSVADKRKNPPWIRRRPV VVEPISDEDWYLFCGDTVEILEGKDAGKQGK VVQVIRQRNWVVVGGLNTHYRYIGKTMDYR GTMIPSEAPLLHRQVKLVDPMDRKPTEIEWR FTEAGERVRVSTRSGRIIPKPEFPRADGIVPET WIGDPRKDTSVEDALERTYVPCLKTLQEEVME AMGIKETR\NTRRSIGIEPGAEQLLPNFCPSLE G  DSLALSPRIECSGAISAHCNLTPPGFTPFSCLS LPSSWAYRCASPHPDNFFVFLVESGFHHVGQ AGLKLLISSDPPTSA/FPKCWDYRRD\SSAPAT FSSYQRNNPDLLINDTIMPNIK SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTI HGGWRHRDHTAIDEWDFNPSKFLIYTCLLL FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV VAGASVGAGVWARNPRYRTEGEACVEFKA MLIAVGIHLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLEEILC SVNILQFIFIALKLDRIIHWPWLVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH VTMAISWITTIVPLLTTEVLLVHRLDGHNTFS YVSIFVPLWLSLTIMATTFRRKGGNHWWF AIRRDF\CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGFEPTLHDCFPRP LGGDTLFHVEYISVHGRERLSAKD PPILRWITPSGKNFFFFFFESEFYSSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1162	2512	A	9343	84	837	QGRFRAFCWQRDFLQPPGMRLSALLALASKV
VVQVIRQRNWVVVGGLNTHYRYIGKTMDYR GTMIPSEAPILLHRQVKLVDPMDRKPTEIEWR FTEAGERVRVSTRSGRIIPKPEFPRADGIVPET WIDGPKDTSVEDALERTYVPCLKTLQEEVME AMGIKETR\NTRSIGIEFGAEQLLPNFCPSLE G  DSLALSPRLECSGAISAHCNLTPPGFTPFSCLS LPSSWAYRCASPHPDNFFVFLVESGFHHVGQ AGLKLLISSDPPTSA/FPKCWDYRRD\SSAPAT FSSYQR\NNPDILL\NDTIMPNIK  1164 2514 A 9347 3 1099 SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTI HGGWR-HIRDHTAIDEWDFPSK-FLYTCLLL FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV VAGASVGAGVWARNPRYRTEGEACVEFKA MLIAVGHILLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNILGFIFIALKLDRIIHWPWLVVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATTFRRGGNHWWF AIRRDF/CQDQLPQFTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGGDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESSFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1	1 20 12	1				
GTMIPSEAPLLHRQVKLVDPMDRKPTEIEWR FTEAGERVRVSTRSGRIIPKPEFPRADGIVPET WIDGPKDTSVEDALERTYVPCLKTLQEEVME AMGIKETR\NTRRSIGIEPGAEQLLPNFCPSLE G  DSLALSPRLECSGAISAHCNLTPPGFTPFSCLS LPSSWAYRCASPHPDNFFVFLVESGFHHVGQ AGLKLLISSDPPTSA/FPKCWDYRRD\SSAPAT FSSYQR\NPPDLIL\NDTIMPNIK  1164 2514 A 9347 3 1099 SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTI HGGWRHHRDHTAIDEWDFPYSKFLLYTCLLL FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV VAGASVGAGVWARN\PRYRTEGEACVEFKA MLIAVGHILLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNILQFIFIALKLDRIIHWPWLVVFVPLWILM SFICLVVLY\TVWSLLFLRSLDVVAEQRRTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATTFRKGGNHWWF AIRRDF/CQDQLPQPTGKPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADDGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1		1	1		ļ	VVEPISDEDWYLFCGDTVEILEGKDAGKQGK
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	000.00	177.	Lero	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of peptide	nou	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	seq-		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
eotide	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	ucaice	1	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
испсс			1 714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		[		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	}	peptide	•	/=possible nucleotide deletion, \=possible
	1	ì		sequence		nucleotide insertion
			+	·		PRPLILYAPAPARPAGTAFIPHSHPPPPDLLRPT
	1	1		1	1	ATPA/TPCPSLPPPPRPLHPTQPSTALLPDPPPW
		l				PLPFPPPSS/RPPRPDCSTSYSPTFPPPT
1168	2518	A	9375	511	15	MMLSEETSAVRPQKQTRFNGAKLVWMLKGS
•					1	PITVTSAVIIVLMLLMM/IFSPWLATHDPNAID
		1			ļ	LTARLLPPSAAHWFGTDEVGRDLFSRVLVGS
	1	l	1			QQSILAGLVVVATTGMIGSPLECLFGELGGRA
		1				DAIFMRVMDIMRS/IPSLVLTMEKTAALGPSL
			l			FNAMQASSEH
1169	2519	A	9377	42	410	GNGRVAPRDPGAVASAEPGLTTHDSGVNPN
						NSARRMEAMASGSNWLSGVNVVLVMAYWS
						LVFVLLFIFAKRQIMRFAMKSLRGPHGPVGH NAPKDLKEEIDILLSRVHNIKYEP\HLLADDDA
	l	<u> </u>			1202	GVSGFSASVLRQRRMEDELEPSLRPRTQIQGR
1170	2520	Α	9378	302	1303	ILLLTICAAGIGGTFQFGYNLSIINAPTLHIQEF
	1	1				TNETWQARTGEPLPDHLVLLMWSLIVSLYPL
		1	Ì	İ	}	GGLFGALLAGPLAITLGRKKSLL\VNNIFVVS
	}	1	1			AAILFGFSRKAGSFEMIMLGRLASWGVNAGV
	1	1	ļ	1	ľ	SMNIQP\MLPGGESAPKELRGAVAMSSAIFTA
		i			1	LGIVMGQVVGLSTTAATGLRGL\AGELEELEE
		1	l l			ERAACQGCRARRPWELFQHRALRRQVTSLV
		}	1			VLGSAMELCGNDSVYAYASSVFRKAGVPEA
			-			KIQYAIIGTGSCELLTAVVSVSLEGALPPPAL
					1	WGGTPRSFALNOFTLQKKKK
1171	2521	A	9381	2	412	RGPASAOEDERARTAPLERVRARGRMTTSSA
11/1	2321	1 ^	7301	_		LFPSLLPCSWSTSNKYLAEFRAGKMSLKGTTE
	1					TPDKRKGLAY/IQQTDDSLIHFCWKDRTSGNV
<u> </u>		-			1	EDDLIIFPDDCEFKRLPQCPNGRVYVLKFKAG
1		1				SKRLFFWMQEP
1172	2522	A	9384	20	355	GWNGRSTEASPAAEAPHVPHKET\KAAMGTQ
				]		CTHGGKVRPDPHDMLTTVVHKIKLFVLCHSL
				-		LQLCAIMISDYLKSSIYTVEKRLGLFRPTSGLL
						ASFNEVGNTALIVLESY  LCQCIVPGQQKETFSLNPSSATVRFYL*LSLQ
1173	2523	A	9393	430	87	QRKEDQ*IIL*YHLNKDCLHIFMSAITLYMKI*
		1		(		KIFVLFDFNIMFETPFYII*FIFLFSQNLKRIRQV
]		1		}		IRPPISFSKINNGP
				<del></del>	1 224	ERLEIGRLGGERGSGPASCLRVIDVSGMWDQ
1174	2524	A	9397	77	374	RLVKLALLQLLRAFYGIKVKGVRVHRDCGTF
		1	1	J		ESSSTLIRVS*FGVPCNALAHFGVTHF*YILDF
	ĺ			1		LGML
1155	1000	+	0200	66	397	HESSRADRDKMDTRGSTYTDADPVNKSGGT
1175	2525	A	9399	100	1 391	AKMNKWSKGKVRDKLNNLVLFDTATYDKL
		1		1		CKEVPNYKLITLAVVSERLKIPGSLARAALHE
}	}	1	1			LLSRGLI*LVIQHIAQVIY
1154	2636	<del> </del>	9408	12	299	LDLTHVLSLSISLTVTILGTTFGMVIPLLDVVY
1176	2526	A	7408	1	273	GERGYAONGDF*DAQLDDYSFSCYSHAQVN
			1	}		GAPNSLTRAYDDP*VKISGLECQKVGALVEV
			<b>\</b>	1		KCLNL
1177	2527	A	9416	12	402	CNFLRSSRIRVHSTPAASTMPPKVDPNEIKVV
1 11//	2321	1	7410	1 -		YLRCTGGEVRATSALAPKIGPLGLSSIKVGVD
				1		FV*ATGDWNVLIISVILTIRILLSHIFVVPPFFCF
1		1		1		DHLIAFWDLQSLIFLHVIFSLFITLLLFCFFSIF
1170	2520	A	9419	142	426	TPLFDLWPRVVLSWLETVLTSLRTRRAASGPP
1178	2528	^	7417	172	1.20	ACRIMPTTVDDVLEHGGEVHFLQKQMLYLL
1		1		1		ALI*DTFAPIYVGIVFLGFTPDHRCRSPGVAEL
1170	2622	<del></del>	9420	1450	1655	LSSAGTKMNLN*KNYWPGASAHACNPSTLG
1179	2529	Α	9420	1430	1033	GQSRCITRSGDRDHPG*HGETPSVLKIQKISRA
1						

WO 01/57188

000 00	CEA TO	Mac	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence				acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ļ	Ì	914	ng to first amino acid		T=Threonine, V=Valine, W=Tryptophan,
	<u> </u>	ļ			of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
	1		l	residue of	sequence	/=possible nucleotide deletion, \=possible
	ı		1	peptide		
		l .		sequence		nucleotide insertion
1180	2530	A	9422	176	375	HRPQTTRPDWKPRT*PQGK*GRLSSEISPASPP
		1		Ì		SRFSRSTKPVPPKADPPARQKLTGVLHAPLLK
			1			L
1181	2531	A	9436	2	274	PIAASLRMYNLQPYTEENLICTAFATMVETVP
						IARTILDRLTGIPHGYCFVE*ADWATADKCVH
	İ	1	1	1		IYNGKPLPGATPLLSLQLHQLAHLGS
1182	2532	A	9442	3	240	VDKCSSKSIVLSEYCPHCMCSLSTDPKPFGQL
1102	2332	1	12			SMILK*MGAGDEKISAMGKARVDHRELYLGL
	1		1	ļ		LYPTEDYKLTFRARH
1102	2533	A	9444	384	3	LKDFQPWALHDWPLFCCCTFLLFLVLECFTR
1183	2533	ΙΛ.	7444	707		KGCSGWAPWLSLQCQHFGRPRWADHLRSGV
	1	1		1		RDQPGQYSKTTFLPKIQKLAGHSGAHL*S*LL
1		1	1	1	1	ERMRWKNRLNPGGRSCSEPRWHHCTPGWAT
				1		ERG
		ــــــــــــــــــــــــــــــــــــــ			655	LSGFKSLMPKIPLQYIYVRVRTTWSFCLPLDG
1184	2534	Α	9462	391	655	RKLMLS*YSK*LT*KYNILPEYSRMTLPPGMV
l	ł	1	1			IHTCNPSTLGGRAGWIV*AQEFET
						RCPMWQGQASRMDPAKAKDREASTCCSLA
1185	2535	A	9467	215	566	WWWGWECWVRALKLSSGPAGPLACWVAK
1		1	1			
1	1	1	1	1		KKSLSLSGPVYPSEKGAGLYVF*DRVSLCHPG
						WSAVVQFWLTAASNSCFSLLSSWDYRCA
1186	2536	A	9468	275	452	HIPQLHTKTHYVPTRMVNKI*QIDNSKPWQR
	1		İ			GG*TGILTHCW*ESKLVQPLWKIVWHYQ
1187	2537	A	9469	388	3	EVAPGPSQILPRRVTDGGDRPQFSLPGPRLPQ
110,		1		1		SSRGAEPCLSNCIHSPAPRKQRMGDSDQ*STP
Ì	1	1	-	1		NPASPHPEAPQEPWDSASGSVGSFSLGRGAK
j	l		ļ	1		ASS*VPGKGRGPRQGSELLAETILELFLALAN
1	j			1		S
1188	2538	A	9471	124	397	TMDKKNRHGNSLDMASEIHMTGPMCLIENTT
1100	2550	1 11	7	1		GRLMANPEALKILSAITQPMVEEAIAGLYRAC
			ļ			*FYLTNNLAGMKKGLCLGSTEQAHTIGI
1189	2539	A	9480	584	769	GHVQSQHFGRPRRADHLRSGDRDHPG*HDET
1109	2339	^	7400	301	'"	PSLLKIQKISWAWWRAPVVPATWEAEAEEW
	1		j			R
1100	2540	$+_{A}$	9483	463	86	VTVGLTLLLRGAPRFTAG*PPSGGGPPLAPLL
1190	2540	^	7403	403		PRQHCTLQTHRHLHPEAPVKV*KT*RLFPGLR
	1		1	ļ		GASSCRRRCNPVLAARKAGSPRSHSTRENC
	1					RRSRCPDTAHRRRRRGRRRNPSCVRSPRWR
			1000	<del> </del>	411	LADALCLSAAATGAVRPGARAQPSTRRRLSP
1191	2541	Α	9489	1	411	SVRVCCRAAAASNLLYSSCLQRHSERASEEG
		· 1		1		ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI
	1	i			1	MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ
					1	
			<u></u>			KEELTAVNVK
1192	2542	A	9497	389	161	VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI*
		1				CEEDERKMAREFLAEFMSTYVMMNIHMIVE
		1			i	KDTYSDHEEINTS
1193	2543	A	9509	186	1	IAKSQ*KRWQRSGAMETLKHGWWECKLVQF
,	-5 .5	1				FGKTFVNVN+S+TYVYPCDKIILLLGLYPTEM
1194	2544	HA-	9512	58	433	PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL
1134	2344	^	73.2		""	LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA
	-			1	i	SSKGOOFRR*KEHPFMLKTLNKLRIEGT*LKI
1		1			1	RRAIYDNPTANIIVEGQKLEAFPLRTGTRQ
L		<del></del> _	+ 25:5	505	1223	GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP
	2545	Α	9515	595	1223	AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC
1195	į.			1	1	TOUGHT TIMESOUGHT TIMESOUGHT ATTENDED
1195		1			1	I DODI CI ADDDDDDD DIYIT VGDGNGRNANI AFPP
1195						PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP
1195						LPRCSCAPLRSASAPQVS*CV*AVNLLPHNL*
1195						LPRCSCAPLRSASAPQVS*CV*AVNLLPHNL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP
1195						LPRCSCAPLRSASAPQVS*CV*AVNLLPHNL*

No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder   No. of mucle outder	CEO #5	CEO TE	14-	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Included	SEQ ID	SEQ ID	Met	1 -	1		D=Aspartic Acid, E=Glutamic Acid,
USSN   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496   Og496		1	liou .				F=Phenylalanine, G=Glycine, H=Histidine,
1994   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914   1914			1				I=Isoleucine, K=Lysine, L=Leucine,
1914		1 •	Ì		1		M=Methionine, N=Asparagine, P=Proline,
amino acid residue of sequence   peptide paptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   pep	•	daice					O=Glutamine, R=Arginine, S=Serine,
Persidue of   peptide   sequence   y=Tyrosine, X=Usknown, "=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=Stop codon,   y=	uence		{	/14			T=Threonine, V=Valine, W=Tryptophan,
peptide			1				Y=Tyrosine, X=Unknown, *=Stop codon,
1196		8	ļ				/=possible nucleotide deletion, \=possible
1196			1			}	nucleotide insertion
AERVAPGWDLHTPYLPRINSRTPHA**PPHA   GYIGALFPMSGQWPGGQ   A   A   9521   289	1196	2546	A	9518		468	
1197   2547			'	1			
HAMRHLTGNTSMAIRI-'ADSRFQVQRARYE		}	1				
HAMRHLIGHTSMAIRIL' ADSREQUÇARAYE   APNWYKYGYG'PYDMLC	1197	2547	A	9521	289	448	IAWLSGLFFPSNQANLCFLCYKLTADSRYRG
1198			ì	1	{		HAMRHLTGNTSMAIRFL*ADSRFQVQRARYE
VKQEPNICHL **ETHEFFRITYRLKEREQKKRK							APNWKYKYGY*IPVDMLC
199	1198	2548	A	9524	204	t	KNKKTTKCLSIVTLNISGPNQ*NKRHRVAEWI
1999							
V*QRGDGKNPGYTHLNRPVGTX    1200   2550   A   9548   186   1		}	}				SSYS
1200	1199	2549	A	9546	1785	1943	GGRFKESKLTNAGWQRNSFFIGPPKSIPWAA
1201   2551   A   9549   591   2   SSVVEPROPRSSIPPLSFYGSSPNWTGG   GSCPSGE*LVSPGSSGPNSTGGSSPNWTGGG   SSVVEPROPRSSIPPLSFYGSSPNWTGGG   GSCPSGE*LVSPGSGRKKYSNSNVTMHETSQ   YHVQHLATTIMDKSEAITSVDDAIRKLVQLSS   YHVQHLATTIMDKSEAITSVDDAIRKLVQLSS   PLPTYQRSQTVLNQLRYPSVLLLVQDSEQSK   PLPTYQRSQTVLNQLRYPSVLLLVQDSEQSK   PLPTYQRSQTVLNQLRYPSVLLLVQDSEQSK   PLPTYQRSQTVLNQLRYPSVLLLVQDSEQSK   PLPTYQRSQTVLNQLRYPSVLLLVQDSEQSK   PLPTYQRSQTVLNQLRYPSVLLLVQDSEQSK   PLPTYQRSQTSTALLTCRLCK   AMRP   KYGNEGHWSRQCPNPGKPIRPCPLCRGPHWK   LDCERPPQGPLPSLPLAKTSYSDLTGLATED   *WGPGMDAPATITIASSKTRVTLWAGRPVFF   LIPYRATYSALPNTSGPTTQSSQVSVVGIDGQV   SKPRATPFLFCSLHTF   SKRFERROKGPREFRKKGREGEGQRD   TRENTRYREKGERGERKKMPHRERKGESQQRD   TRENTRYREKGERGERKKMPHRERKGESQQRD   TRENTRYRELITEKER   EDKRLRLVDGDSRCAGRV*IYHDGFWGTLGD   DGWDLSDAHVVCQKLGCGVAFNATVSAHFC   EGSGPIWLDDLNCTGTESHL WQCPSRGWGQ   HDCRHKEDAGVLCSEFTALR   ARGSCPTREFATANGRMGETKOAPQMLVTFK   DAWYTFREEWRQLULVHRITLYRGMLETC   GLIDTLRINNVPQPDVHLLYRGMLETC   GLIDTLRINNVPQPDVHLLYRGMLETC   GLIDTLRINNVPQPDVHLLYRGMLETC   GLIDTLRINNVPQPDVHLLYRGMLETC   SKIPTIPSSPRLKP*TASSQRNLGQILNWELTAK   SKIPTIPSSPRLKP*TASSQRNLGQILNWFLTAV   NPQLSTFSWQIETKYSTKV1.TGNMEERK   SKIPTIPSSPRLKP*TASSQRNLGQILNWFLTAV   NPQLSTFSWQIETKYSTKV1.TGNMEERK   GLIPTKHTHMQEPPHRYLISTYDDHYNRHG   YNPGLPLRTWNGGKLUW   LRSSPAALLRALCTITVTGTALALRSRVATTN   PDGCRNVLRPKYYRLCDKAESWGIALETVPT   GVAVTSWAIMLTVLTLVCKGQDYNRQKLD   FGILSCISS   SKIPTIPSSPRLKP*TASSQRNLGQILNWELTK   GVAVTSWAIMLTVLTLVCKGQDYNRQKLD   FGILSCIS   SKIPTIPSSPRLKPTATLTGTALALRSRVATTN   PDGCRNVLRPKYYRLCDKAESWGIALETVPT   GVAVTSWAIMLTVLTLVCKGQDYNRQKLD   FGILSCIS   SKIPTIPSSPRLKPTATLTGTALALRSRVATTN   PDGCRNVLRPKYYRLCDKAESWGIALETVPT   GVAVTSWAIMLTAVLTLVCKGQDYNRQKLD   FGILSCIS   SKIPTIPSSPRLKPTATLTGTALALRSRVATTN   PDGCRNVLRPKYYRLCDKAESWGIALETVPT   GVAVTSWAIMLTAVLTLVCKQGDYNRQKLD   FGILSCIS   SKIPTIPSTSCHSSTSTRK   GDPGPTTSKMSIWTSGRTSSSYRHDEKNIVQ   RICHDLLLDKRTVTTALAKAGEDGRAUA   QUENNFTKNIV   RICHDLLLDKRTVTTALAKAGEDGRAUA   QUENNFTKNIV   RICHDLLLDKRTVTTALAKAGEDGRAUA   QUENNFTKNIV   SKIPTIPSTYN   SKIPTIPSTY   SKIPTIPST			İ				V*QRGDGKNPGVTHLNRPVGTX_
1201   2551   A   9549   591   2   SSVVEFRGPRSSLPPLDSTFPCGSSPNVTGGG GSCPSGE*1 VSPGSEQRKYSNSNVIMETSQ YHVQHLATFINDKSEAITSVDDAIRKLVQLSS KEKIWTQEMLLQVNDQSLRLLDIESQELEIDF PLFTVQRSQTVLNQLRYFSVLLLVQDGSQEK GSCPSGE*1 VSPGSEQRKYSNSNVIMETSQ YHVQHLATFINDKSEAITSVDDAIRKLVQLSS KEKIWTQEMLLQVNDQSLRLLDIESQELEIDF PLFTVQRSQTVLNQLRYFSVLLLVQDGSQEK PDVHFFHCDEVEABLVHEYMESALTDCRLGK AMRP	1200	2550	A	9548	186	1	VNAEKEF*KIQHYFMTKSQNKLHIEHTYLKPI
1202   2552   A   9552   428   1			1				KAIYDKWTSDIMLNLQKL*AFFLRVIVRQI
1202   2552   A   9552   428   1	1201	2551	Α	9549	591	2	
						ł	GSCPSGE*LVSPGSEQRRRYSNSNVIMHE1SQ
PLPTYQRSGTVLNQLRYFSVLLLVCQDSEQSK   PDVHFFHCDEVEAELVHEYMESALTDCRLGK   AMRP			İ				YHVQHLATFIMDKSEAITSVDDAIKKLVQLSS
PDVHFFHCDEVEAELVHEYMESALTDCRLGK   AMRP			1				KEKIWIQEMLLQVNDQSLKLLDIESQEELEDE
AMRP			1				PLPI VQKSQI VLNQLK I PSVLLLVCQDSEQSK
1202   2552			ļ			ļ	
LDCERPPQGPLPSLPELAKTSYSDLTGLATED		1				ļ. <u>.</u>	
**WGPGMDAPATTIASSKTRVTLMVAGRPVFF   Li*YRATYSALPNFSGPTQSSQVSVVGIDGQV   SKPRATPH-FCSLHTF   Li*YRATYSALPNFSGPTQSSQVSVVGIDGQV   SKPRATPH-FCSLHTF   SKPRATPH-FCSLHTF   RRKFFRKQKQ*RYREGKQYRQRDKMKEWG   EKEKRRREKGERERKMRHRERKGESQRD   TMENWRVERLTEKER     1204   2554   A   9573   83   415   EDKRLRLVDGDSRC-GGRV*IYHDGWGTICD   GWDLSDAHVVCQKLGCGVAFNATVSAHFC   EGSGPIWLDDLNCTGTESHLWQCPSRGWGQ   HDCRIKEDAGVICSETTALR     1205   2555   A   9577   64   424   ARGSCPTRFRTANGRMGETTDAPQMLVTFK   DVAVTFFREWRQLVLVHRTLYR*GMLETC   GLLDTLRHNVPQPDVVHLLYHGTQLLIVKRE   VSHSPCAGDMRELFTREATLTHPYNNGA     1206   2556   A   9584   38   476   TLGAVLFSEVSKESSTSHSGGQLGRQNRHPKL   SNFITTSSSPRLKF*TASSQRNLGUILNMFLTAV   NPQPLSTPSWQIETKYSTKVLTGNWMEERK   GLPYKHLITHHQEPPHRYLISTYDDHYNRHG   YNPGLSPPLRYWNGQKLLWL     1207   2557   A   9586   2   412   LRSSPAALLRALCITTVTGTALALRSRVATTN   PDGCRNVLRPKYYRLCDKAESWGIALETYPT   GVAVTSWAINLTVLTLVCKQQDYNRQKLP   THILCLL*EKGIFGLTFAFIGLDGSTGPTRFFL   FGILFSICFS     1208   2558   A   9597   122   3   IKNYWPGMVAHACNPSPLGGRGRWIA*AQK   FADAWADAW   KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK   GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIVQ   RIRCHDLLDKRKTVTALKAGEDRAILLGLAM   MYCSIMM*FLLGITLLRSYMQSVWTRESQCT   LINASITETFNC     1210   2560   A   9618   384   2   SLIPDMLMLAEQQQKQKWAVNTQNTAWSNA   DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI   KVQVKNNDLGLQATINNEANWIAHQDDFNW   LLAELNTCQRQETADS***WSPKNSHVGKDS	1202	2552	Α	9552	428	1	L DODD DOODL BELDEL AKTEVEDL TOLLATED
1203   2553   A   9568   517   738   RRKFERKQKQ*RYREGKQYRQRDKMKEWG   EKEKRREKGEREERKMRHRERKGESQRD   TMENWRYERLITEKER     1204   2554   A   9573   83   415   EDKRIRLYDGDSRCAGRV*IYHDGFWGTICD   DGWDLSDAHVVCQKLGCGVAFNATVSAHFC   EGSGPIWLDDLNCTGESHLWQCPSRGWQ   HDCRHKEDAGVICSEFTALR     1205   2555   A   9577   64   424   ARGSCPTRPRTANGRMGETKDAPQMLVTFK   DVAVTFFREEWRQLVLVHRTLYR*GMLETC   GLIDTLRHNVPQPDVVHLLYHGTQLLIVKRE   VSHSPCAGDMRELFTREATLTPHPYNNGA     1206   2556   A   9584   38   476   TLGAVLFSEVSKESSTSHSGGQLGRQNRHPKL   SNFITPSSPRLKF*TASSQRNLGQILNMFLTAV   NPQFLSTPSWQIETKYSTKVLTGNWMEERRK   GLPYKHLITHHQEPPHRYLISTYDDHYNRHG   YNPGLPPLRTWNGQKLLWL     1207   2557   A   9586   2   412   LRSSPAALLRALCITTVTGTALALRSRVATTN   PDGCRNVLRFKYYRLCDKAESWGIALETYTO   GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP   THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFL   FGILFSICFS     1208   2558   A   9597   122   3   IKNYWPGMVAHACNPSPLGGRGRWIA*AQK   FADAWADAW   KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK   GLPYKHTVALTLVCKGQDYNRRQKLP   THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFL   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   FGILFSICFS   F			1				
SKPRATPPLFCSLHTF							
1203							
EKEKRREKGEREERKMRHRERKGESGQRD   TMENWRVERLTEKER			<del> </del>	0560	617	720	DDVEEDVOKO*RVREGKOVRORDKMKEWG
TMENWRVERLTEKER	1203	2553	A	9568	317	/38	EVEK PREK GEREER KMRHRERK GESGORD
1204							
DGWDLSDAHVVCQKLGGGVAFNATVSAHFG			<del> </del>	0677	02	415	
EGSGPIWLDDLNCTGTESHLWQCPSRGWGQ   HDCRHKEDAGVICSEFTALR	1204	2554	A	95/3	83	413	DGWDI SDAHVVCOKI GCGVAFNATVSAHFG
HDCRHKEDAGVICSEFTALR			1	ł	1		EGSGPIWI DDI NCTGTESHLWOCPSRGWGO
1205   2555   A   9577   64   424   ARGSCPTRPRTANGRMGETKDAPQMLVTFK DVAVTFFREEWRQLVLVHRTLYR*GMLETC GLLDTLRHNVPQPDVVHLLYHGTQLLIVKRE VSHSPCAGDMRELFTREATLTPHPYNNGA     1206   2556   A   9584   38   476   TLGAVLFSEVSKESSTSHSGQQLGRQNRHPKL SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV NPQPLSTPSWQIETKYSTKVLTGNWMEERRK GLPYKHLITHHQEPPHRYLISTYDDHYNRHG YNPGLPFLRTWNGQKLLWL     1207   2557   A   9586   2   412   LRSSPAALLRALCITTVTGTALALRSRVATIN PDGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFL FGILFSICFS     1208   2558   A   9597   122   3   IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW     1209   2559   A   9611   148   558   KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC     1210   2560   A   9618   384   2   SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS					1		HDCRHKEDAGVICSEFTALR
DVAVTFFREEWRQLVLVHRTLYR*GMLETC GLLDTLRHNVPQPDVVHLLYHGTQLLIVKRE VSHSPCAGDMRELFTREATLTPHPYNNGA 1206 2556 A 9584 38 476 TLGAVLFSEVSKESSTSHSGQLGRQNRHPKL SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV NPQPLSTPSWQIETKYSTKVLTGNWMEERRK GLPYKHLITHHQEPPHRYLISTYDDHYNRHG YNPGLPPLRTWNGQKLLWL  1207 2557 A 9586 2 412 LRSSPAALLRALCITTVTGTALALRSRVATIN PDGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS  1208 2558 A 9597 122 3 IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1005	2555	+	0577	61	424	ARGSCPTRPRTANGRMGETKDAPOMLVTFK
Coldtentitypopdvvhllyhgtqllivkre vshspcagdmrelftreatltphyynga	1205	2555	A	9311	04	724	DVAVTFFREEWROLVLVHRTLYR*GMLETC
VSHSPCAGDMRELFTREATLTPHPYNNGA			1	ŀ			GLLDTLRHNVPOPDVVHLLYHGTOLLIVKRE
1206   2556   A   9584   38   476   TLGAVLFSEVSKESSTSHSGGQLGRQNRHPKL SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV NPQPLSTPSWQIETKYSTKVLTGNWMEERRK GLPYKHLITHHQEPPHRYLISTYDDHYNRHG YNPGLPPLRTWNGQKLLWL   LRSSPAALLRALCITTVTGTALALRSRVATIN PDGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS   X   9597   122   3   IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW   KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC   SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS			1		1		VSHSPCAGDMRELFTREATLTPHPYNNGA
SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV NPQPLSTPSWQIETKYSTKVLTGNWMEERRK GLPYKHLITHHQEPPHRYLISTYDDHYNRHG YNPGLPPLRTWNGQKLLWL  1207 2557 A 9586 2 412 LRSSPAALLRALCITTVTGTALALRSRVATTN PGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS  1208 2558 A 9597 122 3 IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SIHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1204	2556	1_	0584	38	476	TLGAVLFSEVSKESSTSHSGGOLGRONRHPKL
NPQPLSTPSWQIETKYSTKVLTGNWMEERRK GLPYKHLITHHQEPPHRYLISTYDDHYNRHG YNPGLPPLRTWNGQKLLWL  1207 2557 A 9586 2 412 LRSSPAALLRALCITTVTGTALALRSRVATIN PDGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS  1208 2558 A 9597 122 3 IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1200	2330	1 ^	7504	30	1 ""	SNFITPSSPRLKP*TASSORNLGOILNMFLTAV
Colpykhlithhqepphrylistyddhynrhg		1			1		NPOPLSTPSWQIETKYSTKVLTGNWMEERRK
YNPGLPPLRTWNGQKLLWL		1	1	1	1	1	GLPYKHLITHHQEPPHRYLISTYDDHYNRHG
1207 2557 A 9586 2 412 LRSSPAALLRALCITTVTGTALALRSRVATTN PDGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS  1208 2558 A 9597 122 3 IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS		1					
PDGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS  1208 2558 A 9597 122 3 IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1207	2557	- A	9586	12	412	LRSSPAALLRALCITTVTGTALALRSRVATTN
GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS  1208 2558 A 9597 122 3 IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1407	2331	1^	7,000	1	'	PDGCRNVLRPKYYRLCDKAESWGIALETVPT
THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS  1208 2558 A 9597 122 3 IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS			1	1	1		GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP
FGILFSICFS			1				THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL
1208 2558 A 9597 122 3 IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS		]					FGILFSICFS
FADAWADAW  1209 2559 A 9611 148 558 KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1200	2550	1_	9507	122	3	
1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1208	2338	1^	1 227/	122	٦	FADAWADAW
GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1200	2550	+	0611	148	558	KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK
RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1409	2339	\ \frac{1}{2}	1 3011	170	336	GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ
MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC  1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS		1					RIRDHDLLDKRKTVTALKAGEDRAILLGLAM
1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS							MVCSIMM*FLLGITLLRSYMOSVWTRESOCT
1210 2560 A 9618 384 2 SLHDMLMLAEQQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS			}	ł	1		LLNASITETFNC
DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1210	2660	+	0610	384	12	SI HDMLMI AEOOOKOKWAVNTONTAWSNA
KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS	1410	2560	A	9019	304	1	DSKFGORILEKMEWSKGRGLGVOEOGGPDDI
LLAELNTCQRQETADS***WSPKNSHVGKDS							KVOVKNNDLGLOATINNEANWIAHODDFNW
		1	1		1	1	LLAFLNTCOROFTADS***WSPKNSHVGKDS
t tiri san							GELSAK
	10=	<del> </del>	<del> </del>	1000	1216	610	OKHPGGGQLGRSPQEDSRFHNKASSGVSRVR

	0FA TD	1/-4	CEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq- uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	1	}	7.1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l		peptide		/=possible nucleotide deletion, \=possible
	1	}		sequence		nucleotide insertion
		<del> </del>	<del>                                     </del>	<u> </u>		LGRAWWLTPVIPTLWEAKAGGSPE*D*AGRG
				1		GSRL*SQHFGRPRRVDHLRSAVQDQPGQHGE
		]		1		TPSLLKIQKIN*VWGRRL*SSYSEAEAGESL
1212	2562	A	9623	297	344	QFPVDGDYQKIEKITQLFQAQNLSLCLAMTR
1212	2002	1				TREL*KGGGKGRHE*AVVPFLKKGGYGVKAP
		}				AILNTSNCT*CF*ETKMLSDDPKACVFEVSSA
		ļ				DL*NTSFGVIR
1213	2563	A	9624	2	356	AELSLASTACGRNTSGDSLPDYDRAPISSPLA
	2000					TSGTILSAISCLWDLPTPVLRVGLSCQPSMSSQ
		1	1	1		IPRMYSTDVEAAVNSLEDLYLQAYYAYLCVG
		}			l	LYFHRDDMALEGVSRFL*ELAE
1214	2564	A	9634	776	912	SLSRWVRAKL*VPYNQENCLNPRGGGCSEPR
		ł				SHYCTPAWATEKDS
1215	2565	A	9636	220	426	KPGNFAVSSEY*DITSGQLKTAVRG*IEMTST
		-				EENFGEKLHDIGFGNGFLDKT*KAQATKAKI
			*			DK CFLEDGCTQAS*AEEAAVSPSMAEEEQGSTSC
1216	2566	A	9637	391	76	RERRSIRFKMKNHSPDDTIKENVTISNIRTRKI
						NHLPETERNLLEHGLMYIRLNAAFCSLVAHS
1		1				
}				<u> </u>		LFGFILKAT LHCKMGALETQTHPCSQNMLRSLQKCCCKV
1217	2567	A	9655	2008	2432	EEHHLQPVQVLQTLLHSATAGTGCRRPARPP
		1				PAPPTPTPWRSRQSGKQSERAS*LKGRGRYGL
1					1	GALGGRGGRALGGSRWPPPLPGETLFSGCKH
	ļ	ì				RRRRGSDAAPGEEAGT
L			0650	3	405	HASARALLSPNLSPNNKMAISGGPVLGFFILA
1218	2568	A	9658	3	403	VLMSAOEPWAIKEEHVIIQAEFYLNPDQSGEF
		1		}		MLDFEGEDTFHGDMAKKETVWRLE*LARLD
1	1	1		İ	1	NFEAQRALANIAADQAALEIMDMGSDYTLIP
ì		}				NVPPKVTVL
1219	2569	HA-	9662	3	284	PDWTEKRKMQDTGSILPLHWFGFGYAALVA
1219	2309	1	7002	-		YGGIIGYVKAGSVPSLAAGLLFGSLSGLGAYQ
1		1			İ	LSQDPRNVWVFLATSGTLAGIMGMRFYHSG
		-				KL
1220	2570	A	9669	200	699	LLLTGYIQTLQNQQLSGNQQEMQAVDNLTSA
1220	2370	1	1	į		PGNTSLCTRDYKITQVLFPLLYTVLFFVGLITN
	}	1		ļ	į.	GLAMRIFFQIRSKSNFIIFLKNTVISDLLMILTF
Í			İ		1	PFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYI
1	1	}				SISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL
		1				KERDSSTFSAAMTIMQGMEQAMPGAGPGVP
1221	2571	A	9676	164	562	QLGNMAVIHSHLWKGLQEKFLKGEPKVLGV
						VQILTALMSLSMGITMMCMASNTYGSNPISV
1		1		1		YIGYTIWGSVMFIISGSLSIAAGIRTTKGLVRG
	1		1	1		1
1					+	SLGMNITSS VAKMVKCCSAIGCASRCLPNSKLKGLTFHVF
1222	2572	A	9688	43	412	PTDENIKRKWVLAMKRLDVNAAGIWEPKKG
1		1				DVLCSRHFKKTDFDRSAPNIKLKPGVIPSIFDS
		- 1				PYHLQGKREKLHCRKNFTLKTVPATNYNH
				1200		RTSMGILYSEPICQAAYQNDFGQVWRWVKE
1223	2573	A	9696	308	564	DSSYANVQDGFNGDTPLICACRRGHVRIVSFL
[						LKKECLCQPQKPERENLLALCCE
					(22	DAWASGGELGSLFDHHVQRAVCDTRAKYRE
1224	2574	A	9700	3	632	GRRPRAVKVYTINLESQYLLIQGVPAVGVMK
			}			ELVERFALYGAIEQYNALDEYPAEDFTEVYLI
	l	i	Í			KFMNLQSARTAKRKMDEQSFFGGLLHVCYA
				1	1	PEFETVEETRKKLQMRKAYVVKTTENKDHY
1		1	4	I	1	
1	1					VTKKKLVTEHKDTEDFRODFHSEMSGFCKA
						VTKKKLVTEHKDTEDFRQDFHSEMSGFCKA ALNTSAGNSNPYLPYSCELPLCYFSSK

			- 656	D., 41, 4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod		nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ŀ	in USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ì	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	Ì		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide	Joquani	/=possible nucleotide deletion, \=possible
				sequence	]	nucleotide insertion
1225	2575	A	9710	1	163	RSGCVLRMTEWETGAPAVAETPDIKLFGKWS
1223	23/3	\	77.0	•	1	TDDVHINDISLQDYIAGVRLILL
1226	2576	A	9713	82	492	QGLPSFLPAFGPSGSWLGPAPTLGSSCNTVDT
1220	2370	Α	177.5	02		ICHGYSEIRPLFYLSFCDLLLGLCWLTETLLYG
i .		ĺ	1		1	ASVANKDIICYNLQAVGQIFYISSFLYTVNYI
Ì					· ·	WYLYTELRMKHTQSGQSTSPLVIDYTCRVCQ
		1		ł		MAFVFSSLI
1227	2577	A	9720	3	416	GKWKRTQVPLLGEECADMDLARKEFLRGNG
1227	2311	1	7			LAAGKMNISIDLDTNYAELVLNVGRVTLGEN
	1	Ţ	1			NRKKMKDCQLRKQQNENVSRAVCALLNSGG
	,	1			1	GVIKAEVENKGYSYKKDGIGLDLENSFSNML
						PFVPNFLDFMQNGNYF
1228	2578	A	9723	278	411	EASSSNTVASNVADKTDPHSMNSRVFIGNLN
						TLVLQKSDVEAVF
1229	2579	A	9725	121	902	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDY
	1					GGSGGPYSKQYAGYDYSQQGRFVPPDMMQP
	ļ	1	}		1	QQPYTGQIYQPTQAYTPASPQPFYGNNFEDEP
i	1	1				PLLEELGINFDHIWQKTLTVLHPLKVADGSIM NETDLAGPMVFCLAFGATLLLAGKIQFGYVY
1	1	1		1		GISAIGCLGMFCLLNLMSMTGVSFGCVASVL
	İ			1		GYCLLPMILLSSFAVIFSLQGMVGILLTAGIIG
		1			ì	WCSFSASKIFISALAMEGQQLLVAYPCALLYG
						VFALISVF
	<u> </u>				247	TFVLNMNTPKEEFQDWPIVRIAAHLPDLIVYG
1230	2580	A	9739	11	247	HFSPERPFMDYFDGVLMFVDISGKCKRDVCL
l		1		l i		MWMSNRLAWEFTCRA
			9744	37	1100	TPLFDFWPGFVLSWLQPLSASLRARRAASGPP
1231	2581	Α	9/44	37	1100	ACRIMPTTVDDVLEHGGEFHFFQKQMFFLLA
1		1	Ì			LLSATFAPIYVGIVFLGFTPDHRCRSPGVAELS
				1 .	ļ	LRCGWSPAEELNYTVPGPGPAGEASPRQCRR
}	1					YEVDWNOSTFDCVDPLASLDTNRSRLPLGPC
						RDGWVYETPGSSIVTEFNLVCANSWMLDLFQ
	1				}	SSVNVGFFIGSMSIGYLADRFGRKLCLLTTVLI
					1	NAAAGVLMAISPTYTWMLIFRLIQGLVSKAG
	-	1	٠.	į		WLIGYILITEFVGRRYRRTVGIFYQVAYTVGL
	1	1	ł			LVLAGVAYALPHWRWLQFTVALPNFFFLLY
}	1	]	- }		1	YWCIPESPRWLISQNKNAEAMRIIKHIAKKNG
			}	1		KSLPASL
1232	2582	A	9753	164	517	PGPGMQGPPPITPTSWSLPPWRAYVAAAVLC
.232				1		YINLLNYMNWFIIAGVLLDIQEVFQISDNHAG
		į.				LLQTVFVSCLLLSAPVFGYLGDRHSRKATMS
						FGILLWSGAGLSSSFISPRYSWLF
1233	2583	A	9757	25	419	LPAPWTERVRKSEGLVGTCLGDPMASPRTVT
1233						IVALSVALGLFFVFMGTIKLTPRLSKDAYSEM
					1	KRAYKSYVRALPLIKKMGINSILLRKSIGALE
1	1	- 1		1		VACGIVMTLVPGRPKDVANFFLLLLVLAVLF
					1	FHQLV
1234	2584	A	9765	71	456	RLELDWGFSLHFLPVAYLCPLSSGFEMNVQP
						CSRCGYGVYPAEKISCIDQIWHKACFHCEVC
	1	1		1	İ	KMMLSVNNFVSHQKKPYCHAHNPKNNTFTS
						VYHTPLNLNVRTFPEAISGIHDQEDGEQCKSV
		1				FHWD
1235	2585	A	9767	52	559	IRSGAMSVDKAELCGSLLTWLQTFHVPSPCA
1						SPQDLSSGLAVAYVLNQIDPSWFNEAWLQGI
					1	SEDPGPNWKLKVTSGLLIRGQTGEEMTRDGP
				1		ARHMSWVMGRKRDRCLVINHLFIHSSMEYSP
						CARPGHSARNNTDKNLPHTAILLVTSNTYTTI
	ļ	1				KINFQAGRSGSCL FRGEALTVRFLTKRFIGEYASNFESIYKKHLC
1236	2586	A	9770	352	608	FRUEALI VKFLIKKFIGETASNFESI TAKHLC

			•			/A Alasia C Custaina
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ĺ	09/496	correspondi	to last amino	O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
		<b> </b>	1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
				residue of	sequence	/=possible nucleotide deletion, \=possible
	ļ			peptide	}	nucleotide insertion
			L	sequence		LERKQLNLEIYDPCSQTQKAKFSLTSELHWA
					1	DGFVIVYDISDRSSFAFAKALI
			ļ	1266	515	NILAHYFPFPRLFLLRDSQSNPKAFALTLCHH
1237	2587	Α	9793	266	313	QKIKNFQILPVSIDALTPPLVVCFLVSFLTHFS
	İ	1			-	RYKPTRPVCITQFQGCS
		<u> </u>	10000	537	967	ELGAGRSDREAMEAAVKEEISVEDEAVDKNI
1238	2588	Α	9802	537	907	FRDCNKIAFYRRQKQWLSKKSTYRALLDSVT
	ĺ	1		ì	ļ	TDEDSTRFQINEASKVPLLAEIYGIEGNIFRLK
		l				INEETPLKPRFEVPDVLTSKPSTVRLISCSGDT
		1				GSLILADGKGDLKC
		<del> </del>	0005	105	540	VPGDPAMVRAGAVGAHLPASGLDIFGDLKK
1239	2589	Α	9805	103	340	MNKRQLYYQVLNFAMIVSSALMIWKGLIVLT
		1				GSESPIVVVLSGSMEPAFHRGDLLFLTNFRED
ļ		1	1			PIRAGEIVVFKVEGRDIPIVHRVIKVHEKDNG
1	}	1		1	l	DIKFLTKGDNNEGDDRGSYK
		<del>   </del>	9819	3	305	TDGRDPLPCAARRRGGGGECCGAGWVAEWS
1240	2590	Α	9019	3		POPLDPAMILWMOGFVLEAVACQDNDDYLR
		1				YGILFEDLDCNGDGVVDIIELQEGLRNWSSAF
	ì				i	DPNSEEHG
1041	2591	A	9834	841	1209	SPARGKSNRTDVMITAPKNKKMTENLAAPEA
1241	2391	A	7634	041	.207	LDSSTHSSSTATOSRAKMNTPAPTPSTVPAIPR
						GGSGGPPPCAPHDRVSSVLQCDTQAMDHKTE
ļ		1	1	1	İ	SSHSVVEFLFKRTKTPSPFHPAVRENRN
1242	2592	A	9843	3	589	TISCGPATEPPASLLSSASSDDFCKEKTEDRYS
1242	2392	^	7043	1		LGSSLDSGMRTPLCRICFQGPEQGELLSPCRC
1					Ì	DGSVKCTHQPCLIKWISERGCWSCELCYYKY
	1					HVIAISTKNPLQWQAISLTVIEKVQVAAAILGS
	1	ĺ	1	1		LFLIASISWLIWSTFSPSARWQRQDLLFQICYG
1		İ	ļ			MYGFMDVMIVAVDSEDMVQAAKEVGKRWS
	-					DIPP
1243	2593	A	9846	198	411	WRISHHAGKMPVMKGLLAPQNTFLDTIATRF
12.5	2277			1	}	DGTHSNFILANAQVAKGFPIVYCSDGFCELAG
		}				FARTEVMQ
1244	2594	A	9848	116	650	PICGFLYLCSAMASESSPLLAYRLLGEEGVAL
				}		PANGAGGPGGASARKLSTFLGVVVPTVLSMF
ľ	1	1				SIVVFLRIGFVVGHAGLLQALAMLLVAYFILA
1		1				LTVLSVCAIATNGAVQGGGAYCILQHRWTG VWPVLPAREVMISRTLGPEVGGSIGLMFYLA
		1			1	NVCGCAVSLLGLVESVLDVFGA_
		Ł			1.00	KSKCRFPEGLSEGFGPMRKEALSSGSVQEAE
1245	2595	Α	9849	573	1620	AMLDEPQEQAEGSLTVYVISEHSSLLPQDMM
						SYIGPKRTAVVRGIMHREAFNIIGRRIVQVAQ
		1				AMSLTEDVLAAALADHLPEDKWSAEKRRPL
				}	1	KSSLGYEITFSLLNPDPKSHDVYWDIEGAVRR
		1				YVQPFLNALGAAGNFSVDSQILYYAMLGVNP
1						RFDSASSSYYLDMHSLPHVINPVESRLGSSAA
				1	1	SLYPVLNFLLYVPELAHSPLYIQDKDGAPVAT
	1	1	1	1		NAFHSPRWGGIMVYNVDSKTYNASVLPVRV
		}	}	1		EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL
1						LSGPTSEGLMTWELDRLLWARSVENLATATT
	}	1				TLTSLA
				<del></del>	100	PPQLGAQRVREPRHPDVRAPLRVTSPGLRSRS
1246	2596	A	9850	114	464	ARSLGRRPRIAMVTVGNYCEAEGPVGPAWM
		ì				QDGLSPCFFFTLVPSTRMALGTLALVLALPCK
						RRERPAGADSLSWGAGPRISSYV
						FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF
	0.505	A	9851	2	327	LAKWAWANIKOCOWACCIMIA PENTIKATON
1247	2597	1				
1247	2597					HQFPTDTIQRSKWIRAVNRVDPRSKKIWIPGP
1247	2597					GAILCSKHFQESDFESYGIRRKLKKGAVPSVS LYKVFKYSSRCTS

	· · · · · · · · · · · · · · · · · · ·		7-000		Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ł	in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	1	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence		ì	914	ng to first		T=Threonine, V=Valine, W=Tryptophan,
	1	ì		amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		ŀ	1	residue of	sequence	Y=1 yrosine, X=Unknown, '-stop codon,
	ĺ	ļ	1	peptide	1	/=possible nucleotide deletion, \=possible
	ļ .	1		sequence		nucleotide insertion
1248	2598	Α	9853	58	444	RVDDFVYSKGGKDAGGADVSLACRRQSIPEE
		1	İ	1	1	FRGITVVELIKKEGSTLGLTISGGTDKDGKPR
	1	-				VSNLRPGGLAARSDLLNIGDYIRSVNGIHLTR
	Į.	Į.		ļ		LRHDEIJTLLKNVGERVVLEVEYELPPPGGCP
	1	1	1			WT
1249	2599	A	9856	2	1265	LPPPRPSRHRRGRAGTRASAAAAAGPTVSAV
1247	12377		7000	-		RAPVRGQDSGAGTPQGRLAGRGAHLSRVGA
			1			SGSGVAAGPAARHAPRRRCADAGEAVGASC
	ì			1		GRCAVALLSGVCTLVSTHVCVGSGCPGAAGT
						PMGAGDAGASAESAVTTAPQEPPARPLQAGS
	i					GAGPAPGRAMRSTTLLALLALVLLYLVSGAL
	ì	1	{	1	1	VFRALEQPHEQQAQRELGEVREKFLRAHPCV
		1				SDQELGLLIKEVADALGGGADPETNSTSNSSH
	1			1		SAWDLGSAFFFSGTIITTIGGGGDWHVGGGK
		ł	-			ELPHGGRCRETEGSQVAPRLPASPLCPGYGN
	-					VALRTDAGRLFCIFYALVGIPLFGILLAGVGD
	I.		l			RLGSSLRHGIGHIEAIFLKWHVPPELVRVLSA
}		1	1	1	1	MLFLLIGCLLFVLTPTFVFCYMEDWSKLEAIY
		1			ì	FVIVTLTTVGFGDYVA
	0.00	<del>                                     </del>	9873	2	652	FVVPSPCGGIPGRAPNGASRPTMGNSASRNDF
1250	2600	Α	9873	4	032	EWVYTDQPHTQRRKEILAKYPAIKALMRPDP
1	1	1	ł		i	RLKWAVLVLVLVQMLACWLVRGLAWRWLL
		1			1	FWAYAFGGCVNHSLTLAIHDISHNAAFGTGR
l		ŀ	1		Ĭ	AARNRWLAVFANLPEGVPYAASFKKYHVDH
					ļ	HRYLGGDGLDVDVPTRLEGWFFCTPARKLL
l	ł	1		ł	1	WLVLQPFFYSLRPLCVHPKAVTRMEVLNTLV
		1				
				1.50	1000	QLA PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSR
1251	2601	A	9875	150	1209	LESYRPDTDLSREDTGCNLQHISDRENIDDLN
1	1	1			1	MEFNPSDHPRASTIFLSKSQTDVREKRKSLFIN
İ	1	1				HHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTI
ļ	1	]				KCVALAIYYHIKNRDPDGRMLLDIFDENLHPL
	ŀ	1	<b>.</b>			KCVALAI I THIKNKUPDUKWILLDIPDENLIB L
	i	1	Į.			SKSEVPPDYDKHNPEQKQIYRFVRTLFSAAQL
1	1	1	1			TAECAIVTLYYLERLLTYAEIDICPANWKRIV
	1	1	1		1	LGAILLASKVWDDQAVWNVDYCQILKDITVE
]	1	1	1		1	DMNELERQFLELLQFNINVPSSVYAKYYFDL
1	1			ļ	i	RSLAEANNLSFPLEPLSRERAHKLEAISRLCED
	}				<u> </u>	KYKDLRRSARKRSASADNLTLPRWSPAIIS
1252	2602	A	9879	6	376	KRPDSRPPAQYRAGPTRPRTRGCELLYWKAT
						KAVGIKMGSLSTANVEFCLDVFKELNSNNIG
					1	DNIFFSSLSLLYALSMVLLGARGETEEQLEKV
		1	1			WNSSEVCSEPRSLSCSRSGSAKLILSLYQ
1253	2603	A	9880	180	388	KEQAELLYGLYCQCDLTLSSHPSSVPAMSSC
		1				NFTHATFVLIGIPGLEKAHFWVGFPLLSMYVA
1		1				AMFGNC
1254	2604	A	9881	19	494	VISFQIITDTIMDSSTAHSPVFLVFPPEITASEYE
1237	2004	1.,	'"	1		STELSATIFSTQSPLQKLFARKMKILGTIQILF
1				1		GIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWG
1		1				SVLFINSGAFLIAVKRKTTETLIILSRIMNFLSA
}		1		1		LGAIAGULLTFEFHPRSKLHL
1066	2005		9896	72	386	RPGREORDCFOAPPLGLGGRQTDMMHHPLT
1255	2605	A	9090	1/2	1 300	GATCVGLPNVGMCPQLSGALTFMYLQQGNQ
1		Ì		İ		EATVAPDTMAQPYASAQFAPPQNGIPGEYTA
}	}	1	}			PHPHPAPEYTGQTT
				<u> </u>		SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG
1256	2606	Α	9902	95	399	PROPERTY FOR CANODALA RECEIVED CALA
Í		1				DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH
I .		1	1	1	Ì	T DOTA DENIMIKE CUPSRIEKKET DERKYSLILYH
1	Ī					
1257			9905	374	459	KEELE EHLKSTPNRLGVVAHTCNPSTLGGRGGW

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				Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	beginning	nucleotide	D=Aspartic Acid E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:		location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	corresponding	1=1soleucine K=Lvsine L=Leucine,
eotide	seq-		USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	į	09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
	1			amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	(	residue of	sequence.	/=possible nucleotide deletion, \=possible
	1	ì	\	peptide		/=possible nucleotide deletion, \ possible
	ļ	i	1	sequence	·	nucleotide insertion AGPGVPAVGGRWASGPGLGGRTLCSGPPDH
1258	2608	A	9911	364	1974	AGPGVPAVGGRWASGPGLOGRILCSGFIDII
1230	2000	1.,	1 ,,,,,,			QRRGPSCGASGDPQCVGSPHPQRARPLLARP
	l .		l	1		GARLLPGHLPSPRPPRLPTGQPPAAAFRGPVR
	1	1	ţ	1	}	POGGGHIHPLPTPGGRPCFAVSEGSGSALLLS
	ì	1	1	ì	1	YLGECGSSSYVTGAACISPVLRCREWFEAGLP
i	]		1	1	ì	WPYERGFLLHQKIALSRYATALEDTVDTSRL
			Į.			FRORST REFEEALFCHTKSFPISWDAY WOKND
	}			1		DI DOVDEA AVPVLCICSADDPVCGPPDHILII
	ł	}	1			FI FHSNPYFFLLLSRHGGHCGFLRQEPLPAWS
	1	)	]	1		LIEVIT FOFR AT TEFFRTEERIKGLSKHRASPLU
	1		ì		l .	GRRRGGAL ORREVSSSSNLEEIFNWKRSYTKL
		}	l	j	}	MAAAAGAAAAPGSREPODRPECGAGHPGPR
ĺ	1		1	1	}	YYRHPERWLLRPEAFLGPLRTRAPSAEDSQR
	1	1	1	1	1	ERPAARSGPEMRVRYPVVAAVLAPYLALSQD
	1	1				PMYKSSASGQGASGSYNHVREEMLIKAGGA
	}	}	1			MSRRVVRQSKFRHVFGQAAKADQAYEDIRV
l	1		ł	1		SKVTWDSSFCAVNPKFLAIIVEAGGGGAFIVL
1	ŀ	,	,	1		
		l l	ì		1	PLAK GCFKFIGESTCCWIFPSSVTTQCVVAKAPRAA
1259	2609	A	9919	693	935	GCFKFIGESICCWIFPSSVIIQCVARBIIADII
1239	2005					TLSKAERLRSQPGPEQGGSSYRPRTPTAAAIL
	1	1				PPRPGRSHRKRKLVSTK
1000	2610	A	9921	455	1082	QRSCLCSAIEKDGGDVKALYRRSQALEKLGR
1260	2010	Α	,,,,,	1.55		LDQAVLDLQRCVSLEPKNKVFQEALRNIGGQ
1	}		l			IQEKVRYMSSTDAKVEQMFQILLDPEEKGTE
	1	1	1		1	KKQKASQNLVVLAREDAGAEKIFRSNGVQLL
	1		İ		1	ORI I DMGETDLMLAALRTLVGICSEHQSKI V
1	1					ATLSILGTRRVVSILGVESQAVSLAACHLLQV
	1	1	l l			MEDAI KEGVKKGFRGKEGALIV
				-	438	GERGAFAPGAAOAPKKKKPRPTEGGPGAGSG
1261	2611	A	9928	1	430	PCK DPVRGPTI LHOPKPPKDEFLSSLESYEIAF
1	Ì		ļ			PTPVDHNGALLAFSPPPPORQRRGTGATAES
	ľ	1	1	[		RLFYKEASPSTHFLLNLTRSSRLLAGHVSVEY
1	ŀ	- 1	ì	1	1	WTREGLAWORADRPHCLYA
	1				135	AAEMGRAGAAAVIPGLALLWAVGLGGPPPA
1262	2612	Α	9931	168	435	PPRLPFCLQELQGRHALHTFSLERTCSYQDFL
ļ		1	1			WADEGRLLHVGAQDLATWHTLSPLGLW
		1		1		RMSATSVDQRPKGQGNKVSVQNGSIHQKDG
1263	2613	A	9938	247	488	CNDDDFEPYLRSPDNQSNSYPPMSDPYMPGY
1.203				1		CUDDILER I PROLINGS 11 1 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 11 MPD 1
1		1		l	1	YAPSIGFPYSLGEAAWSQL
1264	2614	A	9941	61	277	ESIGLTALGPRRRPWEHRWSDPITLKMKGWG
1204	2014	10	1			WLALLIGALLGTAWARRSQDLHCGACKAVR
	ļ	1				RRVRQFNIYDY
			9956	12	522	FVASEVSKMPVPASWPHPPGPFLLLTLLLGLT
1265	2615	Α	7770	1 -		EVAGEEELQMIQPEKLLLVTVGKTATLHCTV
		1		1	1	TO I PUGPVI WERGVGPGRELLYNUKEGHEP
l	[		1	l		RVTTVSDLTKRNNMDFSIRISSITPADVGTYY
-	1			- [		CVKFRKGSPDHVEFKSGAGTELSVRGEYSVG
1		1	(	{		EL SOVWWWI SSHPFMN
		_L_			797	PKNNACHLLFTAVCQPRCKHGECIGPNKCKC
1266	2616	A	10002	243	387	HPGYAGKTCNOGRKTV
		J				LPAPASTWSVARETMASSSVPPATVSAATAG
1267	2617	A	10004	36	707	PGPGFGFASKTKKKHFVQQKVKVFRAADPLV
120/	23.7	1				GVFLWGVAHSINELSQVPPPVMLLPDDFKAS
		ĺ				GVFLWGVAHSINELSQVFFFVIVILLI DDI RAS
		-				SKIKVNNHLFHRENLPSHFKFKEYCPQVFRNL
1	1	1		- 1		RDRFGIDDQDYLVSLTRNPPSESEGSDGRFLIS
1			1	1		YDRTLVIKEVSSEDIADMHSNLSNYHQVRPLS
	- 1	ı		l l	1	
					1	SPILSUSSILLTYSSAIVSNRCQLGRKLIGRENP
1268	2618	A	1000	5 2	209	SPILSLSSLLTYSSAIVSNRCQLGRKLIGRENP GEGYELFVPSNGVPAVCHMVGRRPHRAVLSP SQDELEHSLGESAAQGAAGVVLWVSWENTR

PCT/US01/03800

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Institutio,  I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	Q=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	acid residue	T=Threonine, V=Valine, W=Tryptophan,
			1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1 1	residue of	sequence	/=possible nucleotide deletion, \=possible
				peptide		nucleotide insertion
		<u> </u>		sequence		TKVSLGLA
			<u> </u>		688	FGMLKNKGHSSKKDNLAVNAVALQDHILHD
1269	2619	A	10010	245	688	LQLRNLSVADHSKTQVQKKENKSLKRDTKAI
	•					IDTGLKKTTOCPKLEDSEKEYVLDPKPPPLIL
	İ	1	1	1		AQKLGLIGPPPPPLSSDEWEKVKQRSLLQGDS
	ł		1	i		VOPCPICKEEFELRPOVFSIRG
				<u> </u>	588	RVDDFVRPLPPGLMSRSRASIHRGSIPAMSYA
1270	2620	A	10011	2	1 300	PERDVRGPSTHRTOYVHSPYDRPGWNPRFCII
		1		1		SGNOLLMLDEDEIHPLLIRDRRSESSRNKLLR
		1	1	l		RTVSVPVEGRPHGEHEYHLGRSRRKSVPGGK
	ļ	ļ	1	}	}	OVSMEGAPAAPFRPSOGFLSRRLKSSIKRTKS
		1	1	l		QPKLDRTSSFRQILPRFRSADHDRYRGWSMW
		1				DEIDA
			10012	209	363	LPAPPNLSPRLSFGFQFPGGNDNYLTITGPSHP
1271	2621	A	10013	209	303	FLSGAEVSOSCRRRGGRA
		<del></del>	10014	17	388	SAVTISWKWRSVMGIOTSPALLASLGAGLVT
1272	2622	A	10014	1'	1 500	LIGIAVGSYLVRRSRRPOVTLLDPNEKDLLR
ł	}	ı	İ	1		LIDKTLSARSPCKHIYLSTRIDGSLSIRPYTPVT
1	1	1		1		SDEDOGYVDIDIKVYLKGVHPTFPEGGKMSH
		<del></del>	10016	+1	1339	MAARTLGRGVGRLLGSLRGLSGQPARPPCGV
1273	2623	A	10010	1 *	1337	CADDD A ASGPSGSAPAVAAAAAOPGSYPALS
		1	1	1		AGAAREPAAFWGPLARDTLVWDTPYHTYW
1		1	į.		ì	DCDFSTGKIGWFLGGOLNVSVNCLDQHVKKS
<b>!</b>		1				PESVALIWERDEPGTEVRITYRELLETTCRLA
		1	1	1	· ·	NTLKRHGVHRGDRVAIYMPVSPLAVAAMLA
1	1	- {		ļ		CARIGAVHTVIFAGFSAESLAGRINDAKCKVV
				ļ		ITFNQGLRGGRVVELKKIVDEAVKHCPTVQH
	-		ì	}		VLVAHRTDNKVHMGDLDVPLEQEMAKEDP
i	ł	1	1			VCAPESMGSEDMLFMLYTSGSTGMPKGIVHT
	- }	}	Į	l l	1	QAGYLLYAALTHKLVFDHQPGDIFGCVADIG
1		- 1		1	1	WITGHSYVVYGPLCNGATSVLFESTPVYPNA
		- 1		1		GRYWETVERLKINQFYGAPTAVRLLLKYGD
-	1	]	1	1		AWVKKYDRSSLRTLGSVGEPINCEAWEWLH
1		1				RVVGDSRCTLVDTWWQT
1274	2624	A	10017	1	3750	FRPOGTPRSPASHVLTMSAPDEGRRDPPKPKG
12/4	2024	1		1		KTLGSFFGSLPGFSSARNLVANAHSSARARPA
1						ADPTGAPAAEAAQPQAQVAAHPEQTAPWTE KELQPSEKMVSGAKDLVCSKMSRAKDAVSS
1			l			GVASVVDVAKGVVQGGLDTTRSALTGTKEV
-		j	j	}		VSSGVTGAMDMAKGAVQGGLDTSKAVLTG
1		- 1	1	}		TKDTVSTGLTGAVNVAKGTVQAGVDTTKTV
			1	-	1	LTGTKDTVTTGVMGAVNLAKGTVQTGVETS
		-				LTGTKDTVTTGVMGAVNLARGTVQTGVEV KAVLTGTKDAVSTGLTGAVNVARGSIQTGV
		- 1				DTSKTVLTGTKDTVCSGVTGAMNVAKGTIQT
)	Ì		1	ŀ	İ	GVDTSKTVLTGTKDTVCSGVTGAMNVAKGT
1		- 1	1	}	1	GVDTSKTVLTGTKDTVCSGVTGAMNVA
1	1	-	1			IQTGVDTSKTVLTGTKDTVCSGVTGAMNVA KGTIQTGVDTTKTVLTGTKNTVCSGVTGAVN
	1				1	LAKEAIQGGLDTTKSMVMGTKDTMSTGLTG
		l	İ			LAKEAIQGGLDITKSMVMGTKDTMSTGETG AANVAKGAMQTGLNTTQNIATGTKDTVCSG
Ì	1					VTGAMNLARGTIQTGVDTTKIVLTGTKDTVC
1	]	1			1	SGVTGAANVAKGAVQGGLDTTKSVLTGTKD
]		1				AVSTGLTGAVNVAKGTVQTGVDTTKTVLTG
		- 1		1	1	AASIRFIRMANAWRRIAGIAADIIKIAFIA
				ļ	1	THE TOTAL PROPERTY AND THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
						TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV
						TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV
						TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV VIGTKDTMSTGLTGAANVAKGAVQTGVDTA KTVLTGTKDTVTTGLVGAVNVAKGTVQTGM
						TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV VIGTKDTMSTGLIGAANVAKGAVQTGVDTA KTVLTGTKDTVTTGLVGAVNVAKGTVQTGM DTTKTVI TGTKDTIYSGVTSAVNVAKGAVQT
						TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV VIGTKDTMSTGLIGAANVAKGAVQTGVDTA KTVLTGTKDTVTTGLVGAVNVAKGTVQTGM DTTKTVLTGTKDTIYSGVTSAVNVAKGAVQT
						TKDTVCSGVTSAVNVAKGAVQGGLDTTKSV VIGTKDTMSTGLTGAANVAKGAVQTGVDTA KTVLTGTKDTVTTGLVGAVNVAKGTVQTGM

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						Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end nucleotide	D-Acceptic Acid F=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning	location	E-Phenylalanine, G-Glycine, H-Histidine,
nucl-	peptide		in	nucleotide	corresponding	Introducine K=I vsine L=Leucine,
otide	seq-		USSN	location	to last amino	M=Methionine N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	acid residue	O=Glutamine R=Arginine, S=Serine,
uence			914	ng to first		T-Threonine V=Valine, W=1ryptophan,
			1	amino acid	of peptide	Y=Tyrosine, X=Unknown, *=Stop codon,
			ļ ļ	residue of	sequence	/=possible nucleotide deletion, \=possible
	<b>(</b>	i	1	peptide		nucleotide insertion
	1	!	1 1	sequence		VAKGAIQGGLDTTKSVLTGTKDAVSTGLTGA
	<del> </del>					VKLAKGTVQTGMDTTKTVLTGTKDAVCSGV
	}		1 1		}	TGAANVAKGAVQMGVDTAKTVLTGTKDTV
	[	1	1			TGAANVAKGAVQMOVDTAKTVETONIATGTK
	l	Į.	ì			CSGVTGAANVAKGAVQTGLKTTQNIATGTK
	ŀ	}	ł	•		NTLGSGVTGAAKVAKGAVQGGLDTTKSVLT
	}	)	}		}	GTKDAVSTGLTGAVNLAKGTVQTGVDTSKT
	1	ì	1			VLTGTKDTVCSGVTGAVNVAKGTVQTGVDT
	1		1		1	AKTVLSGAKDAVTTGVTGAVNVAKGTVQTG
	1	1			[	I WINGE AVI MCTKDTYFSGV I GAMSMANGA
	]	1	1	4	1	VQGGLDTTKTVLTGTKDAVSAGLMGSGNVA
	Ţ	1	1			TCATUTGI STFONWLPSIPAISWUULISSKI
	1	1	ì		<u> </u>	TONGGEOTAL SPOEAPESGISTPPDVLSVUPER (
	1	1		}	l l	AUTE A A ATTICITATOVA IF LUGAAPUREDIO
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		1	1	1	ļ	I NATECIANT A A SOPGPK VLSAEOUSY F VRLOD I
	1	İ	1	Ì	į.	LGPSFRQRAFEHAVSHLQHGQFQARDTLAQL
	1	1	1	1	1	ODCERI
				<del></del>	415	THARKETCPCKKEIGRNSRSGMYSRKAM
1275	2625	A	10025	124	413	VVDVVSAANTKVFKKKKEKVLAPVIKPVGG
					1	DKNGGTRVVKLPTMPRYYPTEDVPRKLLSHG
	l l	1	1			VVDEC
}	1			l		CCCL PESPER VPSCSRVFCPVPPGGCGLPSPMS
1276	2626	A	10030	3	507	LACERCOPTERWOI PRRYMKHKRDDGPEKUED
1270	2020		ł			EAVDVTPVMTCVFVVMCCSMLVLLYYFYDL
ļ	1	ŀ	1		j	LVYVVIGIFCLASATGLYSCLAPCVRRLPFGK
ł	1	1	{		1	CRIPNNSLPYFHKRPQARMLLLALFCVAVSV
l	1	ł	- (	{		CKINNSTALLING AUGUSSICS
-	1	- 1		1		VWGVFRNEDQ YSRFTVPLPATMASSEVARHLLFQSHMATKT
1277	2627	IA	10035	51	869	TCMSSQGSDDEQIKRENIRSLTMSGHVGFESL
12//	2027	1 "	1000	1	}	TCMSSQGSDDEQIRRENIASETHISOTT GI
		l	İ	Į.		PDQLVNRSIQQGFCFNILCVGETGIGKSTLIDT
1			1	1		LFNTNFEDYESSHFCPNVKLKAQTYELQESN
		}	}	}	l l	VQLKLTIVNTVGFGDQINKEERQLGRSQSTEN
1	į.		1			PQKYRSEQHPVEPKKCTSFWKGALGKWAGIE
Į.	<b>[</b>	ł		l	1	SSGQSAQQPYLPINSPPHRLADVADVHLFSSV
Ì	1	1	1	1		LSGAFGCYHLDVTVNEFKKQQNRDEQEGYS
1		- 1	-			KGDQEQGSWKHGADPLRGGEM
			10036	3	457	T DAEDVRRKKSI RPCCPRDFHAGCLI VSGPSI
1278	2628	A	10030			LVACAVCESI SVOCRYEEKYKIFNKY WURUF
					}	CI DIWLIEMVETGGSEGVVKSDOVIII DIFGUL
1				1	1	TETYTI ENLTADDAGKYRCGIAILQEDGLSG
		1	-			LEI POPEFOVOVI VSSASSTENSVKIP
1			10000	214	435	AIDSI VPMSSWRSCARAPSSESAWKKSAATKK
1279	2629	A	10039	214	455	SRKCLRTKRKRWSSGKGTQMQSTLSETPRRA
l		1	1	(		OMPCMWWYPFWG
1	1				344	DATU/HNAGKEREAVOLMAGAEKRVKASHS
1280	2630	A	10043	2	344	ELDGI EGGNTRIEEACEMYTRAANMEKMAK
1				1	1	NWSA A GNA FCOAAKLHMQLQSKHDSA 1 SF V
1	1			1	}	DAGNAVKKADPOGKTARHVACYLCV
			İ			VIYKLDSSLFSYFIYFFIFETESHFLPLMKWTG
1281	2631	A	10080	620	818	PIMAHCSLKILASRNSADSAFLSAGDTSLSHST
1201	2001	1	}	1		SASIIIRGDKRASGEVGIAPSSRHILLIGEPSAKY
1202	2632	A	10084	3	1640	SASIIIRGUKKASGE VOIAFSKIIIEIGEI BIELF
1282	2032	1 ^	1.000			NGTAIISLVRGPGILGEVTVFWRIFPPSVGEFA
		1				ETSGKLTMRDEQSAVIVVIQALNDDIPEEKSF
1		1	}	1	1	VEEDI TAVSEGGVI SESSSIANII VYASUSFI
				1	}	GREATSHEOLRVSEAORVNITIRSSGUFGHVR
1			1			I WYKTMSGTAFAGI.DFVPAAGELLFEAGEN
	- 1	ļ		Į		PKST HVFIL DDDYPEGPEEFSLTTKVELQGK
	1	- 1	1		į	CVDCTIOENGI OIDOPPEIGNISIVRIUMANUN
ł	l	- 4				
	ł	ĺ		j		AEGIEFDPKYTAFEVEEDVGLIMIPVVRLHGT

550 m	SEQ ID	Met	SEQ	Predicted	Predicted end	Ammo acid sequence (A=Alanine C=Cysteine,
SEQ ID	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of		1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	'		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			! !	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ļ	1	peptide	Jequenes	/=possible nucleotide deletion, \=possible
	l	ļ		sequence		nucleotide insertion
			ļ	sequence		VCVVTADEISOSSSASPGGVDYILHGSTVTFQ
	Ĭ	]	}			HGONI SFINISIIDDNESEFEEPIEILLTGATGG
	Ì	1	1		ļ	AVI GRHI VSRITIAKSDSPFGVIRFLNQSKISIA I
		<b>l</b>				ADDISTMIT SI VI ERTGGLLGEIOVNWETVGPN
	Ì	1	1			SOFALL PONRDIADPVSGLFYFGEGEGGVKILL
		1	1	ļ	}	LTIYPHEEIEVEETFIIKLHLVKGEAKLDSRAK
	Į.	ſ	ļ			DVTLTIQEFGDPNGVVQFAPETLSKKTYSEPL
	1	1	1			ALEGPLLITFFVRRVKGTFGEIM
			1 _			MGSKTLPAPVPIHPSLQLTNYSFLQAVNGLPT
1283	2633	A	10088	316	516	VPSDHLPNLYGFSALHAVHLHQWTLGYPAM
1203	2033	1				
	1	1		ļ		HLXRS
1204	2634	+	10091	2	569	FVSPSRAMASALIYVSKFKSFVILVVTPLLLLP
1284	2034	1,	1.007.	-	1	LVILMPAKFVRCAYVIILMAIYWCTEVIPLAV
ı	1	1		1	1	TSLMPVLLFPLFQILDSRQVCVQYMKDTNML
•	1	\.		1	1	FI GGLIVAVAVERWNLHKRIALRTLLWVGA
	1	Ì	1			KPARLMLGFMGVTALLSMWISNTATTAMMV
	ì	1	1		1	PIVEAILQQMEATSAATEAGLELVDKGKAKE
	1	1	ŀ		1	T D
			10092	290	728	KQSTRPDVMTLYPLHWQEEMSGESVVSSAVP
1285	2635	Α	10092	250	/20	A A A TRITISEK GTSPSSKYVKLNVGGAL Y Y I I
1	i	1	ļ.	}		MOTI TKODTMLKAMFSGRMEVLTDSEGWIL
İ	į	- {	l l	<b>\</b>	1	IDRCGKHFGTILNYLRDGAVPLPESRREIEELL
1	1	Į.			{	AEAKVVLVOGLVEECOAALQV
			10100	<del>                                     </del>	574	RPRGRGAWAGPGGDYSGVRRQQRRRTRISGS
1286	2636	Α	10100	1	374	ORGSDAAGTMGCCTGRCSLICLCALQLVSAL
		l		1		EPOIEDEI GEOWAPILGNFLHIIVVILGLEGIIQ
1	1	1	Į.	· I		VD PR VIMVYTVWTAL WVTWNVFIICFYLE VG
}	- 1		- [	Ì		GLSKDTDLMTFNISVHRSWWREHGPGCVKR
1	ŀ		-	]		VLPPSAHGMMDDYTYVSVTGCIVDFQYLEVI
	}	1	1	l	Ì	TICY
	i i	l				RSRMGDKPIWEQIGSSFIQHYYQLFDNDRTQL
1287	2637	Α	10103	252	376	CATVVSFOL
}					150	MEEEDESRGKTEESGEDRGDGPPDRDPTLSPS
1288	2638	A	10107	1	478	AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL
	}	- [	- 1		1	RWRRCRSPRSEPRSQESGGTDTATVLDMATD
1	ł	ł	- 1			SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM
	1	j				LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG
į	- 1	l l		İ		I
ļ.	1	ì	i	]		LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT
1289	2639	A	10113	237	438	DLREIGHGSFGAAYFARDVRTNEVVAIKKMS
1207				1		
1		ļ				YSG TO THE PROPERTY IN SPRAPITER SPG
1290	2640	A	10114	367	856	RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG
1290	2040	1	1			TEATRPTAMSKSLKKKSHWTSKVHESVIGRN
		1		1	]	PEGQLGFELKGGAENGQFPYLGEVKPGKVAY
1	1				1	ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI
						KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR
	1	1		1		L CAGO
			- 10000	128	591	PTIPETERRSALSCSVLKSEPLPGLOPQASQQR
1291	2641	A	10116	120	371	PRRIPGRROVOVOEGGGSGLRAWVLAMASV
		1		- 1		LGSGRGSGGLSSOLKCKSKRRRRRRSKRKDK
		}		1		VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE
		1		İ		VIKENRNYGNI AARPPPSGDRARGGATR
		ļ				QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR
1292	2642	A	10121	1	749	VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG
1		1				SWESWCCCCLIPADRPWDRGQHWQLEMADI
i	1	- 1			Ì	RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM
Ì	1	1	1	1		RSVHEIRFEAAVAVIQSERANGSIQI INDIAN
ļ		ŀ	1			
				ļ		LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW
						LKFYSFYKQATEGPCKLSRPGFWDPIGKTKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP MTEKVEELLRVIGPFYEIVEDKKSGRSSDITSD

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	peptide		in USSN	location	corresponding	I=Isolencine, K=Lysine, L=Laucine,
otide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
ience		}	914	amino acid	of peptide	T=Threonine V=Valine, W=Tryptophan,
		ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	Ì	1		peptide	Sequence	/=possible nucleotide deletion, \=possible
		1	1	sequence		nucleotide insertion
				sequence	<del> </del>	LGNVLTSTPNAKTVNGKAESSDSGAESEEEE
		ł				AC .
		<del> </del>	10124	2	989	PLMSLVRVVEFVAASSAQKTPSRLENYYMVC
1293	2643	A	10124	2	707	KADEKENOLVHFLRNHKQEKHLVFFRYSSGL
		1	1		}	CGRGIRDSARMCSTCACVEYYGKALEVLVK
		İ	ŀ		1	GVKIMCIHGKMKYKRNKIFMEFRKLQSGILV
			1	i		CTDVMARGIDIPEVNWVLQYDPPSNASAFVH
		1	1			RCGRTARIGHGGSALVFLLPMEESYINFLAIN
		}	l		1	QKCPLQEMKPQRNTADLLPKLKSMALADRA
•		1	1		}	VFEKGMKAFVSYVQAYAKHECNLIFRLKDL
						DFASLARGFALLRMPKMPELRGKQFPDFVPV
	1			1		DVNTDTIPFKDKIREKQRQKLLEQQRREKTEN
		1		Ì		EGRRKFIKNKAWSKQKAKKK
1001	2644	A	10129	91	1042	VTMYKDCIESTGDYFLLCDAEGPWGIILESLA
1294	2044	\ A	10125	**		ILGIVVTILLLLAFLFLMRKIQDCSQWNVLPTQ
			1			LLFLLSVLGLFGLAFAFIIELNQQTAPVRYFLF
		l	1	1	1	GVLFALCFSCLLAHASNLVKLVRGCVSFSWT
		1			İ	TILCIAIGCSLLQIIIATEYVTLIMTRGMMFVN
	1	1.	i	1	1	MTPCQLNVDFVVLLVYVLFLMALTFFVSKAT
			1			FCGPCENWKQHGRLIFITVLFSIIWVVWISML
	1		1			LRGNPQFQRQPQWDDPVVCIALVTNAWVFL
		1		ĺ		LLYIVPELCILYRSCRQECPLQGNACPVTAYQ
		1	1	ļ		HSFQVENQELSRDKWKVLLNSDFLSHSGA
1295	2645	A	10133	376	518	RPRVVTHNSQWCFLPQDHPGWLPGQSGAPG
12/3	20.5		1			GRGAPRQEGPGSSWRQV EWSLDPFMGIMSGQVGDLSPSQEKSLAQFRE
1296	2646	A	10135	3	551	NIQDVLSALPNPDDYFLLRWLQARSFDLQKS
1270	20.0	1		1	1 .	EDMLRKHMEFRKQQDLANILAWQPPEVVRL
}		l			ļ	YNANGICGHDGEGSPVWYHIVGSQDPKGLLL
	1	- {		ļ	1	SASKQELLRDSFRSCELLLRECELQSQKLGKR
	Ì	ł		ļ		VEKIIAIFGLEGLGLRDLWKPGIELLQE
		1				MVSSCCGSVCSDQGCGQDLCQETCCRPSCCE
1297	2647	A	10138	48	407	TTCCRTTCCRPSCCVSSCCRPQCCQSVCCQPT
			l l			CSRPSCCQTTCCRTTCYRPSCCVSSCCRPQCC
						QPVCCQPTCCRPSCCETTCCHPXCC
l .		l				GGNRKSAEMFSQVPRTPASGCYYLNSMTPEC
1298	2648	A	10156	94	453	QEMYLRFDQTTRRSPYRMSRILARHQLVTKI
		1		İ		QQEIEAKEACDWLRAAGFPQYAQLYEDSQFF
ļ					,	INITYAVKNOHDFLEKDLGEPLCRRLNT
					202	PRESELVINGRORVSARFGGSPSKAATVRSQP
1299	2649	A	10161	[ ]	393	ASAOLENMEEAPKRVSLALOLPEHGSKDIGN
1				1		VPGNCSENPCONGGTCVPGADAHSCDCGPG
Į.				1	1	KGRRCELACIKVSRPCTRLFSETKAFPVWEGG
ł			1	1		VCHHV
1					1201	AKIASLERIMPANYTCTRPDGDNTDFRYFIYA
1300	2650	A	10162	98	391	VTYTGILGPGLIGNILALWVFYGYMKETKRA
			1		1	VIFMINLAIADLLQVLSLPLRIFYYLKHDWPF
	1	- 1		}		VPV
					7545	PGID VGITSOTGL SSNLOENCSKLAFISSHGTE
1301	2651	A	10165	] 1	7545	VOI OCMPMEGRGRASSSISDLOGKGFEKGT
1			(	1		EKHVPGVGSARHSPQASAGGSPWQRGKAQT
1		1	1		i	RWLGKPDPGRKRRRGSPQEEGGLRVSAAAR
		1	1			LI CSGANRCKVI VRONSTPNTOOPAVHPSTI
1	-	ļ	1	1		PSRPLPQAGRCLVAPLRPHPDWVAAKTLAK
						LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP
1		- !		1		RTLSVEEPGVECNQLCLYADVTDPVLCLGQH
1	Į	}			İ	DPGVEGKHCEKEKISSSKELKHVHAKSEPSK
1	1	- 1	1	1		ARRLSESLHVVDENKNESKIEREHKRRTSTP
1						
]		- 1				IMEGVQEETDTRDVKRQVERSEICTEEPQKQ

			OF O	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ		nucleotide	D=A spartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ſ	in	nucleotide		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N-Asparagine, 1-1 forms,
uence	}	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	]	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ł	i	ŀ	ĺ	peptide		/=possible nucleotide deletion, \=possible
į.	İ	Ì		sequence	<b>\</b>	nucleotide insertion
	<del> </del>	<del> </del>	<del> </del>	bequeste		KSTLKNEKHLKKDDSETPHLKSLLKKEVKSS
l	ļ		l		}	KEKPEREKTPSEDKLSVKHKYKGDCMHKTG
1			1			DETELHSSEKGLKVEENIQKQSQQTKLSSDDK
1	1		1	1		TERKSKHRNERKLSVLGKDGKPVSEYIIKTDE
Į.					ļ	NVRKENNKKERRLSAEKTKAEHKSRRSSDSK
}	1	]	1	1		IQKDSLGSKQHGITLQRRSESYSEDKCDMDST
1	1	}				NMDSNLKPEEVVHKEKRRTKSLLEEKLVLKS
			ļ			NMDSNLKPEEV VIKERRICKT KSEEDELEEV ETC
1	ł		ł	1		KSKTQGKQVKVVETELQEGATKQATTPKPD
i	1		1			KEKNTEENDSEKQRKSKVEDKPFEETGVEPV
1	ł	1	1			LETASSSAHSTQKDSSHRAKLPLAKEKYKSD
1		1	1			KDSTSTRLERKLSDGHKSRSLKHSSKDIKKKD
			1			ENKSDDKDGKEVDSSHEKARGNSSLMEKKL
1	Ì	1	1	1	1	SRRLCENRRGSLSQEMAKGEEKLAANTLSTP
	1		1	1		SGSSLORPKKSGDMTLIPEQEPMEIDSEPGVE
1				1	1	NVFEVSKTODNRNNNSHQDIDSENMKQKTS
	1	1	1	į.	1	ATVOKDELRTCTADSKATAPAYKPGRGTGV
ł	1	1		1		NSNSEKHADHRSTLTKKMHIQSAVSKMNPGE
ļ		1	ļ	}		KEPIHRGTTEVNIDSETVHRMLLSAPSENDRV
ſ		1	1	1		QKNLKNTAAEEHVAQGDATLEHSTNLDSSPS
i	1		1	Į.		LSSVTVVPLRESYDPDVIPLFDKRTVLEGSTA
ł	1		Ĭ.	1		STSPADHSALPNQSLTVRESEVLKTSDSKEGG
1	1	1	1			EGFTVDTPAKASITSKRHIPEAHQATLLDGKQ
1	1	}	1		1	GKVIMPLGSKLTGVIVENENITKEGGLVDMA
	1	1	1			KKENDLNAEPNLKQTIKATVENGKKDGIAVD
ł		-	ļ	1	}	HVVGLNTEKYAETVKLKHKRSPGKVKDISID
İ	i		1			VERRNENSEVDTSAGSGSAPSVLHQRNGQTE
ı	1	- [	(	1		DVATGPRRAEKTSVATSTEGKDKDVTLSPVK
			1			AGPATTTSSETRQSEVALPCTSIEADEGLIIGT
1		1	ł	İ	İ	HSRNNPLHVGAEASECTVFAAAEEGGAVVTE
1		İ	1	1		HSRNNPLHVGAEASECTVFAAAEEGGAVAEGEDB AADI
1	1		1			GFAESETFLTSTKEGESGECAVAESEDRAADL
1	1					LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE
	l			1		KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG
1	{	ĺ	1	1		TEIRAGSISSEEVDGSQGNMMRMGPKKETEG
	j	-	1		1	TVTCTGAEGRSDNFVICSVTGAGPREERMVT
	j	- }	1		1	GAGVVLGDNDAPPGTSASQEGDGSVNDGTE
	1	1	ŀ	-		GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS
Į.	1	ı	1			SESEENGESAMDSTVAKEGTNVPLVAAGPCD
1	1			1	1	DEGIVTSTGAKEEDEEGEDVVTSTGRGNEIGH
	1		1			ASTCTGLGEESEGVLICESAEGDSQIGTVVEH
		-		-{		VEAEAGAAIMNANENNVDSMSGTEKGSKDT
		1	1			DICSSAKGIVESSVTSAVSGKDEVTPVPGGCE
		]	)	1	1	GPMTSAASDOSDSQLEKVEDTTISTGLVGGS
	1	l	}	J		VDVI VSGEVPECEVAHTSPSEKEDEDITISVE
1		Ì	1			NEECDGLMATTASGDITNQNSLAGGKNQGK
	-	1		ł		VILISTSTTNDYTPOVSAITDVEGGLSDALKTE
	1	1			1	ENMEGTRYTTEEFEAPMPSAVSGDDSQLTAS
1	1	1		1		RSEEKDECAMISTSIGEEFELPISSATTIKCAES
	1	1		1	}	LQPVAAAVEERATGPVLISTADFEGPMPSAPP
				1	İ	LUPVAAA VEEKA I OF VEIST ADFECT VEIST A EVE
1	1	1		1	}	EAESPLASTSKEEKDECALISTSIAEECEASVS
-	1	- (				GVVVESENERAGTVMEEKDGSGIISTSSVEDC
				1	'	EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS
				1		TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA
1		1		1		AIISTSTAECMPISASIDRHEENQLTADNPEGN
			ļ	1	1	GDLSATEVSKHKVPMPSLIAENNCRCPGPVR
		1	.[	1		GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH
		İ	1			PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL
			- [	}	1	HUNAEEKNVLLNSLQKEDKSPETGTAGGSST
			- [	1		ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK
1			1	Į.		DSSVSSTRYLAAVNTGAIKADDMPPVQGTVA
		1		j		EHSFLPAEQQGSEDNLKTSTTKCITGQESKIAP
1		1		.1		ELISITEI VEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

		14-4	CEO 1	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID NO: of	Met hod	SEQ ID NO:	beginning	nucleotide	D=A spartic Acid E=Glutamic Acid.
NO: of	peptide	nod	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nuci-	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uchec		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uenœ			'	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	(		peptide		/=possible nucleotide deletion, \=possible
		1	1	sequence		nucleotide insertion
			1			SHTMIPPATYSVALLAPKCEQDLTIKNDYSGK
			1			WTDQASAEKTGDDNSTRKSFPEEGDIMVTVS
	ì		1			SEENVCDIGNEESPLNVLGGLKLKANLKMEA
						YVPSEEEKNGEILAPPESLCGGKPSGIAELQRE PLLVNESLNVENSGFRTNEEIHSESYNKGEISS
		}		}		GRKDNAEAISGHSVEADPKEVEEEERHMPKR
		1				KRKQHYLSSEDEPDDNPDVLDSRIETAQRQC
	1	1				PETEPHATKEENSRDLEELPKTSSETNSTTSRV
			1	•	1	MEEKDEYSSSETTGEKPEQNDDDTIKSQE
		1				EPSLFPFLRPSPARPPRRPPAFFPSPELAGPEPH
1302	2652	A	10167	321	842	FVFYFFLSYVHPPKELAKYEYMEEQVILTEKG
		(				NSTVAGRGTSVRCLSPSPRPLPPLLPLLADLLE
		1	İ			DGFGEHPFYHCLVAEVPKEHWTPEGNPSPFP
	ł	}	1			EARETKCYVRSSVGCVEPLTTQAEVTENLDR
	1		1	l .		KNSQQVFKLLKKK
	}		<u> </u>		100	NMILLKKRILINSLGEGTINGLLDELLETNV
1303	2653	Α	10171	206	429	LSQEDTEIVKCENVTVIDKARDLLDSVIRKGA
		j				RACEICITYI
	L	1			1624	LCTLSPGISGTAGSCLTTEPGTELGTSFAQNGF
1304	2654	Α	10184	970	1524	VHEAVVI FTOALKLNPODHRLFGNRSFCHER
	1	1			1	LGQPAWALADAQVALTLRPGWPRGLFRLGK
	1	1	1			A LMGLOREREA A A VFOETLRGGSOPDAAKEL
	ł	1	1	1		RSCLLHLTLQGQRGGICAPPLSPGALQPLPHA
İ						FLAPSGLPSLRCPRSTALRSPGLSPLLH
				12	394	TOLLGRRERVDGAAMAACEGRRSGALGSSQ
1305	2655	A	10194	2	374	SDFL TPPVGGAPWAVATTVVMYPPPPPPPHR
1	l l	)	1			DEISVILSEGESYDNSKSWRRRSCWRKWKQL
1		1	1	}		SRLQRNMILFLLAFLLFCGLLFYINLADHWKG
		1	1	Ì	1	IRNTCT
1306	2656	A	10195	1	410	IPGSTISLEGPLSKWTNVMKGWQYRWFVLDY
1300	2030	1	100,70	1		NAGLLSYYTSKDKMMRGSRRGCVRLRGAVI
ł						GIDDEDDSTFTITVDQKTFHFQARDADEREK
ĺ	{					WIHALEETILRHTLQLQVRVFTWFPDSSLVGA
1	1	- [	1.			FFFWLVSGFFFK
1307	2657	A	10205	85	308	QGLPSTMVKLGCSFSGKPGKDPGDQDGAAM
1301		-				DSVPLISPLDISQLQPPLPDQVVIKTQTEYQLS
1	1		}			SPDQQNYTKSR
1308	2658	A	10214	2	453	ECGGIROPGPGPPPALASAPAATMNRVGGSPS AAANYLLCTNCRKVLRKDKRIRVSQPLTRGP
1			1	}		SAFIPEKEVVQANTVDERTNFLVEEYSTSGRL
					İ	DNITQVMSLHTQYLESFLRSQFYMLRMDGPL
			}	1	}	PLPYRHYIAIMAAARHQCSYLINM
				1		RGWPEQQSTGRPRDVARQPRCQKEEGRRLRP
1309	2659	A	10233	45	421	RGWPEQQSTGRPRDVARQPRCQREECRACK RALESRTFQGSERSRWGPPLESTKENVQCGH
				)	1	RALESKI FQGSEKSK WOFF DESTREAM RPAFPNSSWLPFHERLQVQNGECPWQVSIQM
1	{					SRKHLCGGSILHWWWVLTAAHCFRRTLLDM
1				1		
	1					AFQLFNAKCESAFLSKRNPLQRNWTVLYRRK
1310	2660	A	10241	243	442	HKKGQSAEIQKKRTRRAFKFQRAITGASLADI
1			ł		(	MAK
				<del></del>	122	LPGADYGGGHLSLRLFHLLLTSAAWVPDESQ
1311	2661	A	10261	751	176	VTLNSAICVLSTVLIMEFPDLGKHCSEKTCKQ
			1			LDFLPVKCDACKQDFCKDHFPYAAHKCPFAF
		1				QKDVHVPVCPLCNTPIPVKKGQIPDVVVGDHI
1		- 1			}	DRDCDSHPGKKKEKIFTYRCSKEGCKKKEML
						QMVCAQCHGNFCIQHRHPLDHSCRHGSRPTI
1		ł		1		KAG
- 1	1					STSSDEGSPSASTPMINKTGFKFSAEKPVIEVP
<u> </u>						
1312	2662	A	10270	3	669	SMTILDKKDGEQAKALFEKVRKFRAHVEDSD

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	ŀ	in	nucleotide	location	F=Phenylalanine, G=Grycine, ri-ristanic,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	Į	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
donot	[	1	Į	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	i	Ĭ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	1	į.		peptide		/=possible nucleotide deletion, \=possible
	1	1		sequence		nucleotide insertion
		<del> </del>	<del> </del>	1		LIYKLYVVQTVIKTAKFIFILCYTANFVNAISF
	}	1			ł	EHVCKPKVEHLIGYEVFECTHNMAYMLKKL
	ł	1	1		ì	LISYISIICVYGFICLYTLFWLFRIPLKEYSFEKV
	1	ŀ	1		Ì	REESSFSDIPDVKNDFAFLLHMVDQYDQLYS
1	Ì	1	1		1	KRFGVFLSEVSENKLREISLNHEWTFEKL
	ļ	<del>                                     </del>	10287	1221	266	GAHRVLSPAOGAOPRLRSAASVEVSMVGQR
1313	2663	A	10287	1221	200	VLLLVAFLLSGVLLSEAAKILTISTLGGSHYLL
]			1			LDRVSQILQEHGHNVTMLHQSGKFLIPDIKEE
1	1	1	1		]	EKSYQVIRWFSPEDHQKRIKKHFDSYIETALD
ľ		1	1	-	1	GRKESEALVKLMEIFGTQCSYLLSRKDIMDSL
1	ļ	1	1	1	1	KNENYDLVFVEAFDFCSFLIAEKLVKPFVAIL
Í	1	1	1			PTTFGSLDFGLPSPLSYVPVFPSLLTDHMDFW
Į.	l	ł	1			GRVKNFLMFFSFSRSQWDMQSTFDNTIKEHF
Ì	1	1				PEGSRPVLSHLLKAELWFVNSDCAFDFARPL
]	1	1	1	}		LPNTVYIGGLMEKPIKPVPQVSEPSAFSLGFT
1						LPNI V YIGGEMENFINF V PQVSLI SAL SEGI I
1314	2664	A	10288	536	1890	NVQLAKFSSTLVFFFSCDADPSALAKYVLAL
	1	1	ì			VKKDKSEKELKALCIDQLDVFLQKETQIFVEK
		1			1	LFDAVNTKSYLPPPEQPSSGSLKVEFFPPQEK
ļ		j	}	i		DIKKEEITKEEEREKKFSRRLNHSPPQSSSRYR
1	[				l .	ENRSRDERKKDDRSRKRDYDRNPPRRDSYRD
	1				]	RYNRRGRSRSYSRSRSRSWSKERLRERDRD
	1					RSRTRSRSRTRSRERDLVKPKYDLDRTDPLEN
	1	-			1	NYTPVSSVPSISSGHYPVPTLSSTITVIAPTHHG
ſ	1	1			1	NNTTESWSEFHEDQVDHNSYVRPPMPKKRC
ļ	1					RDYDEKGFCMRGDMCPFDHGSDPVVVEDVN
1						LPGMQPFPAQPPVVEGPPPPGLPPPPPILTPPPV
1	1		ì	1		NLRPPVPPPGPLPPSLPPVTGPPPPLPPLQPSG
	Į.		ì			MDAPPNSATSSVPTVVTTGIHHQPPPAPPSLFT
1	l	1	ı		İ	ADTYDTDGYNPEAPSITNTSRPMYRHRVHPR
1						AKLG
1315	2665	A	10293	447	1331	SHPLLSCPEKVSAKLRAAAEAAAEERRTRGA
1313	2003	^	10255	1		GSRGICAGLRSVAPGPEPLKQEEGRREWGSSI
I	ĺ	1			1	GTPSPCGSAOAAAAAAAEEATEKIPALRPALL
1		ļ				WALLALWLCCATPAHALQCRDGYEPCVNEG
1	1	-	ł	1	1	MCVTYHNGTGYCKCPEGFLGEYCQHRDPCE
	ļ	ļ			}	KNRCONGGTCVAOAMLGKATCRCASGFTGE
	1	1				DCOYSTSHPCFVSRPCLNGGTCHMLSRDTYE
1		1	1			CTCOVGFTGRNPKCPGGNLNYQFNGIIVVYS
1		1				GGSVPPSGTKTSKPAEHNAMGTGSKNFASGT
1	1	1				LWVMVSGATSTSTSTL
		<del>-   -</del>	10004	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTG
1316	2666	Α	10294	110	17/2	YSLVOENGORKYGGPPPGWDAAPPERGCEIFI
		1			1	GKLPRDLFEDELIPLCEKIGKIYEMRMMMDF
			1			NGNNRGYAFVTFSNKVEAKNAIKQLNNYEIR
	1			1	}	NGRLLGVCASVDNCRLFVGGIPKTKK
					1066	LLKSCGVLLSGVCIPCEGKGPTVLVIQTAVPQ
1317	2667	Α	10301	158	1956	DRPTKSSMRSAAKPWNPAIRAGGHGPDRVRP
			1			LPAASSGMKSSKSSTSLAFESRLSRLKRASSE
1	]	)		1	1	DTI NUDCETA ACCUMI VVTATA CAICEI TEC
				1	1	DTLNKPGSTAASGVVRLKKTATAGAISELTES
1	1	-				RLRSGTGAFTTTKRTGIPAPREFSVTVSRERSV
1		İ		1		PRGPSNPRKSVSSPTSSNTPTPTKHLRTPSTKP
}	1	1		1		KQENEGGEKAALESQVRELLAEAKAKDSEIN
		1	1	1	1	RLRSELKKYKEKRTLNAEGTDALGPNVDGTS
	1	1	1	1		VSPGDTEPMIRALEEKNKNFQKELSDLEEENR
1						VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ
- 1		-				ESSFGSPTGNOLSSDIDEYKKNIHGNALRTSG
1		1	1	1	1	SSSSDVTKASLSPDASDFEHITAETPSRPLSSTS
1		ļ	1	1	1	3333D4 I KA3C3I DI EDI DI III ETI SIG 2551=
					1	NPFKSSKCSTAGSSPNSVSELSLASLTEKIQKM
						NPFKSSKCSTAGSSPNSVSELSLASLTEKIQKM EENHHSTAEELQATLQELSDQQQMVQELTAE

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nucl-	peptide		in	nucleotide location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN 09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	<b>\</b>		ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ļ	1	1	peptide	3-4	/=possible nucleotide deletion, \=possible
		ļ		sequence		nucleotide insertion
	<del> </del>		+	boquonos		NEKLYDEKTILETSFHQHRERAEQLSQENEKL
	1	]		]		MNLLQERVKNEEPTTQEGKIIELEQKCTGILE
				İ		QGRFEREKLLNIQQQLTCSLRKVEEENQGAL
			,	}		EMIKRLKEENEKLNEFLELERHNNNMMAKTL
			ļ	_		EECRVTLEGLKMENGSLKSHLQG
1318	2668	Α	10303	333	879	GECFIMAAVVQQNDLVFEFASNVMEDERQL
		1	1			GDPAIFPAVIVEHVPGADILNSYAGLACVEEP NDMITESSLDVAEEEIIDDDDDDITLTVEASCH
		1				DGDETIETIEAAEALLNMDSPGPMLDEKRINN
	}		}	ĺ		NIFSSPEDDMVVAPVTHVSVTLDGIPEVMETQ
	1	-	Ì		1	QVQEKYADSPGASSPEQPKRKKK
	1				164	MEVRMSGSVAVTRAIAVPGLLLLIIATALSL
1319	2669	Α	10322	169	654	LIGAKSLPASVVLEAFSGTCQSADCTIVLDAR
		1	ļ			I PRTLAGLLAGGALGLAGALMQTLTRNPLAD
		}	1		į.	PGLLGVNAGASFAIVLGAALFGYSSAQEQLA
	İ	1	1	1	Į	MAFAGALVASLIVAFTGSQGGGQLSPVRLTL
İ		-	}	•	1	AGVXI
1.22	2670	A	10323	441	12	KMNQVAVVIGGGQTLGAFLCHGLAAEGYRV
1320	2070	A	10323	1 77.	1	AVVDIOSDKAANVAOEINAEYGESMAYGFG
ţ	i	- [				ADATSEQSVLALSRGVDEIFGRVDLLVYSAGI
]				1	}	AKAAFISDFQLGDFDRSLQVNLVGYFLCARE
1			ļ	1		FSRLMIRDGIQGRIIQINSKSDE
1321	2671	A	10332	1	453	RHRTAGPGSTISSRTDSASAPAARAMPCEYTY
1321	1		1		}	AKLTSDCSRPSLQWYTRAQSKMRRPRLLLKD ILKCTLLVFGVRILYILKLNYTTEECDMKNMH
				1	-	YVDPDHVKRAQKYAQQVLQKESPPKFAKTS
1	}	1		1		MALLFEHRYSVDLLPFVQKAPTDSEA
			<del> </del>	100	423	EPSNGPVVYSALGNEDDEILLLGKDIIGTFAAS
1322	2672	A	10333	25	423	FRKMRAHOVLTFLLLFVITSGASENASTSRGC
1		1			ļ	GLDLL PONVYLCDLDAIWGIVVEAVAGAGA
ļ						LITLLLMLILLGRLPFIKEKEKKSPAVLHFLFL
		)		ļ	}	LGTLG
1323	2673	+	10334	52	426	SSLGNEDDEILSLAKDITGMFVASHRKMRAH
1323	2073	1 ^	1000			QVLTFLLLFVITSVASENASTSRGCGLDLLPQ
1 .		}		}	1	YVSLCDLDAIWGIVVEAAAGAGALITLLLMLI
		-		1		LLVRLPFFKEKEKKSPVGLHFLFLLGTLGP
1324	2674	A	10336	1	932	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEE
.524		1,				NSVTHHEVKCQGKPLAGIYRKREEKRNAGN
1		1	Ì	1		AVRSAMKSEEQKIKDARKGPLVPFPNQKSEA AEPPKTPPSSCDSTNAAIAKQALKKPIKGKQA
			1		1	PRKKAQGKTQQNRKLTDFYPVRRSSRKSKAE
1			1	1		LOSEERKRIDELIESGKEEGMKIDLIDGKGRG
1		1	1	1		VIATKQFSRGDFVVEYHGDLIEITDAKKREAL
1	'	- (		1		YAQDPSTGCYMYYFQYLSKTYCVDATRETN
				1		RLGRLINHSKCGNCQTKLHDIDGVPHLILIAS
	Ì	1				RDIAAGEELLYDYGDRSKASIEAHPWLKH
					870	PGSTISCSELKGTQCRATAGSRGRRPPMTCWI
1325	2675	A	10338	3	070	RGVTATFGRPAEWPGYLSHLCGRSAAMDLG
		1				PMRKSYRGDREAFEETHLTSLDPVKQFAAWF
i		1				EEAVOCPDIGEANAMCLATCTRDGKPSARMI
1	1	1				LLKGFGKDGFRFFTNFESRKGKELDSNPFASL
1	Ì			Į.		VFYWEPLNROVRVEGPVKKLPEEEAECYFHS
1		1	1		j	RPKSSOIGAVVSHOSSVIPDREYLRKKNEELE
			1	1		OLYODOEVPKPKSWGGYVLYPQVMEFWQG
	-		]		}	QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE
1	}			l	1	DWLYERLAP
1		1 -		<del>-  </del>	984	ARAAAHCGICRLVRWWRKRRSVMGIQTSPV
1326	2676	Α	1 10344	2	704	700 00 00 00 00 00 00 00 00 00 00 00 00
1326	2676	A	10344	2	704	LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT LLDPNEKYLLRLLDKTTVSHNTKRFRFALPTA

SEQ ID   SEQ ID   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   No. of   N	VTSD ISQY VIQP ULIRA EELQ TAD CHPN VQRR ITAW DEQG AHQ
NO. of nucleotide conting sequence   No. of nucleotide content   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   No. of nucleotide   N	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
nucicotide sequence    USSN   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496   O9/496	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
eerde uence    Sequence	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
sequence uence	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
acid residue of peptide residue of peptide sequence  914	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
amino acid residue of peptide sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
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Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide sequence   Poptide seq	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
Incleotide insertion   Sequence   HHTLGLPVGKHIYLSTRIDGSLVIRPYTP   EDQGYVDLVIKVYLKGVHPKFPEGGKM   LDSLKVGDVVEFRGPSGLITYTOKGHFF   NKKSPPEPRVAKKLGMIAGGTGITPMLG, IILKVPEDPTQCFLLFANQTEKDIIL.REDL   ARYPNRFKLWFTLDHPPKDWAYSKGF   MIREHLPAPGDDVLVLLCGPPMVQLA   LDKLGYSQKMRFTY	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
HHTLGLPVGKHIYLSTRIDGSLVIRPYTIP EDQGYVDLVIKVYLKGVHPKFPEGGKM LDSLK VGDVVEFRGPSGLLTYTOKGHFI NKKSPPEPRVAKKLGMIAGGTGITPMLG ILK VPEDPTQCFLLFANQTEKDILLEDL ARYPNRFKLWFTLDHPPKDWAYSKGFI MIRHLPAPGDDVLVLLCGPPPMVQLA LDKLGYSQKMFTY LOSAGEGVTHVLILLESPARPVAAVTQV RYHRLSDMSMLAERRKQKWAVDPQN SNDDSKFGQRMLEKMGWSKGKGLGAA ATDHIKVQVKNNHLGLGATINNEDNWI DDFNQLLAEINTCHGQETTDSSDKKEK LEEKSKISKNRVHYMKFTKGKDLSSRSI DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA GSAAMKVKIKCWNOVATWLWVANDI GCRMAFNGCCPDCKVPGDDCPLVWGQU HMHCILKWLHAQQVQQHCPMCRQEW MCMPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGRILLILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYQDFV LHYMWINPHLCGLLVLASWTMSALY LHYMVINFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTVTM YSLRNKDIKRALGHILLWGTMKGQFFF	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
EDGGYVDLVIKVYLKGVHPKFPEGGKM LDSLKVGDVVEFRGPSGLLTYTOKGHFF NKSPFERVAKKLGMIAGGTGITPMLG ILKVPEDPTQCFLLFANQTEKDILLREDL ARYPNRFKLWFILDHPPKDWAYSKGFN MREHLPAPGDDVLVLLCGPPPMVQLA LDKLGYSQKMRFTY LOSAGEGVTHVLILLESPARPVAAVTQV RYHRLSDMSMLAERRKQKWAVDPQD SNDDSKFGQRMLEKMGWSKGKGLGAG ATDHIKVQVKNNHLGLGATINNEDNWI DDFNQLLAELNTCHGQETTDSSDKEKEK LEEKSKISKNRVHYMKFTKGKDLSSRSI DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQG HMHCILKWLHAQQVQQHCPMCRQEW QMEPGNDTQISEFLLLGFSQEPGLOPFI SMYVLTVLGNLLILLATISDSHLHTPMY LSFADICVTSTTIPKMLMNQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFV LHYMVIMKPHLGGLVLASWTMSAL) LMVVRLSFCTALEPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYGG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHLLWGTMKGQFFI DEFI KSCCCCCT FDEPPPPLDOVQEEE	VQRR VTAD CHPN VQRR VTAW VQRR VQRR VQRR VQRQ AHQ
IDSLKVGDVVEFRGPSGLLTYTIOKGH-INKKSPPEPRVAKKLGMIAGGTGIFPMLG ILKVPFDPTQCFLLFANQTEKDILLREDL ARYPNRFKLWFTLDHPPKDWAYSKGF- MIREHLPAPGDDVLVLLCGPPPMVQLA: LDKLGYSQKMRFTY LOSAGEGVTHVLILLESPARPVAAVTQ\ RYHRLSDMSMLAERRKQKWAVDPQ\ SNDDSKFGQRMLEKMGWSKGKGLGAG ATDHIKVQVKNNHILGLGATINNEDNW\ DDFNQLLAELNTCHGQETTDSSDKKEK LEEKSKISKNRVHYMKFTKGKDLSSRS\ DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDF CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WHAQQVQQHCPMCRQEW OMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFV\ LHYMVIMNPHLCGLLVLASWTMSAL\ LMVVRLSFCTALEPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSVSK AISSAGKKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHLLWGTMKGQFF	ILIRA EELQ TAD CHPN VQRR ITAW DEQG AHQ
1327 2677 A 10345 1 968 LOSAGETOTIVMLC  1327 2677 A 10345 1 968 LOSAGETOTIVALUL COPPPMVQLAL LDKLGYSQKMRFTY  1328 2678 A 10346 173 439 CRAMFOCEPOCKYPGDDCPLVWGQHMHCLKWLHAQQVQHCPMCRQEW  1329 2679 A 10351 3 964 OMEPGNDTQISEFLLLGFSQEPGLOPFL  SMYLVTVLGNLLIILATISDSHLHTPM  LSFADICVTSTTIPKMLMNQTQNKVTI  MQYFFILFAGFENFLLSVMAYDRV  LHYMVIMPHLCGLLVLASWTMSAL  LMVVRLSFCTALEIPHFFCELNQVIQLA  LNHWVIYFTVALLGGPTGILSVSSS  ALSAQQKYKAFSTCASHLSVVSLFYG  YLSSAATRNSHSSATASVMYTVVTPM  VSLRNKGIRRAGHLLWGTMKGQFF  YSLRNKGIRRAGHLLWGTMKGQFF  YSLRNKGIRRAGHLLWGTMKGQFF  YSLRNKGIRRALGIHLLWGTMKGQFF  YSLRNKGIRRAGHLLWGTMKGQFF  YSLRNKGIRRALGIHLLWGTMKGQFF	EELQ /TAD CHPN /QRR /TAW DEQG AHQ
1327 2677 A 10345 1 968 LQSAGEGVTHVLILLESPARPVAAVTQV RYHRLSDMSMLAERRRKQKWAVDPQN SNDDSKFGQRMLEKMGWSKGKGLGAG ATDHIKVQVKNNHLGLGATINNEDNW DDFNQLLAELNTCHGQETTDSSDKEKK LEEKSKISKNRVHYMKFTKGKDLSSRKS CIFICKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKSAPAEEQLRGPC SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQG HMHCLLKWLHAQQVQQHCPMCRQEW GMFGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFV LHYMVIMNPHLCGLLVLASWTMSALN LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGIL YSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLL WGTMKGQFF	TAD CHPN CRR TTAW QEQG AHQ
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1327 2677 A 10345 1 968 LQSAGEGVTHVLILLESPARPVAAVTQV RYHRLSDMSMLAERRRKQKWAVDQV SNDDSKFGQRMLEKMGWSKGKGLGAA ATDHIKVQVKNNHLGLGATINNEDNWI DDFNQLLAELNTCHGQETTDSSDKKEK LEEKSKISKNRVHYMKFTKGKDLSSRSI DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQQHCPMCRQEW HMHCILK WLHAQQVQQHCPMCRQEW SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVALLYWVINSPCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVYTPM YSLRNKDIKRALGHILLWGTMKGQFFI DEFLK SCCCCCLIFDFPPPPLDOVQEEC	EQG AHQ
RYHRLSDMSMLAERRRKQK WAVDIQUE SNIDDSKFGQRMLEKMGWSKGKGLGAG ATDHIKVQVKNNHLGLGATINNEDNWI DDFNQLLAELNTCHGQETTDSSDKKEK LEEKSKISKNRVHYMKFTKGKDLSSRSI DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILKWLHAQQVQHCPMCRQEW GMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFV LHYMVIMNPHLCGLLVLASWTMSALV LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHILLWGTMKGQFFI DEELKSCCCCCT.FDFPPPPLDOVQEEEC	EQG AHQ
RYHKLSDMSMLAEKRRUK WAYDERST SNDDSKFGQRMLEKMGWSKGK.GLGAGERST SNDDSKFGQRMLEKMGWSKGK.GLGAGERST SNDDSKFGQRMLEKMGWSKGK.GLGAGERST SNDDSKFGQRMLEKMGWSKGK.GLGAGERST SNDDSKFGQRMLEKMGWSKGK.GLGAGERST SNDDSKFGQRMLEKMGWSKGK.GLGAGERST SNDDSKFTGARMALKNKPQVPVPGSDISS RKRGKKNKEATGKDVESYLQPKAKR KPERAEAQERVAKKSAPAEEQLRGPC SSKASAQDAGDHVQPA SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDF CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQQHCPMCRQEW SWYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFV LHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHILLWGTMKGQFFI DFPPPPDPPDDOVQEEC	AHQ
ATDHIKVQVKNNHLGLGATINNEDN W. DDFNQLLAELNTCHGQETTDSSDKKEK LEEKSKISKNRVHYMKFTKGKDLSSRSI DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDF CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQHCPMCRQEW GMPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVALHYMVIMNPHLCGLLVLASWTMSALY LHYMVIMNPHLCGLLVLASWTMSALY LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHILLWGTMKGQFFI	AHQ
ATDHIKVQVKNNHLGLGATINNEDN W. DDFNQLLAELNTCHGQETTDSSDKKEK LEEKSKISKNRVHYMKFTKGKDLSSRSI DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDF CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQHCPMCRQEW GMPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVALHYMVIMNPHLCGLLVLASWTMSALY LHYMVIMNPHLCGLLVLASWTMSALY LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHILLWGTMKGQFFI	AHQ
DDFNQLLAELNTCHGQETIDSSDKREK LEEKSKISKNRVHYMKFTKGKDLSSRS) DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKSAPAEEQLRGPC SSKASAQDAGDHVQPA GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQQHCPMCRQEW HMCILK WLHAQQVQQHCPMCRQEW LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFV LHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGGFFI	KSES
LEEKSKISKNRVHYMKFTKGKDLSSRSD DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA  1328 2678 A 10346 173 439 GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQQHCPMCRQEW GMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVALHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHLLWGTMKGQFFI	1010
DCIFGKRQSKKTPEGDASPSTPEENETT TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA  GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQQHCPMCRQEW QMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFV LHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSA AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHLLWGTMKGQFFI TIGEYFAKRMAALKNKPQVPA  BELKSCCCCLEDPPPPPLDOVQEEEC	CIDE 1
TIQEYFAKRMAALKNKPQVPVPGSDISI RKRGKKRNKEATGKDVESYLQPKAKR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA  1328 2678 A 10346 173 439 GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQQHCPMCRQEW QMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVALHYMVIMNPHLCGLLVLASWTMSALY LHYMVIMNPHLCGLLVLASWTMSALY LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHLLWGTMKGQFFI DELKSCCCCCLFDFPPPPLDOVQEEEC	LISAL
RKRGKKRNKEATGKDVESYLQFRARR KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA  GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILKWLHAQQVQHCPMCRQEW QMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVA LHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHLLWGTMKGQFFI	TQVE
KPERAEAQERVAKKKSAPAEEQLRGPC SSKASAQDAGDHVQPA  GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQHCPMCRQEW OMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVA LHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHLLWGTMKGQFFI	HTEG
I 328 2678 A 10346 173 439 GSAAMKVKIKCWNGVATWLWVANDI CRMAFNGCCPDCKVPGDDCPLVWGQC HMHCILK WLHAQQVQHCPMCRQEW QMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVALHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGHLLWGTMKGQFFI	wpo
1328 2678 A 10346 173 439 GSAAMKVKIKCWNGVATWLWVANDER CRMAFNGCCPDCKVPGDDCPLVWGGC HMHCILK WLHAQQVQHCPMCRQEW OMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVALHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	``- \
CRMAFNGCCPDCKVPGDDCPLVWGQQ HMHCILKWLHAQQVQQHCPMCRQEW OMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVA LHYMVIMNPHLCGLLVLASWTMSALI LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI TDELKSCCCCCLFDFPPPPLDQVQEEEC	NICGI
CRMAFNGCCPDCKVPGDDCPLVWGQU HMHCILKWLHAQQVQQHCPMCRQEW OMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFV LHYMVIMNPHLCGLLVLASWTMSALV LHYMVIMNPHLCGLLVLASWTMSALV LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI TDELKSCCCCCLFDFPPPPLDQVQEEEC	CLICE
HMHCILKWLHAQQVQQHCPMCRQEW  QMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVA LHYMVIMNPHLCGLLVLASWTMSALI LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI  TEELKSCCCCCLFDFPPPPLDQVQEEEC	SHCF
1329 2679 A 10351 3 964 QMEPGNDTQISEFLLLGFSQEPGLQPFL SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVA LHYMVIMNPHLCGLLVLASWTMSALV LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI TDELKSCCCCCLFDFPPPPLDQVQEEEC	Krke [
SMYLVTVLGNLLIILATISDSHLHTPMY LSFADICVTSTTIPKMLMNIQTQNKVIT MQMYFFILFAGFENFLLSVMAYDRFVA LHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	FGLFL [
LSFADICVTSTTIPKMLMNIQTQNKVII MQMYFFILFAGFENFLLSVMAYDRFVA LHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	LLF2M
MQMYFFILFAGFENFLLSVMAYDRFVA LHYMVIMNPHLCGLLVLASWTMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	YIACL
LHYMVIMNPHLCGLLVLASWIMSALY LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	JCHP
LMVVRLSFCTALEIPHFFCELNQVIQLA LNHMVIYFTVALLGGGPLTGILYSYSG AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	SLLOI
LNHMVIYFTVALLGGGPLTGILYSYSK AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	CSDSF
AISSAQGKYKAFSTCASHLSVVSLFYG YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	HISSE
YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	ATLCV
YLSSAATRNSHSSATASVMYTVVTPM YSLRNKDIKRALGIHLLWGTMKGQFFI	TILGY
DELK SCCCCLEDEPPPPLDOVQEEEC	NPFI
DELK SCCCCLEDEPPPPLDOVQEEEC	KCP
1220 2680 A 1030Z 34 2575	EVERV
	SNULE
TDPPNWOOLVSREVLLGLKPCEIKRQE	VINEL
FYTERAHVRTLKVLDQVFYQRVSREG	ILSPSE
LRKIFSNLEDILQLHIGLNEQMKAVRK	RNETS
LRKIPSNLEDILQLAID LANGE A A A A	ECSNO
VIDQIGEDLLTWFSGPGEEKLKHAAAT	ממין ממי
PFALEMIKSRQKKDSRFQTFVQDAESN	PLUMT
LOLKDIIPTQMQRLTKYPLLLDNIATY	LINE WILL
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PI EDVORRI DTSSLKLSEYPNVEELRO	PDPIK
DVMIHEGPI VWKVNRDKTIDLYTLLL	FDITA
I LOKODDRI VLRCHSKILASTADSKH	[F2LAI
KLSTVLVRQVATDNKALFVISMSDNG	AOIYE
LVAQTVSEKTVWQDLICRMAASVKE	
LVAQTVSEKIVWQDLICKMAASVAL	STKPI
PLPQSTPGEGDNDEEDPSKLKEEQHGI	)21Khi
OSPODIO GLESTLISSK POSHSLSTSGN	SVTGL
	SVTGL SEVRD
HI PVSEERWALDALRNLGLLKQLLVC	STRPI SVTGL SEVRD (IAIPDS
EV SVOEDWOHEPRYRTASOGPOIDS	STAPI SVTGL SEVRD (IAIPDS
NILL A VHSGEGHMPFRTGTGDIATCYS	SYTGL SEVRD SEVRD MAIPDS QLGLT MQLGLT
SFAPRDSVGLAPQDSQASNILVMDHM	SYTGL SEVRD SEVRD SEVRD SEVENDS SEVENDSE SEVENDSE SEVENDSE SEVENDSE
MPTMEPEGGLDDSGEHFFDAREAHSI	SYTGL SEVRD SEVRD SEVRD SEVENDS SEVENDSE SEVENDSE SEVENDSE SEVENDSE
MPTMEPEGGLDUSGERFFUAREARISE	SYTGL SEVRD LAIPDS QLGLT TIQNSE PRTSTE
GDGAVNKEEKDVNLRISGNYLILDGY	STAPI SVTGL SEVRD LAIPDS QLGLT VIQNSE PRTSTE IMTPE DENPSE
SSTDEEVASSLTLQPMTGIPAVESTHQ	STRPI SVTGL SEVRD SIAIPDS SQLGLT FIQNSE PRTSTE IMTPE DENPSE DPVQE
ONTHSDGAISPFTPEFLVOORWGAME	STRPI SVTGL SEVRD SIAIPDS SQLGLT FIQNSE PRTSTE IMTPE DENPSE DPVQE QQHSP
OSPSSCADSOSOIMEYIHKIEADLEHL	ISTRPI SEVRD PLAIPDS PQLGLT PIQNSE PRTSTE IMTPE PENPSE DPVQE QQHSP YSCFEI
SYTILCORLAGSALTDKHSDKS	ISTRPI SEVRD PLAIPDS PQLGLT PIQNSE PRTSTE IMTPE PENPSE DPVQE QQHSP YSCFEI
07.252	ISTRPI SEVRD PLAIPDS PQLGLT PIQNSE PRTSTE IMTPE PENPSE DPVQE QQHSP YSCFEI

					ra cara	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Mct	SEQ	Predicted	Predicted end ; nucleotide	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	ļ	USSN	location	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence		1	914	ng to first	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	}		amino acid	1 1 1	Y=Tyrosine, X=Unknown, *=Stop codon,
) [	Ì		1	residue of	sequence	/=possible nucleotide deletion, \=possible
1		ļ	ļ	peptide		nucleotide insertion
				sequence		AVEFAEGALTMAPWPELGDAQPNPDKYLEG
1331	2681	A	10353	1	2100	AAGQQPTAPDKSKETNKTDNTEAPVTKIELLP
1	l	ł	{			
<b>,</b>	1	1			1	SYSTATLIDEPTEVDDPWNLPTLQDSGIKWSE
1				1		RDTKGKILCFFQGIGRLILLLGFLYFFVCSLDIL
1		1		!		SSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIG
ì		1	1	1		VLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIP
		1	1			IIMGANIGTSITNTIVALMQVGDRSEFRRAFA
		İ	1	ł		GATVHDFFNWLSVLVLLPVEVATHYLEITQL
1	Ļ					IVESFHFKNGEDAPDLLKVITKPFTKLIVQLDK
	ļ	1		1	1	KVISQIAMNDEKAKNKSLVKIWCKTFTNKTQ
1	1	1	{		1	INVTVPSTANCTSPSLCWTDGIQNWTMKNVT
1		1	ľ			YKENIAKCQHIFVNFHLPDLAVGTILLILSLLV
	ĺ		j		j	LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP
		1	1		)	FPFAWLTGYLAILVGAGMTFIVQSSSVFTSAL
ĺ		1				TPLIGIGVITIERAYPLTLGSNIGTTTTAILAAL
1		1	1		1	ASPGNALRSSLQIALCHFFFNISGILLWYPIPFT
)			1			RLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIP
			j		1	LTVFGLSLAGWRVLVGVGVPVVFIIILVLCLR
1		1	ľ			LLQSRCPRVLPKKLQNWNFLPLWMRSLKPW
1			1			DAVVSKFTGCFQMRCCCCCRVCCRACCLLC
1		1	ì		į.	GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET
1		ł	1			FDNITISREAQGEVPASDSKTECTAL
1332	2682	Α	10354	30	1377	SQQGSQPHRQGPPSLLTAPHSLDLPALPPGPR
1						GŚQGKLRRVLVPMSVKPSWGPGPSEGVTAVP
Ī	!	1	1			TSDLGEIHNWTELLDLFNHTLSECHVELSQST
i		1	Į.			KRVVLFALYLAMFVVGLVENLLVICVNWRG
1						SGRAGLMNLYILNMAIADLGIVLSLPVWMLE
)	j	1	J			VTLDYTWLWGSFSCRFTHYFYFVNMYSSIFF
1	-	ŀ	į	1		LVCLSVDRYVTLTSASPSWQRYQHRVRRAM
1		1		{		CAGIWVLSAIIPLPEVVHIQLVEGPEPMCLFM
		I			1	APFETYSTWALAVALSTTILGFLLPFPLITVFN
1	}	1	1		1	VLTACRLRQPGQPKSRRHCLLLCAYVAVFV
	1	1	J			MCWLPYHVTLLLLTLHGTHISLHCHLVHLLY
			1			FFYDVIDCFSMLHCVINPILYNFLSPHFRGRLL
ļ			Ì			NAVVHYLPKDQTKAGTCASSSSCSTQHSIIIT
}		}	ł		1	KGDSQPAAAAPHPEPSLSFQAHHLLPNTSPISP
1		}	-	1	1 .	TQPLTPS
1333	2683	A	10358	2	884	AAGAGADGREPASERASRAEPPAVAMGQND
		1			1	LMGTAEDFADQFLRVTKQYLPHVARLCLIST
	1	1				FLEDGIRMWFQWSEQRDYIDTTWNCGYLLA
1	1	1		1		SSFVFLNLLGQLTGCVLVLSRNFVQYACFGLF
						GIIALQTIAYSILWDLKFLMRNLALGGGLLLL
1					1	LAESRSEGKSMFAGVPTMRESSPKQYMQLGG
1					}	RVLLVLMFMTLLHFDASFFSIVQNIVGTALMI
	1	1		1		LVAIGFKTKLAALTLVVWLFAINVYFNAFWT
		1			}	IPVYKPMHDFLKYDFFQTMSVIGGLLLVVAL
	1			1	1	GPGGVSMDEKKKEW
1334	2684	A	10367	59	1562	OAWSLOVALSPFFFPASPSNSFAAAVPQLLFP
1334	2084	^	10307	37	1502	ELPLPHVPGQESAKRRSARRFLIMSELTKELM
		1				ELVWGTKSSPGLSDTIFCRWTQGFVFSESEGS
				1	1	ALEQFEGGPCAVIAPVQAFLLKKLLFSSEKSS
]				1		WRDCSQEEQKELLCHTLCDILESACCDHSGS
				j	}	YCLVSWLRGKTTEETASISGSPAESSCQVEHS
			1	}	1	SALAVEELGFERFHALIQKRSFRSLPELKDAV
	1					LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN
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			j			EIEDASEPLIDPVYGHGSQSLINLLLTGHAVSN
						VWDGDRECSGMKLLGIHEQAAVGFLTLMEA
						VWDGDRECSGMKLLGIHEQAAVGFLTLMEA LRYCKVGSYLKISKIPYLDCLASETHLTVFFA
						VWDGDRECSGMKLLGIHEQAAVGFLTLMEA

					Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EQ ID	SEQ ID	Met	SEQ	Predicted	nucleotide	D=A spartic Acid E=Glutamic Acid,
10: of	NO: of	hod	ID NO:	beginning nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		in	location	corresponding	1=Isoleucine, K=Lysine, L=Leucine,
otide	seq-		USSN	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence		09/496	ng to first	acid residue	O=Glutamine R=Arginine, S=Serine,
uence		Į	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	l	Ì	( )	residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1	1	1		Sequence	/-possible nucleotide deletion, -possible
	}	}	1	peptide	}	nucleotide insertion
		l	<u> </u>	sequence		LGUIL GPEL OFFEDOGSSGPESFTVYHYNGL
						KOSNYNEKVMYVEGTAVVMGFEDPMLQTD
		Ì	1	Ì	ļ	DIDING CI OTK WPYIELLWIIDK SPSLN
		}				TRTKRRLGREKAMASPPRGWGCGELLLPFML
1335	2685	Α	10375	82	2929	LGTLCEPGSGQIRYSMPEELDKGSFVGNIAKD
			1			LGLEPQELAERGVRIVSRGRTQLFALNPRSGS
			1	1		LVTAGRIDREELCAQSPLCVVNFNILVENKM
			4	(		KIYGVEVEIIDINDNFPRFRDEELKVKVNENA
		1	Į.		1	AAGTRLVLPFARDADVGVNSLRSYQLSSNLH
	\	}	1	Į.		FSLDVVSGTDGQKYPELVLEQPLDREKETVH
	į.	}	1		}	DLLLTALDGGDPVLSGTTHIRVTVLDANDNA
	1	1	1	1		PLFTPSEYSVSVPENIPVGTRLLMLTATDPDE
	İ	ſ	1	1	}	GINGKLTYSFRNEEEKISETFQLDSNLGEISTL
	1	1	1	1		QSLDYEESRFYLMEVVAQDGGALVASAKVV
	}		ŀ		į.	VTVQDVNDNAPEVILTSLTSSISEDCLPGTVIA
	}		}	1	1	LFSVHDGDSGENGEIACSIPRNLPFKLEKSVD
			1		1	NYYHLLTTRDLDREETSDYNITLTVMDHGTP
	1	1	1	1		PLSTESHIPLKVADVNDNPPNFPQASYSTSVT
	ł	1	1	1		ENNPRGVSIFSVTAHDPDSGDNARVTYSLAE
	}			1	1	DTFQGAPLSSYVSINSDTGVLYALRSFDYEQL
	1	1	1	1	Į.	RDLQLWVTASDSGNPPLSSNVSLSLFVLDQN
	l l		]	1	}	DNTPEILYPALPTDGSTGVELAPRSAEPGYLV
	į.	1	1	1		TKVVAVDKDSGQNAWLSYRLLKASEPGLFA
		1	1			VGLHTGEVRTARALLDRDALKQSLVVAVED
	j	}	1		1	HGQPPLSATFTVTVAVADRIPDILADLGSIKTP
	ļ.	1	1	1		IDPEDLDLTLYLVVAVAAVSCVFLAFVIVLLV
	Ì	1	1	ł	1	LRLRRWHKSRLLQAEGSRLAGVPASHFVGV
	1	1	1			DGVRAFLQTYSHEVSLTADSRKSHLIFPQPNY
ł	ì	1		1		ADTLLSEESCEKSEPLLMSDKVDANKEERRV
}			i			QQAPPNTDWRFSQAQRPGTSGSQNGDDTGT
1	1		1	1	1	WPNNQFDTEMLQAMILASASEAADGSSTLGG
			- 1	}		GAGTMGLSARYGPQFTLQHVLQGELGSDYR
Ì	i	i	j	)		QNVYIPGSNATLTNAAGKRDGKAPAGGNGN
i	l	Į	1	ì		QNVYIPGSNATLINAAGRADGRATAGE.
ì	1	- 1	1			KKKSGKKEKK RPRRRQPSFSCRVLVLEDPPCFRFTNSMNQEK
1336	2686	A	10379	1	557	RPRRRQPSFSCRVLVLEDFFCFRITHSMITQLE
1,550	2000			ł	ĺ	LAKLQAQVRIGGKGTARRKKKVVHRTATAD DKKLQSSLKKLAVNNIAGIEEVNMIKDDGTVI
	1	1	]	Ì		DKKLQSSLKKLAVNNIAGIEEVIVINGDOTVI
			1			HFNNPKVQASLSANTFAITGHAEAKPITEMLP
ł		1	1	1		GILSQLGADSLTSLRKLAEQFPRQVLDSKAPK
}		}		1		PEDIDEEDDDVPDLVENFDEASKNEAN PEDIDEEDDDVPDLVENFDEASKNEAN
1222	2607	A	10380	1	1263	IPGSTISWSPAAARGLSVCRCCRLHPASAMDL
1337	2687	Α.	1,0000	] -		FGDLPEPERSPRPAAGKEAQKGPLLFDDLPPA
ł				1		SSTDSGSGGPLLFDDLPPASSGDSGSLATSISQ
			1			MVKTEGKGAKRKTSEEEKNGSEELVEKKVC
}		1		1		KASSVIEGLKGYVAERKGEREEMQDAHYILN
1	1	)	Į			DITEECRPPSSLITRVSYFAVFDGHGGIKASKE
1						A A ONT HONLIRK FPK GDVISVEKTVKRCLLD
	1	1			ļ	TEKHTDEEFLKOASSOKPAWKDGSTATCVL
1	- 1	- 1	- {	Í	ĺ	VIDNII VIANI GDSRAILCRYNEESUKHAALSI
}	- 1		1	1	1	CKEHNPTOYEERMRIOKAGGNVRDGRVLGV
-				1	j	LEVSRSIGDGOYKRCGVTSVPDIRRCQLTPNL
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1						NVTVMVVRIGH
		1				GPSQSMAAGELEGGKPLSGLLNALAQDTFHO
1338	2688	A	10385	3	589	YPGITEELLRSQLYPEVPPEEFRPFLAKMRGII
1 220				}		KSIASADMDFNQLEAFLTAQTKKQGGITSDQ
1	Ì	- 1	1	1		AAVISKFWKSHKTKIRESLMNQSRWNSGLRO
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Peptide   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence		1	Ì	1			V=Tyrosine, X=Unknown, *=Stop codon,
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SNIVEIKVI.RKESMEJ.VKJ.THINTIGH TLHHWSWASDMPLECAHFVEIRCYIDNL. GLEEWSDWSPVKNISWIPDSQTKVFPQDK VGSDITFCCVSQEKVI.SALIGHTNCPLIHLI NVAKKRNISWASSGTNIVFTTEDNIFGTV AGYPPDTPQQLNCETHDLKEICSWNFGR LVGPRATSYTLVESFSGK.VYRLKRAEATT YQLLFQMLPNQEIYNFTLNAHNPLGRSQS VNITEKVYPHTPTSFK.VKDINSTAVKLSW GNFAKINFLCEIEIKKSNSVQEQRNVTIKG NSSYLVALDKLNPYTLYTFRIRCSTETFWI SKWSNKKQHLTTEASPSKGPDTWREWSS KNLITYWKPLPINEANGKILSYNVSCSSDE SI.SEIPDPQHKAEIRLDKNDYIISVVAKNS' SPPSKIASMEIPNDLLKIEQVVGMGKGILL HYDPMITCDYVIKWCNSSRSEPCLMDWI PSNSTETVIESDEFRPGIRYNFFLYGCROQ QLIRSMIGYTEELAPIVAPNFTVEDTSADS KWEDPVEELRGFLRGYLJFYGKGERDTS RVLESGRSDIK.VKNITDISQKTLRIADLQG YHLVLRAYTDGGVGPEKSMYVVTEENS IIALLIPVAVAVIVGVYTSILCYRKREWIKE PDPNFENCKALQFQKSVCEGSSALKTLEI CTPNNVEVLETRSAFPKIEDTEVSPVAER RSDAKPENHVVESYCPPIEEEIPNFAADE TAQVIYIDVQSMYQPQAKPEEEQENDPVG GYKPQMHLPINSTVEDIAAEEDLDKTAGY QANNVTNWLVSPSPRSIDSNSEIVSFGSI NSRQFLIPPKDEDSPKSNGGGWSFTNFFQ ND  1341 2691 A 10392 1 5057 MLPPKHLSATKKEWKEPLISTELVLEQY PEKLKPWVRAKKPENCEKLYTLLENYER QPEGESLHGVLVVSAGLRCHUTLLENYER QPEGESLHGVLVVSAGLRCHUTLLENYER QPEGESLHGVLVVSAGLRCHUTLENYER ATKSVSTHAQGDAAQGLGGTIVKMWAR LATGVLLDDNISDYSDDDMTRNRESS SVHSSSGDRDWDRRGRSRDTEPRDRWSI NPRSRMPPRUSLIPVAKTSTEMDREDDI RSYRSDDAESTYONVVDLAEEDRRPDNIS		1	1	1	1		IPDTPEILNI SADESTSTLYLKWNDRGSVFPHR
TLHHWSWASDMPLECALHFVEERCYIDNL GLEE WSDWSPVKNISWPDSOTK VPPOKK VGSDITFCCVSQEKVLSALIGHTNCPLIHLI NVAIKIRNISVSASSGTINVVFTTEDNIFGTV AGYPDTPQQLNCETHDLKEICSWNPGR LVGPRATSYTL VËSFSGKYVRLKRAEAPT YQLLFQMLPNQEIYNFTLNAHNPLGRSQS VNITEKVYPHTPITSFK VKDINSTAVYLSWI GNFAKINFLCEIEKKSNYQEQRNYTIKG NSSYLVALDKLNPYTLYTFRIRGSTETFWI SKWSNKKQHLTTEASPSKGPDTWREWSS KNLIIYWKPI.PINEANGKLISYNNSCSSDE SLSEIPDPOHKREILDKINDYIISVVAKNS' SPPSKIASMEIPDDLKIEQV VGMGKGILL HYDPNITCDYVIKWCNSSRSEPCLMDW' PSNSTETVIESDEFROIR YNFFLYGCRNQ QLLRSMIGYIEELAPIVAPNFTVEDTSADS K WEDIPVEELRGFLGYLFYFGKGFENTS RVLESGRSDIKVKNITDISQKTLRIADLQG YHLVLRAYTDGGVGPEKSMYVVTKENS' IIAILIPVAVAVIVGVVTSILCYRKREWIKE PDIPNPENCKALQFQKSVCEGSSALKTLEI CTPNNVEVLETRSAFPKIEDTEIVSPVAER RSDAKPENHVVESVCPPIEEEIPNPAADE TAQVIYIDVQSMYQPQAKPEEEQENDPVC GYKPQMHLPINSTVEDIAAEEDLDKTAG' QANVNTWNLVSPDSPRSIDSNSEIVSFGSI NSRQFLIPPKDEDSPKSNGGGWSFTNFFQ ND  1341 2691 A 10392 1 5057 MLPPKHLSATKPKKSWAPNLYELDSDLT DVIIGEGFTDSEFFHQRFRNLIYVEFVGPR IKLRNLCLDWLQPETRTKEEIIELLVLEQY PEKLKPWRAKKPENCEKLVTLLENYKE QPEGESLHGVLVVSAGLRCPLGLSASTLL SGLDNSLSWAAVGMSCVLWDIELHHDFL ATKSVSTHAQGDAAQGLGGTIVMWAR LATGVLLDDNNSDVTSDDDMTRNRESS SVHSFSGDRDWDRRGRSRDTEPRDRWSI NPRSRMPPRDLSLPVVAKTSFEMDREDD RAYFSRSONDAKTSSENDREDD	1	1	1	1	}	l	CHUTWEIN VI DKESMEI VKI VTHNTTI NGKD
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VGSDITFCCVSQEKVISALIGHTNCPLIHLI NVAIKIRNISVSASSGITNVYTTEDNIFGTV AGYPPDTPQQLNCETHDLKEIICSWNPGR LVGPRATSYTLVESFSGKYVRLKRAEAFT YQLLFQMLPQEIVNFTLNAHNPLGRSQS VNITEKVPHTPTSFKVKDINSTAVALSW GNFAKINFLCEIEIKKSNSVQEQRNVTIKG NSSYLVALDKLNPYTLYTFRIRCSTETFWI SKWSNKKQHLTTEASPSKGPDTWREWSS KNLIIYWKPLPINEANGKILSYNVSCSDE SLSEIPDPQHKAEIRLDKNDYIISVVAKNS SPPSKIASMEIPNDDLKIEQVVGMGKGILL HYDPNMTCDYNKWCNSSRSEPCLMDWF PSNSTETVIESDEFRPGIRYNFFLYGCRNQ QLLRSMIGYIEELAPIVAPNFTVEDTSADS KWEDIPVEELRGFLRGYLFYFGKGERDTS RVLESGRSDIKVKNITDISQKTLRIADLQG YHLVLRAYTDGGVGPEKSMYVVTKENS IIAILIPVAVAVIVGVYTSILCYRKREWIKE PDIPNFENCKALQFQKSVCEGSSALKTLEI CTPNNVEVLETRSAPPKEUDTEIVSPVAER RSDAKPENHVVESYCPPIIEEEIPNPAADE TAQVIYIDVQSMYQPQAKPEEEQENDPV GYKPQMHLPINSTVEDIAAEEDLDKTAGI QANVNTWNLVSPDSFRSIDSNSEIVSFGSI NSRQFLIPPKDEDSPKSNGGGWSFTNFFQ ND MLPPKHLSATKPKKSWAPNLYELDSDLT DVIIGEGPTDSFFFHQRFRNLIYVEFVGFR IKLRNLCLDWLQPETRTKEEIIELLVLEQY PEKLKPWVRAKKPENCEKLYTLLENYKE QPEGESLHGVLVVSAGIRGPLGSASTILL SGLDNSLSWAAVGMSCVLWDIELHHDFI ATKSVSTHAQGDAAQGLGGTIVRMWAR LATGVLLDDNNSDVTSDDDMTRNRESS SVHSFSGDRDWDRRGRSRDTEPPDRWSI NPRSRMPRRDLSLPVVAKTSFEMDREDDI RAYFSRSDDAESYONVVDLAEDRKPHNI	1	1	1	1	1		TEHHWOWASDMPLECAIRE VEIKC I IDIALAIS
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EQ ID IO: of	SEQ ID NO: of	Met hod	SEQ ID NO: in	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence		1	/	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	i		Ì	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
		į		sequence		nucleotide insertion
		<del> </del>	1			SQVGGKRFECKDCGETFNKSAALAEHRKIHA RGYLVECKNQECEEAFMPSPTFSELQKIYGK
	}					DKFYECRVCKETFLHSSALIEHQKIHFGDDKD
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	ł			<b>\</b>		KEKMYECK V CGETFLHSSSLKEHQKIHTRGN
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		1				GYEKSVIHSGPFTESQKSHTITRPLESDEDEKA
						FTISSNPYENQKIPTKENVYEAKSYERSVIHSL
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		}	1		(	GLWALIQAKYSTIEFDFLGYAIVRFNQYFKM
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1343	2693	-	10394	102	839	PEAQTSAVLAREKGHLPTMRHEAPMQMAS
1343	2093		1.337			QDARYGQKDSSDQNFDYMFKLLIIGNSSVGI
		- 1				TSFLFRYADDSFTSAFVSTVGIDFKVKTVFK
				1		EKRIKLQIWDTAGQERYRTITTAYYRGAMG
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1344	2694	10	1 1037.	, I –		LQQRTPAEMSPVLHFYVRPSGHEGAASGHT

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						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutaine Acid,
	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-			USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
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		1	İ	amino acid		Y=Tyrosine, X=Unknown, *=Stop codon,
	]			residue of	sequence	/=possible nucleotide deletion, \=possible
	ł	{	1	peptide		/=possible nucleotide deletion, (-possible
	1	}		sequence	1	nucleotide insertion
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		1	1	1	}	KMNRVIRACVEAPKGNPICSLHDQGAGGNG
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1343	2093	1 1	1 1007			RVAMHYQMSVTLKYEIKKLIYVHLVIWLLLV
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1347	269	7 1	1040	)2   153	1969	KHRQENNALDMAPEIHMTGPMCLIENTNGEL VANPEALKILSAITQPVVVVAIVGLYRTGKSY

EO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
EO ID		hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
O: of	NO: of	nou	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
ucl-	peptide	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
otide	seq-	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
eq-	uence	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ence	ł		914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	}	1	residue of	sequence	V=Tyrosine X=Unknown, *=Stop codon,
	1	1	{		Sequence	/=possible nucleotide deletion, \=possible
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		1				PUDLY PEHTLYLLDTEGLGDVKKGDNQNDS
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		1	1			YMKNSFKDVDHLFQKKLAAQLDKKRDDFCK
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1240	2698	A	10404	5	892	TQLPAPLSGVLSRLQLGSGAPLLTWVQETAG
1348	2090	^	10.0.			VAGGAPRRTPVTMWRLLARASAPLLRVPLS
	1	. ]	ļ	1	1	DSWALLPASAGVKTLLPVPSFEDVSIPEKPKL
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1		1			1	VTIEEFIESCQKDENIMRSMQLFDNVI
1		1	1			

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1350.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-1350, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).
- 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1351-2700, the mature protein portion thereof, or the active domain thereof.
- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-1350.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

Pages 340 to 1963 of this application contain amino acid sequence listings. They can be obtained at the address given below.

Les pages 340 to 1963 de cette demande contiennent des listages des séquences d'acides aminés. Elles peuvent être obtenues à l'adresse indiquée ci-dessous.

World Intellectual Property Organization 34, chemin des Colombettes CH-1211 Genève 20

## (19) World Intellectual Property Organization International Bureau



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(43) International Publication Date 9 August 2001 (09.08.2001)

(10) International Publication Number WO 01/57188 A3

(51) International Patent Classification7: C07K 5/00, A61K 39/395, C12Q 1/68 C07H 21/04.

PCT/US01/03800 (21) International Application Number:

(22) International Filing Date: 5 February 2001 (05.02.2001)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

09/496,914 09/560.875 3 February 2000 (03.02.2000) US 27 April 2000 (27.04.2000)

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US Filed on

09/496,914 (CIP) 3 February 2000 (03.02.2000)

LIS

09/560,875 (CIP)

Filed on

27 April 2000 (27.04.2000)

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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU. ID. IL. IN. IS. JP. KE, KG, KP, KR, KZ, LC, LK, LR. LS. LT. LU. LV. MA. MD. MG. MK. MN. MW. MX. MZ. NO. NZ. PL. PT, RO. RU. SD. SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT. LU. MC. NL. PT. SE, TR), OAPI patent (BF, BJ, CF, CG. CI. CM. GA. GN. GW. ML. MR. NE. SN, TD, TG).

## Published:

- with international search report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau
- (88) Date of publication of the international search report: 28 February 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.